

GenCore version 5.1.4
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OM protein - protein search, using SW model

Run on: September 30, 2003, 10:07:04, 1 Search time 41.0833 Seconds

(with-out alignment)
42.499 Million full updates/sec

Title: US-09-787-443-1

Perfect score: 11

Sequence: 1 ASKKPKRNKA 11

Scoring table: CLICG

Gapop 60.0, Gapext 60.0

Searched: 1107863 seqs, 154726574 residues

Word size: 3

Total number of hits satisfying chosen parameters: 27822

Minimum BB seq length: 8

Maximum BB seq length: 15

Post-processing: Listing first 500 summaries

Database: A_Geneseq_19Jun01.*

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red. No. is the number of results predicted by blast to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DE	ID	Description
1	11	100.0	11	21	AAV85527	NCAM Igl binding p
2	11	100.0	11	23	ABG69429	Human neural cell
3	6	54.5	11	21	AAV85531	NCAM Igl binding p
4	6	54.5	11	21	AAV85532	NCAM Igl binding p
5	5	45.5	11	21	AAV85533	NCAM Igl binding p
6	5	45.5	14	22	AAV85534	Human peptide 453
7	4	36.4	8	15	AAV85535	peptide signal seq
8	4	36.4	8	16	AAV85536	peptide signal seq
9	4	36.4	8	22	AAV85537	SV40 V1 protein

10	4	36.4	9	16	AAV85538	Rapla (172-180) pe
11	4	36.4	9	21	AAV85539	HIA A24 binding TA
12	4	36.4	9	21	AAV85540	HIA B7 binding TAD
13	4	36.4	9	21	AAV85541	HIA B8 binding TAD
14	4	36.4	9	22	AAV85542	Human TALG-12 immu
15	4	36.4	9	22	AAV85543	Human TALG-12 immu
16	4	36.4	9	22	AAV85544	Human TALG-12 immu
17	4	36.4	9	23	AAV85545	Transcription fact
18	4	36.4	10	12	AAV85546	LHRH analogue 2
19	4	36.4	10	12	AAV85547	Gonadotropin relea
20	4	36.4	10	18	AAV85548	Human platelet gly
21	4	36.4	10	19	AAV85549	Human amphirequin
22	4	36.4	10	19	AAV85550	Mimotope capable o
23	4	36.4	10	22	AAV85551	Mycoplasma genital
24	4	36.4	10	22	AAV85552	Human complementa
25	4	36.4	10	22	AAV85553	Human complementa
26	4	36.4	10	22	AAV85554	Human complementa
27	4	36.4	10	22	AAV85555	Human complementa
28	4	36.4	10	22	AAV85556	Human complementa
29	4	36.4	10	22	AAV85557	Human complementa
30	4	36.4	10	22	AAV85558	Saccharomyces cere
31	4	36.4	10	22	AAV85559	Saccharomyces cere
32	4	36.4	10	22	AAV85560	Target cyclic pept
33	4	36.4	10	23	AAV85561	Human respiratory
34	4	36.4	11	19	AAV85562	PTP activity deter
35	4	36.4	11	19	AAV85563	NCAM Igl binding p
36	4	36.4	11	21	AAV85564	NCAM Igl binding p
37	4	36.4	11	23	AAV85565	Nuclear protein nu
38	4	36.4	12	19	AAV85566	Human neurofilamen
39	4	36.4	12	21	AAV85567	Antigenic peptide
40	4	36.4	12	23	AAV85568	Human Ghrelin (C-t
41	4	36.4	12	23	AAV85569	Recombinant transp
42	4	36.4	12	23	AAV85570	Human respiratory
43	4	36.4	12	23	AAV85571	Nuclear protein nu
44	4	36.4	13	12	AAV85572	Anti-rhodopsin mon
45	4	36.4	13	15	AAV85573	PDGF-activity-disp
46	4	36.4	13	20	AAV85574	Putative HS bindin
47	4	36.4	13	21	AAV85575	Signal peptidase i
48	4	36.4	13	21	AAV85576	Signal peptidase i
49	4	36.4	13	23	AAV85577	Signal peptidase i
50	4	36.4	13	23	AAV85578	Rat C/RAP-beta pep
51	4	36.4	13	23	AAV85579	Phosphorylated epi
52	4	36.4	13	23	AAV85580	S. cerevisiae 3-is
53	4	36.4	14	21	AAV85581	Peptide conveying
54	4	36.4	14	23	AAV85582	Human Sox-11 trans
55	4	36.4	15	18	AAV85583	Peptide #3 derived
56	4	36.4	15	18	AAV85584	Peptide #4 derived
57	4	36.4	15	18	AAV85585	p53 activating pep
58	4	36.4	15	20	AAV85586	KDR/Flk-1 targetin
59	4	36.4	15	20	AAV85587	Histone H1S 3 deri
60	4	36.4	15	20	AAV85588	Histone H1S-3 deri
61	4	36.4	15	21	AAV85589	Signal peptidase i
62	4	36.4	15	21	AAV85590	Human histone H1 p
63	4	36.4	15	21	AAV85591	Human histone H1 p
64	4	36.4	15	22	AAV85592	Unique region #2 o
65	4	36.4	15	23	AAV85593	Human SHARP 1 tran
66	4	36.4	15	23	AAV85594	Caspase cleavage s
67	4	36.4	15	23	AAV85595	Human ubiquitin-bi
68	4	36.4	15	24	AAV85596	Muskmelon 9-hydrox
69	4	36.4	15	24	AAV85597	Sequence of cyclic
70	4	36.4	15	24	AAV85598	Formula 1B for new
71	4	36.4	15	24	AAV85599	Synthetic substrat
72	4	36.4	15	24	AAV85600	PE-Lys246, 247, 24
73	4	36.4	15	24	AAV85601	ID2 plasmidom sur
74	4	36.4	15	24	AAV85602	Angiotensin-conver
75	4	36.4	15	24	AAV85603	Sequence of the NH
76	4	36.4	15	24	AAV85604	Hepatitis C virus
77	4	36.4	15	24	AAV85605	Sm B/B' epitope 47
78	4	36.4	15	24	AAV85606	Sm B/B' epitope 76
79	4	36.4	15	24	AAV85607	Sm B/B' epitope 77
80	4	36.4	15	24	AAV85608	Sm B/B' epitope 78
81	4	36.4	15	24	AAV85609	Sm B/B' epitope 79
82	4	36.4	15	24	AAV85610	Sm B/B' epitope 80

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84	27.3	8	15	AA342229	HIV derived HLA do	157	8	22	ARP21778	HIV All motif tat
85	27.3	8	15	AA371199	Hepatitis C Virus	158	8	22	ARP21802	HIV All motif vif
86	27.3	8	15	AA372203	Hepatitis C Virus	159	8	22	ARP21814	HIV All motif vif
87	27.3	8	15	AA372202	Hepatitis C Virus	160	8	22	ARP21850	HIV All motif vif
88	27.3	8	15	AA372202	Hepatitis C Virus	161	8	22	AA372955	Human papilloma #127
89	27.3	8	15	AA372203	Hepatitis C Virus	162	8	22	AA372972	p21 C-terminus del
90	27.3	8	15	AA372203	Hepatitis C Virus	163	8	22	AA372990	p21-activated prot
91	27.3	8	15	AA372203	Hepatitis C Virus	164	8	22	AA372990	HLA-B8 octamer #31
92	27.3	8	15	AA372203	Hepatitis C Virus	165	8	22	AA372990	HLA-B8 octamer #21
93	27.3	8	15	AA372203	Hepatitis C Virus	166	8	22	AA372990	HLA-B8 octamer #28
94	27.3	8	15	AA372203	Hepatitis C Virus	167	8	22	AA372990	HLA-B8 octamer #20
95	27.3	8	15	AA372203	Hepatitis C Virus	168	8	22	AA372990	HLA-B8 octamer #35
96	27.3	8	15	AA372203	Hepatitis C Virus	169	8	22	AA372990	Myristic acid link
97	27.3	8	15	AA372203	Hepatitis C Virus	170	8	22	AA372990	HBs-17 epitope pep
98	27.3	8	15	AA372203	Hepatitis C Virus	171	8	22	AA372990	Nuclear localisati
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376	3	27.3	9	22	ABP16443	HIV b27 Super motif	449	3	27.3	9	22	AA008125	HLA-A1 nonamer #20
377	3	27.3	9	22	ABP16458	HIV b27 Super motif	450	3	27.3	9	22	AA008139	HLA-B *0702 noname
378	3	27.3	9	22	ABP17271	HIV b27 Super motif	451	3	27.3	9	22	AA008160	HLA-B *0702 noname
379	3	27.3	9	22	ABP17334	HIV b27 Super motif	452	3	27.3	9	22	AA008198	HLA-B *2705 noname
380	3	27.3	9	22	ABP17347	HIV b27 Super motif	453	3	27.3	9	22	AA008229	HLA-B *2705 noname
381	3	27.3	9	22	ABP17341	HIV b27 Super motif	454	3	27.3	9	22	AA008298	HLA-A *0201 noname
382	3	27.3	9	22	ABP17899	HIV b27 Super motif	455	3	27.3	9	22	AA008436	HLA-B *2705 noname
383	3	27.3	9	22	ABP18001	HIV b27 Super motif	456	3	27.3	9	22	AA008437	HLA-B *2705 noname
384	3	27.3	9	22	ABP18296	HIV b27 Super motif	457	3	27.3	9	22	AA008561	HLA-A1 nonamer #38
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386	3	27.3	9	22	ABP18474	HIV b27 Super motif	459	3	27.3	9	22	AA008665	HLA-B *0702 noname
387	3	27.3	9	22	ABP19133	HIV b27 Super motif	460	3	27.3	9	22	AA008954	HLA-B *0702 noname
388	3	27.3	9	22	ABP19157	HIV b27 Super motif	461	3	27.3	9	22	AA008978	HLA-A *0201 noname
389	3	27.3	9	22	ABP19336	HIV b27 Super motif	462	3	27.3	9	22	AA008988	HLA-A26 nonamer #3
390	3	27.3	9	22	ABP19522	HIV b27 Super motif	463	3	27.3	9	22	AA008988	HLA-A26 nonamer #7
391	3	27.3	9	22	ABP20458	HIV b27 Super motif	464	3	27.3	9	22	AA009447	HLA-B8 nonamer #4
392	3	27.3	9	22	ABP20636	HIV b27 Super motif	465	3	27.3	9	22	AA009448	HLA-B8 nonamer #5
393	3	27.3	9	22	ABP20769	HIV b27 Super motif	466	3	27.3	9	22	AA009661	HLA-B8 nonamer #18
394	3	27.3	9	22	ABP20769	HIV b27 Super motif	467	3	27.3	9	22	AA011026	HLA-A26 nonamer #9
395	3	27.3	9	22	ABP20934	HIV b27 Super motif	468	3	27.3	9	22	AA011506	HLA-B *1510 noname
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405	3	27.3	9	22	ABP22031	HIV b27 Super motif	478	3	27.3	9	22	AA012259	HLA-B8 nonamer #33
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415	3	27.3	9	22	ABP22031	HIV b27 Super motif	488	3	27.3	9	22	AA012649	HLA-B *1510 noname
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421	3	27.3	9	22	ABP22031	HIV b27 Super motif	494	3	27.3	9	22	AA012649	HLA-B *1510 noname
422	3	27.3	9	22	ABP22031	HIV b27 Super motif	495	3	27.3	9	22	AA012649	HLA-B *1510 noname
423	3	27.3	9	22	ABP22031	HIV b27 Super motif	496	3	27.3	9	22	AA012649	HLA-B *1510 noname
424	3	27.3	9	22	ABP22031	HIV b27 Super motif	497	3	27.3	9	22	AA012649	HLA-B *1510 noname
425	3	27.3	9	22	ABP22031	HIV b27 Super motif	498	3	27.3	9	22	AA012649	HLA-B *1510 noname
426	3	27.3	9	22	ABP22031	HIV b27 Super motif	499	3	27.3	9	22	AA012649	HLA-B *1510 noname
427	3	27.3	9	22	ABP22031	HIV b27 Super motif	500	3	27.3	9	22	AA012649	HLA-B *1510 noname
428	3	27.3	9	22	ABP22031	HIV b27 Super motif	501	3	27.3	9	22	AA012649	HLA-B *1510 noname
429	3	27.3	9	22	ABP22031	HIV b27 Super motif	502	3	27.3	9	22	AA012649	HLA-B *1510 noname
430	3	27.3	9	22	ABP22031	HIV b27 Super motif	503	3	27.3	9	22	AA012649	HLA-B *1510 noname
431	3	27.3	9	22	ABP22031	HIV b27 Super motif	504	3	27.3	9	22	AA012649	HLA-B *1510 noname
432	3	27.3	9	22	ABP22031	HIV b27 Super motif	505	3	27.3	9	22	AA012649	HLA-B *1510 noname
433	3	27.3	9	22	ABP22031	HIV b27 Super motif	506	3	27.3	9	22	AA012649	HLA-B *1510 noname
434	3	27.3	9	22	ABP22031	HIV b27 Super motif	507	3	27.3	9	22	AA012649	HLA-B *1510 noname
435	3	27.3	9	22	ABP22031	HIV b27 Super motif	508	3	27.3	9	22	AA012649	HLA-B *1510 noname
436	3	27.3	9	22	ABP22031	HIV b27 Super motif	509	3	27.3	9	22	AA012649	HLA-B *1510 noname
437	3	27.3	9	22	ABP22031	HIV b27 Super motif	510	3	27.3	9	22	AA012649	HLA-B *1510 noname
438	3	27.3	9	22	ABP22031	HIV b27 Super motif	511	3	27.3	9	22	AA012649	HLA-B *1510 noname
439	3	27.3	9	22	ABP22031	HIV b27 Super motif	512	3	27.3	9	22	AA012649	HLA-B *1510 noname
440	3	27.3	9	22	ABP22031	HIV b27 Super motif	513	3	27.3	9	22	AA012649	HLA-B *1510 noname
441	3	27.3	9	22	ABP22031	HIV b27 Super motif	514	3	27.3	9	22	AA012649	HLA-B *1510 noname
442	3	27.3	9	22	ABP22031	HIV b27 Super motif	515	3	27.3	9	22	AA012649	HLA-B *1510 noname
443	3	27.3	9	22	ABP22031	HIV b27 Super motif	516	3	27.3	9	22	AA012649	HLA-B *1510 noname
444	3	27.3	9	22	ABP22031	HIV b27 Super motif	517	3	27.3	9	22	AA012649	HLA-B *1510 noname
445	3	27.3	9	22	ABP22031	HIV b27 Super motif	518	3	27.3	9	22	AA012649	HLA-B *1510 noname
446	3	27.3	9	22	ABP22031	HIV b27 Super motif	519	3	27.3	9	22	AA012649	HLA-B *1510 noname
447	3	27.3	9	22	ABP22031	HIV b27 Super motif	520	3	27.3	9	22	AA012649	HLA-B *1510 noname

ALIGNMENTS

RESULT 1

AA008527 standard; peptide: 11 AA.

XX

AA008527

XX

07 A00-200 (first entry)

XX

NCAM 140 binding peptide 03

XX

NCAM 140 adhesion molecule; 1q1; immunoglobulin domain 1;

KW

neurotrophin receptor; proliferation; nerve damage; sclerosis;

KW

impairment of neuronal cell; stroke; Parkinson's disease; memory; schizophrenia;

KW

Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

KW

treatment; prostate; nerve guide; treatment; nervous system.

CC from NCAM presenting cells, and is also capable of promoting the proliferation of NCAM presenting cells; the present sequence represents a peptide, peptide used in the identification of these binding peptides which can be used in the compound; the compound may be used in the treatment of normal, degenerated or damaged NCAM presenting cells. The compound may in particular be used to treat diseases of the central and peripheral nervous systems such as post-operative nerve damage, traumatic nerve damage, impaired myelination of nerve fibres, conditions resulting from a stroke, Parkinson's disease, Alzheimer's disease, dementia, sclerosis, nerve degeneration associated with diabetes mellitus, disorders affecting the circadian clock or neuromuscular transmission and schizophrenia. Conditions affecting the muscles may also be treated with the compound, such as conditions associated with impaired function of neuromuscular connections (e.g. genetic or traumatic shock or traumatic atrophic muscle disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus types 1 and 2), kidney (e.g. nephrosis), heart, liver and bowel may also be treated using the compound. The compound is used in a prosthetic nerve guide, and also to stimulate the ability to learn, and to stimulate the memory of a subject.

XX Sequence 11 AA:
 SQ Query Match 54.5% Score 61 DB 21 Length 11
 Best Local Similarity 100.0% Pred. No. 51
 Mismatches 6 Conservative 0 Mismatches 0 Gaps 0

LY 6 KPNKA 11
 LR 6 KPNKA 11

RESULT:
 1. AAY8954 standard; peptide: 11 AA
 A: AAY8954
 XX AAY8954
 DE 07 APR 2002 (first entry)
 XX 07 APR 2002 (first entry)
 DE NCAM 1q1 binding peptide 117 used as a control peptide
 XX NCAM: neural cell adhesion molecule 1q1, immunoglobulin domain 1, neurite outgrowth promoter; proliferation, nerve damage, dementia, Alzheimer's disease; striated muscle disease; memory, schizophrenia; Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis; treatment; prosthetic nerve guide; treatment; nervous system; synthesis

XX Synthesis:
 XX W020014744 A2
 XX 06 APR 2002
 XX 23 SEP 1999 9360-EX-0500
 XX 29 SEP 1999 98DK-0001242
 XX 29 APR 1999 95DK-0000592
 XX (KUNN) BOCK L C B.
 XX (BOCK) BOCK E.
 XX (KUNN) BOCK A.
 XX (KUNN) BOCK X.
 XX (KUNN) BOCK Y.
 XX (KUNN) BOCK Z.
 XX (KUNN) BOCK A.
 XX (KUNN) BOCK B.
 XX (KUNN) BOCK C.
 XX (KUNN) BOCK D.
 XX (KUNN) BOCK E.
 XX (KUNN) BOCK F.
 XX (KUNN) BOCK G.
 XX (KUNN) BOCK H.
 XX (KUNN) BOCK I.
 XX (KUNN) BOCK J.
 XX (KUNN) BOCK K.
 XX (KUNN) BOCK L.
 XX (KUNN) BOCK M.
 XX (KUNN) BOCK N.
 XX (KUNN) BOCK O.
 XX (KUNN) BOCK P.
 XX (KUNN) BOCK Q.
 XX (KUNN) BOCK R.
 XX (KUNN) BOCK S.
 XX (KUNN) BOCK T.
 XX (KUNN) BOCK U.
 XX (KUNN) BOCK V.
 XX (KUNN) BOCK W.
 XX (KUNN) BOCK X.
 XX (KUNN) BOCK Y.
 XX (KUNN) BOCK Z.

XX Compositions that bind neural cell adhesion molecules useful for treating disorders of the nervous system and muscles e.g. Alzheimer's and Parkinson's diseases

XX Example 5: Fig 2: 11pp: English.

XX Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule. NCAM is found in three forms, two of which are transmembrane forms, while the third is attached via a lipid anchor to the cell membrane. All three NCAM forms have an extracellular structure consisting of five immunoglobulin domains (Ig domains). The Ig domains are numbered 1 to 5 from the N-terminal. The invention relates to a compound containing a peptide which binds to the NCAM 1q1 domain. The compound binds to NCAM 1q1/1q2 domains, and is capable of stimulating or promoting neurite outgrowth from NCAM presenting cells, and is also capable of promoting the proliferation of NCAM presenting cells. The present sequence represents a control peptide used in the identification of those binding peptides which can be used in the compound. The compound may be used in the treatment of normal, degenerated or damaged NCAM presenting cells. The compound may in particular be used to treat diseases of the central and peripheral nervous systems such as post-operative nerve damage, traumatic nerve damage, impaired myelination of nerve fibres, conditions resulting from a stroke, Parkinson's disease, Alzheimer's disease, dementia, sclerosis, nerve degeneration associated with diabetes mellitus, disorders affecting the circadian clock or neuromuscular transmission and schizophrenia. Conditions affecting the muscles may also be treated with the compound, such as conditions associated with impaired function of neuromuscular connections (e.g. genetic or traumatic shock or traumatic atrophic muscle disorders). Conditions of the gonads, pancreas (e.g. diabetes mellitus types 1 and 2), kidney (e.g. nephrosis), heart, liver and bowel may also be treated using the compound. The compound is used in a prosthetic nerve guide, and also to stimulate the ability to learn, and to stimulate the memory of a subject.

XX Sequence 11 AA:
 SQ Query Match 45.5% Score 5; DB 21 Length 11
 Best Local Similarity 100.0% Pred. No. 51
 Mismatches 5 Conservative 0 Mismatches 0 Gaps 0

LY 1 ASKKP 5
 LR 1 ASKKP 5

RESULT:
 1. AAY9418 standard; peptide: 14 AA
 A: AAY9418
 XX AAY9418
 XX 24 JAN 2002 (first entry)
 XX Human peptide 1693 encoded by a SNP oligonucleotide.
 XX Immunosuppressive; immunostimulatory; anti-inflammatory; cytostatic; neuroprotective; antitumor; gene therapy; vaccine; amylose; cancer; amyloid protein; angiotensin; apoptosis related protein; cadherin; cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor; complement related protein; cytochrome; kinesin; cytokine; interferon; interleukin; G protein coupled receptor; thioesterase; inflammation; multifactorial disease; autoimmune disease; infection; nervous system disease

XX Home sapiens
 XX W020014744 A2
 XX 05 JUL 2001
 XX 28 SEP 2000 9360-EX-0500
 XX 28 SEP 2000 9360-EX-0500

16 25 MAR 1994 9405 0175414
 17 25 MAR 1994 24005 0173419
 18 (CUBA) CERAJEN CORP.
 19 STRICKER PA. Teach M;
 20 WPI, 2401 465210/30;
 21 polymorphic nucleic acids encoding and antibodies against S. Typhimurium,
 22 *sequences and histones, useful for diagnosing and treating, and*
 23 *character, and immune diseases and infections*
 24 *base-pairing, page 0619; 4143pp; English*
 25 The present invention relates to combinations (see Abstracts 85, 4670)
 26 of modified polypeptide variants of proteins related to antibodies, antigens,
 27 proteins, and peptides, apoptosis related proteins, cellular signaling,
 28 polynucleotides, oncogenes, histones, kinases, and other structural factors,
 29 immunological related proteins, cytokines, kinases, cytokines,
 30 interferons, interleukins, and protein-coupled receptors and tyrosinases.
 31 The present sequence is a peptide molecule, in such modified form
 32 of oligonucleotides and the peptides encoded by them may be used in the
 33 prevention, diagnosis and treatment of diseases associated with
 34 inappropriate expression of the proteins listed above, disorders that may
 35 be prevented, diagnosed and/or treated with a multifactorial diseases
 36 with a genetic component, such as autoimmune diseases (e.g., rheumatoid
 37 arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus,
 38 and thymic disease), inflammatory diseases (e.g., Crohn's disease, ulcerative
 39 colitis, Crohn's disease and kidney, leukodystrophies, diseases of the nervous
 40 system and an infection of pathogenic organisms.
 41 Sequence: 14 AA;
 42 *Quality Match* 45.54% *Score* 41 *DB* 15; *length* 8;
 43 *best Local Similarity* 100.00% *Prog. No.* 9, 90105;
 44 *Matches* 4; *Conservative* 0; *Mismatches* 0; *Days* 0;
 45 *Key* 1 KKPK 7
 46 *Modified-site* 1
 47 *Modified-site* 1
 48 *Modified-site* 1
 49 *Modified-site* 1
 50 *Modified-site* 1
 51 *Modified-site* 1
 52 *Modified-site* 1
 53 *Modified-site* 1
 54 *Modified-site* 1
 55 *Modified-site* 1
 56 *Modified-site* 1
 57 *Modified-site* 1
 58 *Modified-site* 1
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 93 *Modified-site* 1
 94 *Modified-site* 1
 95 *Modified-site* 1
 96 *Modified-site* 1
 97 *Modified-site* 1
 98 *Modified-site* 1
 99 *Modified-site* 1
 100 *Modified-site* 1

101 their synthetic analogues for treating or preventing, e.g.,
 102 cardiovascular and autoimmune disease, infections and cancer.
 103 Claim 38; Page 17; 28pp; English.
 104 The sequence is that of a signal sequence analogous to that of
 105 a platelet-derived growth factor chain A.
 106 See also AAF 0441/3;
 107 (Updated in 25-MAR-2003 to correct PN field.)
 108 Sequence: 8 AA;
 109 *Quality Match* 46.44% *Score* 41 *DB* 15; *length* 8;
 110 *best Local Similarity* 100.00% *Prog. No.* 9, 90105;
 111 *Matches* 4; *Conservative* 0; *Mismatches* 0; *Days* 0;
 112 *Key* 1 KKPK 4
 113 *Modified-site* 1
 114 *Modified-site* 1
 115 *Modified-site* 1
 116 *Modified-site* 1
 117 *Modified-site* 1
 118 *Modified-site* 1
 119 *Modified-site* 1
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 197 *Modified-site* 1
 198 *Modified-site* 1
 199 *Modified-site* 1
 200 *Modified-site* 1

```

CC Metastatic spreading.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 8 AA.
Query Match 36.4% Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASKK 4
DB 3 ASKK 6

RESULT 9
AAM51526
AC AAM51526 standard; peptide: 8 AA.
XX AAM51526;
UT 02 JAN 2002 (first entry)
DE SV40 VP1 protein nuclear localisation signal.
XX
XX SV40; simian virus 40; VP1; capsid; virus like particles;
XX nuclear localisation signal; VP1.
XX
OS Rhesus macaque polyoma virus.
XX
PN JP2001160777.A.
XX
XX 26 JUN 2001
XX
XX 09 JUL 1999; 99JP-0249140.
XX
XX 30 JUL 1999; 99JP-0249140.
XX
XX (HANEZ) HANJIA H.
XX
XX WPI: 2001 594954/68.
XX
XX New virus like particles from VP1 capsid protein of adenovirus
XX virus, comprise a peptide containing a nuclear-shifting signal
XX connected to its N-terminal.
XX
XX Claim 6; Page 2; 3pp; Japanese.
XX
XX The present sequence is provided in a specifically claimed example of a
XX virus-like particle-forming protein, and a peptide containing a
XX nuclear shifting signal, at its N-terminus, for forming virus-like
XX particles by shifting to the nucleus of a mammalian cell in which it
XX is expressed. The method is used for forming virus-like particles
XX from the VP1 capsid protein of adenovirus (AAV).
XX
SQ Sequence 8 AA.
Query Match 36.4% Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKKK 6
DB 3 KKKK 6

RESULT 10
AAR78787
LC AAR78787 standard; peptide: 8 AA.
XX AAR78787;
AC AAR78787;
XX
XX 25-MAR-2004 (updated)
UT 25-NOV 1995 (first entry)

```

```

XX
DE Rapia (172-183) peptide sequence.
XX
XX superoxide inhibition; phagocyte; GTP-binding; G protein; Rap;
XX mastoparan; antiinflammatory; inflammation; ICS4; GAP.
XX
XX Synthetic.
XX
XX W09503859-A1.
XX
XX 09 FEB 1995.
XX
XX 29-JUL 1994; 94W0-050843.
XX
XX 02 APR-1993; 94US-010244.
XX
XX 15-NOV-1993; 93US-C15652.
XX
XX (SURI) SCRIPPS RES INST.
XX
XX Bokoch GM, Carnutte JJ;
XX
XX WPI: 1995 082927/11.
XX
XX New peptide(s) inhibiting superoxide produ. in phagocyte(s)
XX derived e.g. from GTP binding proteins or mastoparan, useful for
XX inhibiting inflammation, e.g. in cases of autoimmune disease,
XX gout, asthma, etc.
XX
XX Claim 5; Page 9; 10pp; English.
XX
XX An optionally substituted, non-toxic, peptide of not more than 40
XX amino acids in length is claimed, the peptide being capable of
XX inhibiting superoxide produ. in phagocytic cells and therefore being
XX useful in inhibiting inflammation and treating inflammatory disorders
XX such as autoimmune diseases, gout, ARDS, asthma, myocardial
XX infarction and various dermatological disorders. Preferably the
XX protein is a low mol. wt. GTP binding protein (LWBG), a mastoparan,
XX or an ICS4 peptide.
XX
XX The present sequence is a specifically claimed example of a
XX preferred peptide.
XX
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 9 AA.
Query Match 36.4% Score 4; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKKK 6
DB 3 KKKK 6

RESULT 11
AAR32302
ID AAR32302 standard; Peptide: 9 AA.
XX
XX AAR32302;
AC AAR32302;
XX
XX 11-JAN 2001 (first entry)
XX
XX HLA A24 binding TAC3-12 peptide SEQ ID 86.
XX
XX Transmembrane serine protease; TADC-12; chromosome 17; vaccination;
XX tumor associated differentially-expressed gene 12; cystostatic; human;
XX malignant hyperplasia; cancer; ovary; breast; lung; colon; prostate.
XX
XX Homo sapiens.
XX
XX W0200052044-A1.
XX
XX 09-SEP-2000.
XX

```


PT cancers including ovarian cancer.

PS Example 14: Page 50; 118pp; English.

XX This invention relates to a novel Transmembrane Serine Protease called

CC Tumour Associated Differentially Expressed Gene-12 (TAGD-12). TAGD-12 is

CC located on chromosome 17. Sequences AA93846, AA93847, and AA932256-932259

CC represent human TAGD-12 cDNA and their corresponding protein sequences.

CC A splice variant of TAGD-12 (TAGD-12v) leads to a 33 kDa protein

CC product. TAGD-12 is overexpressed in ovarian carcinomas. TAGD-12

CC exhibits cytoskeletal activity, and can be used in vaccines and in gene

CC therapy. TAGD-12 nucleotide and protein sequences are used in the

CC diagnosis of malignant hyperplasia and cancers of the ovary, breast,

CC lung, colon, prostate and other cancers where TAGD-12 is overexpressed.

CC TAGD-12 is particularly used as tumour marker for early disease

CC diagnosis. TAGD-12 proteins or fragments can be used to vaccinate at-

CC t-risk individuals, with cancer, suspected of having a cancer or at risk of

CC getting cancer. Sequences AA93846, AA93847 represent PCR primers used for

CC amplifying the TAGD-12 cDNA sequence, and in the quantitative analysis of

CC TAGD-12 mRNA. AA932256 represents a peptide fragment of TAGD-12, used to

CC create anti-TAGD-12 antibodies. Sequences AA932251-932253 represent

CC TAGD-12 peptides which target HLA, and may be used in a vaccine or for

CC immune stimulation.

XX Sequence: 9 AA:

Query Match: 36.4%; Score 4; DB 21; Length 9;

Best Local Similarity: 100.0%; Pred. No. 9.3e+05;

Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 4 KPRK 7

DE 1111

DE 5 KPRK 6

RESULT 14

AA938984

CC AA938984 standard; Peptide: 9 AA.

XX AA938984

XX 29-JAN-2002 (first entry)

XX Human TAGD-12 immunogenic peptide. Seq ID 20.

XX Human Tumour Associated Differentially Expressed Gene-12 (TAGD-12)

XX cytoskeletal activity. TAGD-12 is a transmembrane serine protease.

XX CDLK-A domain; Serine domain; protease domain; vaccine; immunogenic peptide.

XX Homo sapiens.

XX US6294563-B1.

XX 25-SEP-2001.

XX 02-MAR-2000; 2600JS 0518046.

XX 03-MAR-1999; 99JS 0261416.

XX (YAK) UNIV ARKANSAS.

XX Collected in Underwood Lab.

XX WPI: 2001-647267/74.

XX Tumour associated differentially expressed gene-12 and its encoded

XX protein, useful for detecting early and treating cancer, particularly

XX ovarian and other malignancies.

XX Example 14: Column 23; 63pp; English.

CC The invention relates to DNA encoding Tumour Associated Differentially

CC Expressed Gene-12 (TAGD-12) protein, the TAGD-12 protein, a vector

CC expressing the TAGD-12 protein, a host cell containing the vector and

CC antisense molecules directed against the nucleic acid. The TAGD-12

CC protein and DNA are useful for detecting early and treating cancer,

CC particularly ovarian and other malignancies (e.g. by gene therapy). The

CC TAGD-12 protein (and peptides derived from it) is useful as a vaccine

CC for treating cancer. TAGD-12 is a transmembrane serine protease which

CC contains an ILK-A (not defined) domain, an SRCR (not defined) domain and

CC a protease domain. The present sequence represents an immunogenic

CC peptide derived from the TAGD-12 protein.

XX Sequence: 9 AA:

Query Match: 36.4%; Score 4; DB 21; Length 9;

Best Local Similarity: 100.0%; Pred. No. 9.3e+05;

CC expressing the TAGD-12 protein, a host cell containing the vector and

CC antisense molecules directed against the nucleic acid. The TAGD-12

CC protein and DNA are useful for detecting early and treating cancer,

CC particularly ovarian and other malignancies (e.g. by gene therapy). The

CC TAGD-12 protein (and peptides derived from it) is useful as a vaccine

CC for treating cancer. TAGD-12 is a transmembrane serine protease which

CC contains an ILK-A (not defined) domain, an SRCR (not defined) domain and

CC a protease domain. The present sequence represents an immunogenic

CC peptide derived from the TAGD-12 protein.

XX Sequence: 9 AA:

Query Match: 36.4%; Score 4; DB 21; Length 9;

Best Local Similarity: 100.0%; Pred. No. 9.3e+05;

Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 4 KPRK 7

DE 1111

DE 3 KPRK 6

RESULT 15

AA069607

CC AA069607 standard; Peptide: 9 AA.

XX AA069607

XX 29-JAN-2002 (first entry)

XX Human TAGD-12 immunogenic peptide. Seq ID 109.

XX Human Tumour Associated Differentially Expressed Gene-12; TAGD-12;

XX cytoskeletal activity; transmembrane serine protease;

XX CDLK-A domain; Serine domain; protease domain; vaccine; immunogenic peptide.

XX Homo sapiens.

XX US6294563-B1.

XX 25-SEP-2001.

XX 02-MAR-2000; 2600JS 0518046.

XX 03-MAR-1999; 99JS 0261416.

XX (YAK) UNIV ARKANSAS.

XX Collected in Underwood Lab.

XX WPI: 2001-647267/74.

XX Tumour associated differentially expressed gene-12 and its encoded

XX protein, useful for detecting early and treating cancer, particularly

XX ovarian and other malignancies.

XX Example 14: Column 23; 63pp; English.

CC The invention relates to DNA encoding Tumour Associated Differentially

CC Expressed Gene-12 (TAGD-12) protein, the TAGD-12 protein, a vector

CC expressing the TAGD-12 protein, a host cell containing the vector and

CC antisense molecules directed against the nucleic acid. The TAGD-12

CC protein and DNA are useful for detecting early and treating cancer,

CC particularly ovarian and other malignancies (e.g. by gene therapy). The

CC TAGD-12 protein (and peptides derived from it) is useful as a vaccine

CC for treating cancer. TAGD-12 is a transmembrane serine protease which

CC contains an ILK-A (not defined) domain, an SRCR (not defined) domain and

CC a protease domain. The present sequence represents an immunogenic

CC peptide derived from the TAGD-12 protein.

XX Sequence: 9 AA:

Query Match: 36.4%; Score 4; DB 21; Length 9;

Best Local Similarity: 100.0%; Pred. No. 9.3e+05;

CC To monoclonal antibody C-14. The invention also provides an associated
 CC molecule capable of binding the mimotopes, where the molecule can be
 CC an antibody, a second peptide, a carbohydrate, a DNA molecule, an RNA
 CC molecule, or other naturally or chemically synthesized molecules. These
 CC molecules are called anti-mimotopes and can act as anti-thrombotic
 CC drugs. A method has also been described for modulating the adhesion
 CC aggregation or agglutination of platelets, where the method comprises
 CC screening platelets and exposing them to an anti-thrombotic molecule. The
 CC exposure affects von Willebrand factor interaction with platelets
 CC through the glycoprotein IIb/III receptor, which mediates the adhesion,
 CC aggregation, or agglutination of the platelets. The peptide mimotopes
 CC mimic platelet epitopes.

XX
 XX
 SQ Sequence 10 AA:

Query Match: 96.4%; Score 4; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKKP 5
 I I I
 D 2 SKKP 5

RESULT 24
 AAM44266
 ID AAM44266 standard; Peptide: 10 AA
 AC AAM44266
 XX
 XX
 QI 22-047 2401 (first entry)
 XX
 DE Mycoplasma genitalium intermolecular complementary peptide; SEQ ID 595
 XX
 KW Mycoplasma genitalium complementary peptide; ligand;
 KW protein-protein interaction; drug design; intermolecular;
 KW intramolecular;
 XX
 XX Mycoplasma genitalium;
 CS Mycoplasma genitalium;
 EN W.200142278 A2
 ID 14 JUN 2001
 XX
 PE 13-DEC 2001; 2003WO-GR04776;
 XX
 XX 13 DEC 1999; 9903-0029464
 XX (PCT) EP01EOM LTD.
 XX Roberts GW, Heal JR;
 XX WPI: 2001-514249/56
 XX
 XX Example 2; Page 132; 16pp; English.
 XX
 XX The present sequence is one of a large number of complementary peptide
 XX ligands generated from Mycoplasma genitalium genome sequences. These
 XX specific complementary peptides interact with their relevant target
 XX proteins encoded by the microbial genome. They are capable of
 XX antagonising or agonising specific interaction of a protein with
 XX another protein or receptor and are thus useful as reagents and drugs,
 XX and as lead ligands to facilitate drug design and development. They
 XX are useful as tools for functional genomic studies, reagents for the
 XX configuration of high-throughput screens, as a starting point for
 XX medicinal chemistry manipulation, for peptide synthesis and as
 XX therapeutic agents. The analysis and deposition of peptide sequences
 XX facilitates understanding of protein-protein interactions. The method

CC allows for analysis of an entire database at a time, thus overcoming
 CC sampling problems. The set of complementary peptides includes both
 CC intermolecular (between proteins) and intramolecular (within a
 CC protein) sequences.

XX
 XX
 SQ Sequence 10 AA:

Query Match: 96.4%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKKP 5
 I I I
 D 2 SKKP 5

RESULT 24
 AAG94727
 ID AAG94727 standard; Peptide: 10 AA
 XX
 XX AAG94727
 AC AAG94727
 XX
 DI 18-SEP-2001 (first entry)
 XX
 DE Human complementary peptide; ligand; drug discovery;
 KW Human complementary peptide; ligand; drug discovery; drug design;
 XX
 XX Homo sapiens;
 CS Homo sapiens;
 EN W0200142277 A2
 XX
 XX 14 JUN 2001
 XX
 PE 13-DEC 2001; 2003WO-GR04776;
 XX
 XX 13-DEC-1999; 9903-0029464
 XX (PCT) EP01EOM LTD.
 XX Roberts GW, Heal JR;
 XX WPI: 2001-495419/44
 XX
 XX Example 4; Page 171; 64pp; English.
 XX
 XX The invention relates to a set of complementary peptide ligands
 XX generated from the human genome. The complementary peptides
 XX interact with their relevant target proteins encoded in the human
 XX genome. They can be used as reagents in drug discovery and as lead
 XX ligands to facilitate drug design and development. The present
 XX sequence is a complementary peptide provided in the specification.

XX
 XX
 SQ Sequence 10 AA:

Query Match: 96.4%; Score 4; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASKK 4
 I I I
 D 7 ASKK 10

RESULT 25
 AAG95284
 ID AAG95284 standard; Peptide: 10 AA
 XX

```

AC AAG59264;
XX
XX In SEP 2001 (first entry)
XX
XX Human complementary peptides SEQ ID NO: 1128
XX
XX Human complementary peptides SEQ ID NO: 1129
XX
XX Homo Sapiens
XX
XX W200142277-A2;
XX
XX 14 JUN 2001;
XX
XX 13 SEP 2001; Z00060:GB04776;
XX
XX 13 SEP 1999; 99GB 0029464;
XX
XX (PROT.) PRODEM LTD;
XX
XX Roberts GW, Head JR;
XX
XX WPL 2001-408419/43;
XX
XX A set of peptide ligands consisting of specific complementary peptides
XX to proteins encoded by genes of the human genome, useful in an assay
XX for screening and identifying of one or more novel peptides which are
XX drug candidates or pro-drugs
XX
XX Example 4; Page 45; 14pp; English;
XX
XX The invention relates to a set of complementary peptide ligands
XX generated from the human genome. The complementary peptides
XX interact with their relevant target proteins encoded in the human
XX genome. They can be used as reagents in drug discovery and as lead
XX ligands to facilitate drug design and development. The present
XX sequence is a complementary peptide provided in the specification.
XX
XX Sequence ID AA;
XX
XX Query Match 36.4%; Score 4; DB 22; length 10;
XX Best Local Similarity 100.0%; Pred. No. 5.5e-02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4 KKKK 6
XX 7 KKKK 10
XX
XX RESULT 26
XX AAG59264;
XX
XX AAG59264 standard; Peptide: 10 AA;
XX
XX AAG5927;
XX
XX 16 SEP 2001 (first entry)
XX
XX Human complementary peptide; SEQ ID NO: 3121;
XX
XX Human complementary peptide; ligand; drug discovery; drug design;
XX
XX Homo Sapiens;
XX
XX W0200142277-A2;
XX
XX 14 JUN 2001;
XX
XX 13 SEP 2001; Z00060:GB04776;
XX
XX 13 SEP 1999; 99GB 0029464;
XX
XX (PROT.) PRODEM LTD;
XX
XX Roberts GW, Head JR;
XX
XX WPL 2001-408419/43;
XX
XX A set of peptide ligands consisting of specific complementary peptides
XX to proteins encoded by genes of the human genome, useful in an assay
XX for screening and identifying of one or more novel peptides which are
XX drug candidates or pro-drugs
XX
XX Example 4; Page 45; 14pp; English;
XX
XX The invention relates to a set of complementary peptide ligands
XX generated from the human genome. The complementary peptides
XX interact with their relevant target proteins encoded in the human
XX genome. They can be used as reagents in drug discovery and as lead
XX ligands to facilitate drug design and development. The present
XX sequence is a complementary peptide provided in the specification.
XX
XX Sequence ID AA;
XX
XX Query Match 36.4%; Score 4; DB 22; length 10;
XX Best Local Similarity 100.0%; Pred. No. 5.5e-02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4 KKKK 6
XX 7 KKKK 10
XX
XX RESULT 26
XX AAG59264;
XX
XX AAG59264 standard; Peptide: 10 AA;
XX
XX AAG5927;
XX
XX 16 SEP 2001 (first entry)
XX
XX Human complementary peptide; SEQ ID NO: 3121;
XX
XX Human complementary peptide; ligand; drug discovery; drug design;
XX
XX Homo Sapiens;
XX
XX W200142277-A2;
XX
XX 14 JUN 2001;
XX
XX 13 SEP 2001; Z00060:GB04776;
XX
XX 13 SEP 1999; 99GB 0029464;
XX
XX (PROT.) PRODEM LTD;
XX
XX Roberts GW, Head JR;
XX
XX WPL 2001-408419/43;
XX
XX A set of peptide ligands consisting of specific complementary peptides
XX to proteins encoded by genes of the human genome, useful in an assay
XX for screening and identifying of one or more novel peptides which are
XX drug candidates or pro-drugs
XX
XX Example 4; Page 45; 14pp; English;
XX
XX The invention relates to a set of complementary peptide ligands
XX generated from the human genome. The complementary peptides
XX interact with their relevant target proteins encoded in the human
XX genome. They can be used as reagents in drug discovery and as lead
XX ligands to facilitate drug design and development. The present
XX sequence is a complementary peptide provided in the specification.
XX
XX Sequence ID AA;
XX

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PI Roberts GW, Head JR;
XX
XX WPL 2001-408419/43;
XX
XX A set of peptide ligands consisting of specific complementary peptides
XX to proteins encoded by genes of the human genome, useful in an assay
XX for screening and identifying of one or more novel peptides which are
XX drug candidates or pro-drugs
XX
XX Example 4; Page 45; 14pp; English;
XX
XX The invention relates to a set of complementary peptide ligands
XX generated from the human genome. The complementary peptides
XX interact with their relevant target proteins encoded in the human
XX genome. They can be used as reagents in drug discovery and as lead
XX ligands to facilitate drug design and development. The present
XX sequence is a complementary peptide provided in the specification.
XX
XX Sequence ID AA;
XX
XX Query Match 36.4%; Score 4; DB 22; length 10;
XX Best Local Similarity 100.0%; Pred. No. 5.5e-02;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4 KKKK 7
XX 5 KKKK 8
XX
XX RESULT 27
XX AAG5927;
XX
XX AAG5927 standard; Peptide: 10 AA;
XX
XX AAG5927;
XX
XX 16 SEP 2001 (first entry)
XX
XX Human complementary peptide; SEQ ID NO: 3121;
XX
XX Human complementary peptide; ligand; drug discovery; drug design;
XX
XX Homo Sapiens;
XX
XX W0200142277-A2;
XX
XX 14 JUN 2001;
XX
XX 13 SEP 2001; Z00060:GB04776;
XX
XX 13 SEP 1999; 99GB 0029464;
XX
XX (PROT.) PRODEM LTD;
XX
XX Roberts GW, Head JR;
XX
XX WPL 2001-408419/43;
XX
XX A set of peptide ligands consisting of specific complementary peptides
XX to proteins encoded by genes of the human genome, useful in an assay
XX for screening and identifying of one or more novel peptides which are
XX drug candidates or pro-drugs
XX
XX Example 4; Page 45; 14pp; English;
XX
XX The invention relates to a set of complementary peptide ligands
XX generated from the human genome. The complementary peptides
XX interact with their relevant target proteins encoded in the human
XX genome. They can be used as reagents in drug discovery and as lead
XX ligands to facilitate drug design and development. The present
XX sequence is a complementary peptide provided in the specification.
XX
XX Sequence ID AA;
XX

```


AAFL7417;
 18 AUG-2002 (first entry)
 Human respiratory syncytial virus (HRSV-G) Type A peptide, NLS 36;
 Mevlin; cosmetic; membrane translocator; antithrombotic; anti-fibrotic;
 pestivirus infection; pharmacological; drug delivery system; virotoxin;
 vaccine; human respiratory syncytial virus, HRSV;
 Human respiratory syncytial virus;
 Key: Location/Qualifiers
 Modified site 1 /note= "Biotinylated lys"
 WO200200882-A2.
 04-JAN-2002.
 29-JUN-2001: 2001WO-NI00484.
 28-JUN-2000: 2000EP-0202255.
 (HRSV) ID-DELYSTAD INST DIERKHOFFERIJ EN DIERGEZ.
 Lunediijk JMW;
 WPI: 2002 149522/18.
 Novel isolated, synthetic or recombinant transport peptide module
 called movin; useful for preparation of pharmaceutical/cosmetic
 composition capable of membrane transport or capable of eliciting
 antibiotic activity
 Disclosure: Page 58; 78pp; English.
 The invention relates to an isolated, synthetic or recombinant transport
 peptide module called movin. The peptide or its functional equivalent
 comprises a sequence that is identical to an amino acid sequence of a
 peptide capable of binding heparin. The peptide module is useful for
 the preparation of a pharmaceutical or cosmetic composition capable of
 membrane translocation or capable of eliciting antibiotic activity. The
 peptide module is useful type specific diagnosis of infection such as
 pestivirus infection, for transport of substances into a cell, as
 antibacterial, for detecting the presence or absence of an antibody
 directed against pestivirus in a sample, to obtain antibodies which are
 specific for pestivirus types and/or subtypes, for differentiating an
 animal from another animal, for preparation of a vaccine system capable of
 inducing antibodies (a vaccine), as drug delivery system, to provide for
 synergy in antibacterial activity, translocation of translocation, and
 in vaccines to prevent infection with pestivirus. A pharmaceutical
 composition is useful for the prophylaxis of pestivirus infections.
 The present sequence is human respiratory syncytial virus (HRSV-G)
 Type A peptide which is a heparin binding peptide.
 Sequence 10 AA;
 Query Match 36.4%; Score 4; DB 2x; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5,9e-02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;
 QY 4 KKPK 6
 1 1 1
 6 KKPK 9
 RESULT 34
 AAWS3153
 ID AAWS3153 standard; peptide; 11 AA.
 AC
 AAWS3153;
 XX
 AAWS3153;
 XX

DT 14-JUL-1998 (first entry)
 XX PTP activity determining peptide substrate 8.
 DE
 XX Protein tyrosine phosphatase; PTP; peptide substrate; phosphorylation.
 KW
 XX Synthetic.
 OS
 XX US5739278-A.
 PN
 XX 14-APR-1998.
 PD
 XX 30-MAR-1995; 55US-0416035.
 PF
 XX 10-MAY-1993; 94US-0059949.
 PR
 XX 30-MAR-1995; 55US-0416035.
 PA (UNIV) UNIV WASHINGTON.
 XX
 XX COOL DE, Daum G, Fischer EH;
 PI
 XX WPI: 1998-250491/22.
 DR
 XX New nona peptide, phosphorylated derivative and related compositions
 PT - useful for measuring activity of protein tyrosine phosphatases
 PT
 XX Disclosure: Columns 13-14; 5pp; English.
 PS
 XX
 CC This peptide substrate can be used for the determination of activity of
 CC protein tyrosine phosphatases (PTP). The peptides with a tyrosine residue
 CC phosphorylated and related compositions containing the peptides are
 CC useful for determining the amount or presence of PTP. Determination of
 CC PTP activity by prior art methods could be affected by a number of
 CC factors, including the type of enzyme being assayed, the conditions under
 CC which the assay was performed and the presence of external effectors. The
 CC peptide of the current invention, when used as a substrate for
 CC determination purposes is not subject to the limitations of prior art
 CC methods. The new determination method is highly sensitive, with the assay
 CC permitting the detection and characterization of a wide variety of PTP's.
 CC Due to the increased sensitivity of the methods, PTP's can be detected in
 CC situations where only limiting amounts of samples, e.g tissue extracts or
 CC immunoprecipitates, are available.
 CC
 SQ Sequence 11 AA;
 Query Match 46.4%; Score 4; DB 19; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5,9e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASKK 4
 1 1
 7 ASKK 10
 DB
 RESULT 35
 AAY88555
 ID AAY88555 standard; peptide; 11 AA.
 XX
 AC AAY88555;
 XX
 XX 07-AUG-2000 (first entry)
 DT
 XX NCAM Igl binding peptide 118 used as a control peptide.
 DE
 XX NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;
 KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
 KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
 KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
 KW treatment; prosthetic nerve guide; treatment; nervous system.
 XX
 XX Synthetic.
 OS
 XX WO200018401-A2.
 PN

```

XX 06-APR-2000.
XX 23-SEP-1999; 99WO-DK00500.
XX 29-SEP-1998; 98DK-0001232.
XX 29-APR-1999; 99DK-0000592.
XX (RONN/) RONN L C B.
XX (BOCK/) BOCK E.
XX (HOLM/) HOLM A.
XX (OLSE/) OLSEN M.
XX (JENSE/) JENSEN P H.
XX (POUL/) POULSEN F M.
XX (SORO/) SOROKA V.
XX (RALE/) RALETS I.
XX (BEKE/) BEREZIN V.
XX Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
XX Poulsen FM, Soroka V, Ralets I, Berezin V;
XX WPI: 2000-293111/25.
XX Compositions that bind neural cell adhesion molecules useful for
XX treating disorders of the nervous system and muscles e.g. Alzheimer's
XX and Parkinson's diseases -
XX Example 5; Fig 7; 119pp; English.
XX Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
XX NCAM is found in three forms, two of which are transmembrane forms, while
XX the third is attached via a lipid anchor to the cell membrane. All three
XX NCAM forms have an extracellular structure consisting five immunoglobulin
XX domains (Ig domains). The Ig domains are numbered 1 to 5 from the
XX N-terminal. The invention relates to a compound containing a peptide
XX which binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Iq2
XX from NCAM presenting cells, and is also capable of promoting the
XX proliferation of NCAM presenting cells. The present sequence represents a
XX control peptide used in the identification of those binding peptides
XX which can be used in the compound. The compound may be used in the
XX treatment of normal, degenerated or damaged NCAM presenting cells.
XX peripheral nervous systems such as post operative nerve damage, traumatic
XX nerve damage, impaired myelination of nerve fibres, conditions resulting
XX from a stroke, Parkinson's disease, Alzheimer's disease, dementias,
XX sclerosis, nerve degeneration associated with diabetes mellitus,
XX disorders affecting the circadian clock or neuro-muscular transmission
XX and schizophrenia. Conditions affecting the muscles may also be treated
XX with the compound, such as conditions associated with impaired function
XX of neuromuscular connections (e.g. genetic or traumatic shock or
XX traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
XX (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
XX liver and bowel may also be treated using the compound. The compound is
XX used in a prosthetic nerve guide, and also to stimulate the ability to
XX learn, and to stimulate the memory of a subject.
XX Sequence 11 AA:
XX
XX Query Match 36.4% Score 4: 18 21 Length 11;
XX Best Local Similarity 100.0% Prod. No. 5,30-02;
XX Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 8 NIKA 11
XX 11.1
XX 8 NIKA 11
XX
XX RESULT 36
XX AAY8556
XX ID AAY8556 standard; peptide: 1: AA.
XX

```

```

AC AAY8556;
XX 07-AUG-2000 (first entry)
XX NCAM Ig1 binding peptide 119 used as a control peptide.
XX
XX NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;
XX neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
XX impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
XX Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
XX treatment; prosthetic nerve guide; treatment; nervous system.
XX Synthetic.
XX WO2000C18801-A2.
XX 06-APR-2000.
XX 23-SEP-1999; 99WO-DK00500.
XX 29-SEP-1998; 98DK-0001232.
XX 29-APR-1999; 99DK-0000592.
XX (RONN/) RONN L C B.
XX (BOCK/) BOCK E.
XX (HOLM/) HOLM A.
XX (OLSE/) OLSEN M.
XX (OSTE/) OSTERGAARD S.
XX (JENSE/) JENSEN P H.
XX (POUL/) POULSEN F M.
XX (SORO/) SOROKA V.
XX (RALE/) RALETS I.
XX (BEKE/) BEREZIN V.
XX Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
XX Poulsen FM, Soroka V, Ralets I, Berezin V;
XX WPI: 2000-293111/25.
XX Compositions that bind neural cell adhesion molecules useful for
XX treating disorders of the nervous system and muscles e.g. Alzheimer's
XX and Parkinson's diseases -
XX Example 5; Fig 7; 119pp; English.
XX Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
XX NCAM is found in three forms, two of which are transmembrane forms, while
XX the third is attached via a lipid anchor to the cell membrane. All three
XX NCAM forms have an extracellular structure consisting five immunoglobulin
XX domains (Ig domains). The Ig domains are numbered 1 to 5 from the
XX N-terminal. The invention relates to a compound containing a peptide
XX which binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Iq2
XX domains, and is capable of stimulating or promoting neurite outgrowth
XX from NCAM presenting cells, and is also capable of promoting the
XX proliferation of NCAM presenting cells. The present sequence represents a
XX control peptide used in the identification of those binding peptides
XX which can be used in the compound. The compound may be used in the
XX treatment of normal, degenerated or damaged NCAM presenting cells.
XX peripheral nervous systems such as post operative nerve damage, traumatic
XX nerve damage, impaired myelination of nerve fibres, conditions resulting
XX from a stroke, Parkinson's disease, Alzheimer's disease, dementias,
XX sclerosis, nerve degeneration associated with diabetes mellitus,
XX disorders affecting the circadian clock or neuro-muscular transmission
XX and schizophrenia. Conditions affecting the muscles may also be treated
XX with the compound, such as conditions associated with impaired function
XX of neuromuscular connections (e.g. genetic or traumatic shock or
XX traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
XX (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
XX liver and bowel may also be treated using the compound. The compound is
XX used in a prosthetic nerve guide, and also to stimulate the ability to
XX learn, and to stimulate the memory of a subject.
XX

```

Seq	Sequence	11 AA;	Best Local Similarity	100.0%;	Pred. No. 5.9e+02;	Mismatches	0;	Indels	0;	Gaps	0;
	Query Match	36.4%;	Score 4;	DB 23;	Length 11;						
	Best Local Similarity	100.0%;	Pred. No. 5.9e+02;								
	Matches	4;	Conservative	0;	Mismatches	0;					
QY	R NIKA 11										
DB	1111										
	8 NIKA 11										
RESULT 47											
ABH74833											
ID	ABH74833	standard:	Peptide: 11 AA.								
XX	AC	ABH74833									
XX	XX										
XX	XX	18 APR 2002	(first entry)								
DE	Nuclear protein nuclear localisation signal: peptide SEQ ID NO:517.										
XX	Fusogenic nuclear localisation signal: NLS: encapsulation; lipogene;										
KW	liposome micelle; karyophilic; cytostatic; antitumour; solid tumour;										
KW	peptide lipid polynucleotide complex; neoplastic disease; gene therapy;										
KW	breast carcinoma, prostate carcinoma.										
XX	Paracanthous aneliosis.										
OS	W6200194836-A2.										
XX	13-DEC-2001.										
XX	08-JUN-2001: 2001WO-US18657.										
XX	09-JUN-2003: 2000US-210925P.										
PA	(B-04L/) BOBILIKAS T.										
PA	Boulikas T;										
PI	WPI: 2002 164295/21.										
XX	Encapsulation of plasmid DNA (lipogenes) and therapeutic agents with										
PT	nuclear localization signal/tusogenic peptide conjugates into targeted										
PT	liposome complexes.										
XX	Claim 14: Page 85; 107pp; English.										
PS	The present invention describes a method for producing micelles with										
XX	entrapped therapeutic agents. The method comprises: (1) combining										
CC	negatively charged agent with a cationic lipid in a ratio where 30-99 %										
CC	of the negatively charged atoms are neutralised by positive charges on										
CC	lipid molecules to form an electrostatic micelle complex in 20-80 %										
CC	ethanol; and (2) combining the micelle complex of (a) with fusogenic-										
CC	karyophilic peptide conjugates in a 0.0-0.5 ratio, therefore producing										
CC	micelles with entrapped therapeutic agents. Also described is a method										
CC	for delivering a therapeutic agent in vivo, comprising the administration										
CC	of the micelle. ABH74256 to ABH74858 represent specifically claimed										
CC	nuclear localisation signal (NLS) peptides for use in the method as the										
CC	tusogenic-karyophilic peptides. The micelles produced can have cytostatic										
CC	and antitumour activities. The peptide-lipid-polynucleotide complexes										
CC	produced are useful for inhibiting the progression of neoplastic										
CC	diseases. The invention relates to the field of gene therapy and is										
CC	directed toward methods for producing peptide-lipid-polynucleotide										
CC	complexes suitable for delivery of polynucleotides. The encapsulated										
CC	molecules display therapeutic efficacy in eradicating solid tumours										
CC	including but not limited to breast carcinoma or prostate carcinoma.										
CC	ABH74235 to ABH74255 are used in the exemplification of the present										
CC	invention.										
XX	Sequence	11 AA;									
Query Match		36.4%;	Score 4;	DB 23;	Length 11;						

Best Local Similarity	100.0%;	Pred. No. 5.9e+02;	Mismatches	0;	Indels	0;	Gaps	0;
Matches	4;	Conservative	0;					
QY	3 KRPK 6							
	1111							
DB	5 KRPK 8							
RESULT 38								
AAV20609								
ID	AAV20609	standard:	Protein: 12 AA.					
XX	AC	AAV20609;						
XX	XX							
DE	22-JUL-1999	(first entry)						
XX	XX	Human neurofilament-L mutant protein fragment 116.						
XX	XX	Human: beta-amyloid precursor protein; beta-APP; diagnosis; cancer;						
KW	frameshift mutation; age-related disease; neurodegenerative disorder;							
KW	Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;							
KW	Huntington's disease; multiple sclerosis; alcoholic liver disease;							
KW	diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;							
KW	ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;							
KW	neurofilament-F; presenilin 1; presenilin II; cellular tumour antigen;							
KW	glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;							
KW	bel-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;							
KW	high mobility group protein-C; neuroendocrine specific protein A.							
XX	XX	Synthetic.						
OS	OS	Homo sapiens.						
XX	XX	W09845322-A2.						
PN	15-OCT-1998.							
XX	XX	02-APR-1998: 98WO-IB00705.						
PD	XX	10-APR-1997: 97US-0043163.						
PF	XX	(UYUT-) RIJKSUNIV UTRECHT.						
PK	XX	(ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.						
XX	XX	(UYRO-) UNIV ROTTERDAM ERASMUS.						
XX	XX	Burbach JPH, Grosveld FG, Van Leeuwen FW;						
XX	XX	WPI: 1998-609901/51.						
DR	XX	N PSDB: AAX75758.						
XX	XX	Diagnosing disease by detecting frameshift mutations in RNA or						
PT	XX	corresponding protein mutations - used to diagnose cancer and						
PT	XX	neurological diseases, particularly Alzheimer's disease, and also						
PT	XX	for treatment and prevention with specific ribozymes or wild-type						
XX	XX	RNA						
PS	XX	Disclosure: Figure 7: 258pp; English.						
XX	XX	This invention describes a novel method for the diagnosis of a disease						
CC	XX	caused by, or associated with, an RNA molecule that has a frameshift						
CC	XX	mutation. The method is used to diagnose age-related diseases, especially						
CC	XX	cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's						
CC	XX	disease, Down's syndrome, myotonic dystrophy, Huntington's disease,						
CC	XX	multiple sclerosis, alcoholic liver disease, diabetes mellitus type II						
CC	XX	and many others listed) or susceptibility to these disorders. The method						
CC	XX	allows a definitive diagnosis of Alzheimer's disease in living patients,						
CC	XX	at an early stage. It is based on the observation that disease may be						
CC	XX	caused by mutations in RNA rather than DNA. The invention describes the						
CC	XX	used of neuronal system RNA molecules, specifically proteins including						
CC	XX	beta-amyloid precursor protein (beta-APP), the microtubule associated						
CC	XX	proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule						
CC	XX	associated protein 2 (MAP2), neurofilament-L, neurofilament-M,						
CC	XX	neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic						
CC	XX	protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma						

CC 2 (bel 2) proto-oncogene, seraphorin 11L, BDNF 1, high mobility group
 CC protein-C (HMGp-C) and neuroendocrine specific protein A.
 XX
 SQ Sequence 12 AA;
 Query Match 36.48; Score 4; E0 19; Length 12;
 Best Local Similarity 100.00; Prod. No. 6.40-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KKKP 6
 II
 DB 8 KKKP 11
 RESULT 39
 AAB19494
 ID AAB19434 standard; peptide; 12 AA.
 AX AAB19494;
 XX
 DT 06-MAR-2001 (first entry)
 XX
 EE Antigenic peptide derived from gamma hydroxy butyrate dehydrogenase.
 KW Gamma-aminobutyric acid; GABA; GABA transaminase; GABA-T;
 KW gamma hydroxy butyrate dehydrogenase; GHBH; succinic semialdehyde;
 KW gamma hydroxybutyrate;
 XX
 OS Synthetic;
 OS Arabidopsis thaliana.
 XX
 DN W02C0061763 A2.
 XX
 PD 19-OCT-2000.
 XX
 PF 06-APR-2000; 2000WO-CA00378.
 XX
 PR 09-APR-1999; 99US-012851R.
 XX
 PA (UNCL) UNIV GUELPH.
 XX
 PI Sheilp HJ, Reitzkreuz KE, Van Gassenbroekere JF;
 XX
 DR WP1; 2000-579492/66.
 XX
 PT Novel proteins related to gamma-aminobutyrate aminotransferase (GABA-T) and gamma hydroxy butyrate dehydrogenase (GHBH) useful for
 PT screening and isolation of homologous genes from other organisms.
 XX
 PS Example 3; Page 26; 48pp; English.
 XX
 CC The present sequence represents a peptide derived from a plant
 CC gamma-hydroxy butyrate dehydrogenase (GHBH), which was used to raise
 CC antibodies. The specification also describes a plant gamma-aminobutyric
 CC acid (GABA) transaminase (GABA-T). The proteins are involved in the
 CC metabolism of GABA in plants. GABA-T is used to transaminate GABA
 CC to form succinic semialdehyde, which may be converted to gamma
 CC hydroxybutyrate by GHBH. The polynucleotides are used to produce
 CC GABA-T and GHBH recombinantly. The proteins are useful for screening
 CC and isolation of homologous genes from other organisms.
 SQ Sequence 12 AA;
 Query Match 36.48; Score 4; E0 21; Length 12;
 Best Local Similarity 100.00; Prod. No. 6.40-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SKKP 5
 II
 DB 8 SKKP 11
 RESULT 40

AAU99715
 ID AAU99715 standard; Peptide; 12 AA.
 XX
 AC AAU99715;
 XX
 DT 24-SEP-2002 (first entry)
 XX
 DE Human Ghrelin (C-terminus) peptide sequence.
 XX
 KW Human; angiotensin converting enzyme-2; ACE-2; body weight disorder;
 KW muscle mass; body fat; obesity; diabetes; atherosclerosis; weight loss;
 KW lipid metabolism; weight gain; anorexia; cachexia; bulimia; sepsis;
 KW familial partial lipodystrophy; hypercholesterolaemia; hyperlipidaemia;
 KW aberrant metabolic rate; heart failure; left ventricular hypertrophy;
 KW neurodegenerative disorder; peptide hormone; cytokine processing;
 KW myocardial infarction; cardiomyopathy; inflammatory bowel disease;
 KW systemic inflammation response syndrome; polytrauma; pain; stroke;
 KW bone destruction; rheumatoid arthritis; osteoarthritis; asthma;
 KW periodontal disease; dysmenorrhoea; premature labour; brain oedema;
 KW focal injury; diffuse axonal injury; reperfusion injury; scar formation;
 KW cerebral vasospasm; subarachnoid haemorrhage; allergic disorder;
 KW adult respiratory distress syndrome; wound healing; appetite;
 KW body mass index; Ghrelin.
 XX
 OS Homo sapiens.
 XX
 PN W020023997-A2.
 XX
 PD 23-MAY-2002.
 XX
 PF 31-OCT-2001; 2001WO-US45703.
 XX
 PR 01-NOV-2000; 2000US-0704216.
 PR 29-MAY-2001; 2001US-0870382.
 PR 19-OCT-2001; 2001US-371741P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Acton SL, Ocain ID, Gould AE, Dales NA, Guan B, Brown JA;
 PI Patane M, Kadambi VJ, Solomon M, Stricker-Krongrad A;
 XX
 DR WP1; 2002-547572/58.
 XX
 PT Treating body weight disorder and increasing muscle mass comprises
 PT administering angiotensin converting enzyme-2 modulating compound.
 XX
 PS Example 1b; Page 221; 395pp; English.
 XX
 CC The present invention describes a new method of treating a body weight
 CC disorder, increasing muscle mass and decreasing body fat by
 CC administration of angiotensin converting enzyme (ACE)-2 modulating
 CC compound. The invention can be used for treating body weight disorders,
 CC particularly obesity of at least grade 1, diabetes, atherosclerosis and
 CC a state associated with lipid metabolism. The method is used for treating
 CC rapid weight loss, rapid weight gain, anorexia, cachexia, bulimia,
 CC generalised partial lipodystrophy, familial partial lipodystrophy,
 CC hypercholesterolaemia, hyperlipidaemia, an aberrant metabolic rate,
 CC congestive heart failure, chronic heart failure, left ventricular
 CC hypertrophy, acute heart failure, neurodegenerative disorders (e.g.
 CC Alzheimer's disease, Parkinson's disease and Huntington's disease),
 CC diseases associated with peptide hormones or cytokine processing,
 CC myocardial infarction, cardiomyopathy, systemic inflammation response
 CC syndrome, sepsis, polytrauma, inflammatory bowel disease, acute and
 CC chronic pain, bone destruction in rheumatoid arthritis and osteoarthritis
 CC and periodontal disease, dysmenorrhoea, premature labour, brain oedema
 CC following focal injury, diffuse axonal injury, stroke, reperfusion
 CC injury, cerebral vasospasm after subarachnoid haemorrhage, allergic
 CC disorders including asthma, adult respiratory distress syndrome, wound
 CC healing and scar formation. The invention decreases the appetite,
 CC increases muscle mass and decreases body fat of subject having body mass
 CC index of greater than 25 (preferably 24.9)kg/m². The present amino
 CC acid sequence represents the human Ghrelin (C-terminus) peptide that was
 CC used in the invention for hydrolysis of biologically active peptides

Query Match 36.4%; Score 4; DB 23; Length 12;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Sequence 12 AA;

QY 2 SKKP 5

DB 1,11

2 SKKP 5

RESULT 41

AAE17344

ID: AAE17344 standard; peptide: 12 AA.

XX AC AAE17344;

DT 18-APR-2002 (first entry)

XX Recombinant; transport peptide module #11.

XX Moving; cosmetic; membrane translocation; antibacterial; antibiotic;
KW pestivirus infection; pharmaceutical; drug-delivery system; virucide;
KW vaccine.

XX Unidentified.

XX W0200200882-A2.

XX 03 JAN-2002.

XX 28-JUN-2001; 2001WO-NL00484.

XX 28-JUN-2000; 2000EP-0202255.

XX (ID:E-) ID-LELYSTAD INST DIERHOUTERIJ EN DIERGEZ.

XX Langedijk JPM;

XX WPI: 2002-139922/18.

XX Novel isolated, synthetic or recombinant transport peptide module
called movin, useful for preparation of pharmaceutical/cosmetic
composition capable of membrane transport or capable of eliciting
antibiotic activity.

XX Claim 6; Page 64; 78pp; English.

XX The invention relates to an isolated, synthetic or recombinant transport
peptide module called movin. The peptide or its functional equivalent
comprises a sequence that is identical to an amino acid sequence of a
peptide capable of binding heparin. The invention also relates to
transport peptides, for example derived from the first protein of
pestiviruses for type-specific diagnosis of infection. The peptide module
is useful for the preparation of a pharmaceutical or cosmetic composition
capable of membrane translocation or capable of eliciting antibiotic
activity. The peptide module is useful type-specific diagnosis of
infection such as pestivirus infection, for transport of substances into
a cell, as antibacterial, for detection the presence or absence of an
antibody directed against pestivirus in a sample, to obtain antibodies
which are specific for pestivirus types and/or subtypes, for
differentiating an animal from another animal, for preparation of a
composition capable of inducing antibodies (a vaccine), as drug-delivery
system, to provide for synergy in antibacterial activity, transportation
or translocation, and in vaccines to prevent infection with pestivirus.
XX A pharmaceutical composition is useful for the prophylaxis of pestivirus
infections. The present sequence is a recombinant transport peptide
module used in the invention.

XX Sequence 12 AA;

Query Match 36.4%; Score 4; DB 23; Length 12;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6

DB 1111

9 KKPK 12

RESULT 42

AAE17424

ID: AAE17424 standard; peptide: 12 AA.

XX AC AAE17424;

DT 18-APR-2002 (first entry)

XX Human respiratory syncytial virus (HRSV) type B region 2 peptide.

XX Moving; cosmetic; membrane translocation; antibacterial; antibiotic;
KW pestivirus infection; pharmaceutical; drug-delivery system; virucide;
KW vaccine; human respiratory syncytial virus; HRSV.

XX Human respiratory syncytial virus.

XX Key location/Qualifiers

FT Modified-site 1 /note: "Biotinylated Lys"

FT W0200200882-A2.

XX 03-JAN-2002.

XX 28-JUN-2001; 2001WO-NL00484.

XX 28-JUN-2000; 2000EP-0202255.

XX (ID:E-) ID-LELYSTAD INST DIERHOUTERIJ EN DIERGEZ.

XX Langedijk JPM;

XX WPI: 2002-139922/18.

XX Novel isolated, synthetic or recombinant transport peptide module
called movin, useful for preparation of pharmaceutical/cosmetic
composition capable of membrane transport or capable of eliciting
antibiotic activity.

XX Disclosure: Page 64; 78pp; English.

XX The invention relates to an isolated, synthetic or recombinant transport
peptide module called movin. The peptide or its functional equivalent
comprises a sequence that is identical to an amino acid sequence of a
peptide capable of binding heparin. The peptide module is useful for
the preparation of a pharmaceutical or cosmetic composition capable of
membrane translocation or capable of eliciting antibiotic activity. The
peptide module is useful type-specific diagnosis of infection such as
pestivirus infection, for transport of substances into a cell, as
antibacterial, for detecting the presence or absence of an antibody
directed against pestivirus in a sample, to obtain antibodies which are
specific for pestivirus types and/or subtypes, for differentiating an
animal from another animal, for preparation of a composition capable of
inducing antibodies (a vaccine), as drug-delivery system, to provide for
synergy in antibacterial activity, transportation or translocation, and
in vaccines to prevent infection with pestivirus. A pharmaceutical
composition is useful for the prophylaxis of pestivirus infections.
XX The present sequence is human respiratory syncytial virus (HRSV-G)
type A peptide which is a heparin binding peptide.

XX Sequence 12 AA;

Query Match 36.4%; Score 4; DB 23; Length 12;

Best Local Similarity 100.0%; Pred. No. 6.3e+02;

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KKPK 6
 III
 BB 9 KKPK 12

RESULT 43
 ID ABB74843 standard; Peptide: 12 AA.
 AC ABB74844;
 XX 18-APR-2002 (first entry)
 DE Nuclear protein nuclear localisation signal peptide SEQ ID NO:40?
 XX Fusoquinol: nuclear localisation signal; NLS; encapsulation; liposome;
 KW liposome; micelle; karyophilic; cytostatic; anti-tumor; solid tumor;
 KW Peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;
 KW breast carcinoma; prostate carcinoma;
 XX Acetabula;
 GS W028019486 A2;
 PN 13 DEC 2001;
 XX 08 JUN 2001; 2001WG-US18657;
 PF 09 JUN 2001; 2001WG-US210925P;
 PR (publ.) BOLLIKAS T;
 XX Bollikas T;
 PI WPI: 2002 164295/21;
 XX Encapsulation of plasmid DNA (liposomes) and therapeutic agents with
 TT nuclear localization signal/liposome peptide complexes into targeted
 ET liposome complexes;
 XX Claim 14; Page 85; 107pp; English;
 PS The present invention describes a method for producing micelles with
 CC entrapped therapeutic agents. The method comprises (a) combining
 CC negatively charged agent with a cationic lipid to form a complex where the cationic
 CC lipid molecules to form an entrapped polynucleotide complex in 20-40% w/w
 CC ethanol; and (b) combining the polynucleotide complex with fusogenic
 CC karyophilic peptide conjugates in a 1:1 molar ratio to form producing
 CC micelles with entrapped therapeutic agents. An agent used as a method
 CC for delivering a therapeutic agent in vivo might select the administration
 CC of the micelle. ABB74256 to ABB74494 represent specifically claimed
 CC nuclear localisation signal (NLS) peptides for use in the method as the
 CC fusogenic karyophilic peptides. The micelles produced can have cytostatic
 CC and anti-tumour activities. The peptide lipid conjugated complexes
 CC produced are useful for inhibiting the progression of neoplastic
 CC diseases. The invention relates to the field of gene therapy and is
 CC directed toward methods for producing peptide-lipid polynucleotide
 CC complexes suitable for delivery of polynucleotides. The encapsulated
 CC molecules display therapeutic efficacy in various solid and soft tumors
 CC including but not limited to breast carcinoma of prostate carcinoma.
 CC ABB74245 to ABB74255 are used in the exemplification of the present
 CC invention.
 XX Sequence 12 AA;
 SQ Query Match 36.4%; Score 4; DB 21; Length 12;
 Best Local Similarity 100.0%; Prod. No. 6; Re402;
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 3 KKPK 6
 III
 BB 9 KKPK 12

DB 2 KKPK 5
 III

RESULT 44
 ID AAB11344 standard; peptide: 13 AA.
 XX AAB11344;
 AC AAB11344;
 XX 25-MAR-2003 (updated)
 DT 05-JUN-1991 (first entry)
 XX Anti-rhodopsin monoclonal antibody epitope.
 DE Monoclonal antibody: rhodopsin; metarhodopsin.
 KW Paracetopos defleini.
 XX Paracetopos defleini.
 PN EP420151-A.
 XX 03-APR-1991.
 PD 25 SEP-1990; 90EP 0118499.
 PF 40-MAY-1990; 90JP-0148269.
 PR 27-SEP-1989; 89JP-0249148.
 KR 28-FEB-1990; 90JP 0045410.
 XX (H11A) HITACHI LTD.
 PA Ishibashi T, Kozuka H, Yoshino S, Shimizu N, Tsuda M;
 PI Imazeki S;
 XX WPI: 1991-095637/14;
 CR Monoclonal antibodies specific to rhodopsin - useful for
 PT immobilising rhodopsin or monitoring its photochemical reactions
 XX Claim 9; Page 15; 21pp; English.
 PS Anti rhodopsin antibodies having a greater affinity for metarhodopsin
 CC than for rhodopsin; recognising this sequence, were produced by
 CC conventional hybridoma techniques.
 CC The peptide is the hydrophilic region connecting the third helix
 CC to the fourth helix of the N-terminus of the octopus rhodopsin.
 CC Both antibodies Ig and pH were reactive with this peptide.
 CC (Updated on 25 MAR 2003 to correct PA field.)
 XX Sequence 13 AA;
 SQ Query Match 36.4%; Score 4; DB 12; Length 13;
 Best Local Similarity 100.0%; Prod. No. 6; Re402;
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 3 ASKK 4
 III
 DB 8 ASKK 11

RESULT 45
 AAR47395
 ID AAR47395 standard; peptide: 13 AA.
 XX AAR47395;
 AC AAR47395;
 XX 25-MAR-2003 (updated)
 DT 29-JUN-1994 (first entry)
 XX PGE-activity-displaying peptide.
 DE Platelet derived growth factor; A-chain; therapy; assay agent;
 KW mitogen; chemotactic agent; wound healing; vascular disease effects;

KW injury: calcium uptake modulation.
 GS Synthetic.
 XX W0942576-A2.
 PN
 XX 24-DEC-1993.
 PD
 XX 03-JUN-1993; 93WO-US05325.
 PF
 XX 05-JUN-1992; 92US-0894497.
 PK
 XX (SMK) SK: INI.
 PA
 XX Judd AK;
 PI
 XX WPI: 1994-007454/01.
 DR
 XX Peptide(s) having platelet derived growth factor activity - derived
 PT from platelet-derived growth factor A and B chain sequences, useful
 PI in therapy and as assay agents
 XX
 XX Claim 1: Page 50; 58pp; English.
 PS
 XX The sequence is that of a peptide corresponding to platelet derived
 CC growth factor (PDGF) A-chain amino acids 65-78. It shows PDGF
 CC activity and can be used in assays for PDGF. It may also be used as
 CC a mitogen and a chemotactic agent for use in wound healing, in the
 CC alleviation of the effects of vascular disease or injury and in the
 CC modulation of calcium uptake into the cells. The peptide is also
 CC easier to produce than native PDGF.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 XX Sequence 13 AA:
 SG
 Query Match 36.4%; Score 4; DB 10; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KKPK 6
 DB 9 KKPK 12
 I I I I
 RESULT 46
 AAW5068
 ID AAW5068 standard; Protein: 13 AA.
 XX
 XX AAW5068;
 AC
 XX 20-MAY 1999 (first entry)
 DT
 XX Putative HS binding domain of HSV gp glycoprotein.
 DE
 XX Herpes simplex virus; HSV; viral envelope protein; non native ligand;
 KW gene therapy; ectopic infection; gp glycoprotein; HS binding domain.
 KW
 XX Herpes simplex virus.
 GS
 XX W039526583-A1.
 PN
 XX 11 FEB-1999.
 PD
 XX 31-JUL-1998; 98WO-US16051.
 PF
 XX 31-JUL-1997; 97US-0054329.
 PK
 XX (JYP1-) UNIV PITTSBURGH.
 PA
 XX Glorioso JC, Laquerre S;
 PI
 XX WPI: 1995-153808/13.
 DR
 XX N-PSDB: AAX22297.
 DR

XX New herpes simplex virus including non-native ligand for use in gene
 PT therapy - has specific affinity for particular cells and reduced
 PT affinity for native host cells, resulting in reduced ectopic
 PT expression
 XX
 XX Example 1: Fig 1: 40pp; English.
 PS
 XX The invention relates to targeting Herpes simplex virus (HSV) vectors,
 CC chiefly by modifying viral proteins. The invention provides a HSV having
 CC an envelope that includes a non-native ligand. The HSV vector binds to
 CC the surface of selected cells and can be internalised, i.e. it is a gene
 CC therapy targeting vector for specific cell types. It may also be used to
 CC study attachment to, and infection of, cells by HSV, while the non-native
 CC ligand-envelope protein chimeras are reagents for receptor-ligand assays
 CC and as adhesion promoters in vitro or in vivo. The new HSV vectors can
 CC deliver genes with minimal ectopic infection, particularly when the
 CC natural broad cell range of HSV is altered by deletion of native ligands.
 CC These vectors are safe and can be produced efficiently. The present
 CC sequence represents a putative binding domain of the HS ligand of the HSV
 CC gp glycoprotein. A region from this sequence can be deleted to create a
 CC modified HSV lacking its native ligand.
 XX
 XX Sequence 13 AA:
 SG
 Query Match 36.4%; Score 4; DB 20; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KKPK 6
 DB 9 KKPK 12
 I I I I
 RESULT 47
 AAB08046
 ID AAB08046 standard; Peptide: 13 AA.
 XX
 XX AAB08046;
 AC
 XX 04-DEC-2000 (first entry)
 DT
 XX Signal peptidase inhibitor peptide compound E18.
 DE
 XX Enzyme substrate: bacterial signal peptidase; Staphylococcus aureus SpsB;
 KW Escherichia coli leader peptidase; signal peptidase inhibitor;
 KW bacterial infection;
 XX Synthetic.
 QS
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "decanoyl attached to residue"
 FT Modified-site 13 /note= "hydroxy attached to residue"
 FT
 XX W0200046250-A1.
 PN
 XX 10-AUG-2000.
 PD
 XX 01-FEB-2000; 2000WO-EP00751.
 PF
 XX 03-FEB-1999; 99GB-0002399.
 PR
 XX (SMK) SMITHKLINE BEECHAM PLC.
 PA
 XX Ashman S, Black MT, Bruton G, Humphries AJ, Moore KJM;
 PI
 XX WPI: 2000-514950/46.
 DR
 XX New peptide compound used as enzyme substrates for bacterial signal
 PT peptidases in assays to detect inhibitors of the peptidases.
 PT
 XX

PS Example 18: Page 17: 36pp; English.

CC The specification describes peptide compounds, which are used as enzyme
 CC substrates for bacterial signal peptidases, in particular Staphylococcus
 CC aureus SpsB and Escherichia coli leader peptidases. They are useful in
 CC assay systems for testing for signal peptidase inhibitors. The assay is
 CC used to test for inhibition of cleavage at specified time points or the
 CC rate of cleavage. Compounds identified by the assay as inhibitors of
 CC cleavage by the peptidases may be used to treat bacterial infections.
 CC The present sequence represents a peptide compound of the invention,
 CC which is used as a signal peptidase inhibitor in the course of the
 CC invention.

XX
 XX
 XX Sequence 13 AA;

Query Match: 36.4%; Score 4; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASKK 4

DB 4 ASKK 11

RESULT 4B

AAB08047

ID AAB08047 standard; Peptide: 13 AA

XX

AC AAB08047;

XX

XX

DT 04-DEC-2000 (first entry)

DE

DE Signal peptidase inhibitor peptide compound.

XX

XX Enzyme substrate; bacterial signal peptidase; Staphylococcus aureus SpsB;

XX Escherichia coli leader peptidase; signal peptidase inhibitor;

XX bacterial infection.

XX Synthetic.

XX

XX Key Location/Qualifiers

FT Modified-site 1 /note- "decanoyl attached to residue"

FT Modified-site 11 Lys(fluorescein 5/6 carbonyl) or Lys(TAMRA);

FT Modified-site 11 /note- "biotin-X, TAMRA or fluorescein 5/6 carbonyl

FT Modified-site 13 attached"

FT Modified-site 13 /note- "hydroxyl attached to residue"

XX W0200046250-A1.

XX 10 AUG 2000.

XX

XX 01-FEB-2000: 2000MO-EP00751.

XX

XX 03-FEB-1999: 99GB-0002399.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Ashman S, Black MT, Bruton G, Humphries AJ, Moore KJM;

XX WPI: 2000-514950/46.

XX

XX New peptide compound used as enzyme substrates for bacterial signal
 XX peptidases in assays to detect inhibitors of the peptidases -

XX Example 19: Page 18: 36pp; English.

CC The specification describes peptide compounds, which are used as enzyme
 CC substrates for bacterial signal peptidases, in particular Staphylococcus
 CC aureus SpsB and Escherichia coli leader peptidases. They are useful in
 CC assay systems for testing for signal peptidase inhibitors. The assay is

CC used to test for inhibition of cleavage at specified time points or the
 CC rate of cleavage. Compounds identified by the assay as inhibitors of
 CC cleavage by the peptidases may be used to treat bacterial infections.
 CC The present sequence represents a peptide compound of the invention,
 CC which is used as a signal peptidase inhibitor in the course of the
 CC invention.

XX
 XX
 XX Sequence 13 AA;

Query Match: 36.4%; Score 4; DB 21; Length 13;
 Best Local Similarity 100.0%; Pred. No. 6.8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASKK 4

DB 8 ASKK 11

RESULT 49

AAB08048

ID AAB08048 standard; Peptide: 13 AA.

XX

AC AAB08048;

XX

XX

DT 04-DEC-2000 (first entry)

DE

DE Signal peptidase inhibitor peptide compound.

XX

XX Enzyme substrate; bacterial signal peptidase; Staphylococcus aureus SpsB;

XX Escherichia coli leader peptidase; signal peptidase inhibitor;

XX bacterial infection.

XX Synthetic.

XX

XX Key Location/Qualifiers

FT Modified-site 1 /note- "decanoyl attached to residue"

FT Modified-site 4 /note- "biotin-X or fluorescein-5/6-carbonyl attached"

FT Modified-site 11 /note- "fluorescein-5/6-carbonyl, TAMRA or biotin-X is

FT Modified-site 13 attached"

FT Modified-site 13 /note- "hydroxyl attached to residue"

XX W0200046250-A1.

XX 10 AUG 2000.

XX

XX 01-FEB-2000: 2000MO-EP00751.

XX

XX 03-FEB-1999: 99GB-0002399.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Ashman S, Black MT, Bruton G, Humphries AJ, Moore KJM;

XX WPI: 2000-514950/46.

XX

XX New peptide compound used as enzyme substrates for bacterial signal
 XX peptidases in assays to detect inhibitors of the peptidases -

XX Example 20: Page 20: 36pp; English.

CC The specification describes peptide compounds, which are used as enzyme
 CC substrates for bacterial signal peptidases, in particular Staphylococcus
 CC aureus SpsB and Escherichia coli leader peptidases. They are useful in
 CC assay systems for testing for signal peptidase inhibitors. The assay is
 CC used to test for inhibition of cleavage at specified time points or the
 CC rate of cleavage. Compounds identified by the assay as inhibitors of
 CC cleavage by the peptidases may be used to treat bacterial infections.
 CC The present sequence represents a peptide compound of the invention,
 CC which is used as a signal peptidase inhibitor in the course of the

Search completed: September 30, 2003, 10:24:32
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CC Invention.
XX
SQ Sequence 13 AA;
    Query Match 36.4%; Score 4; 18 21; Length 18;
    Best Local Similarity 100.0%; Pred. No. 6, 8+02;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASKK 4
   1111
LB 8 ASKK 11

RESULT 50
AA015448
ID AA015448 standard; Peptide: 13 AA.
XX
AC AA015448;
XX
DT 27-SEP-2002 (first entry);
XX
DE Rat C/EBP-beta peptide epitope.
XX
KW Rat; CCAAT/Enhancer binding protein; apoptosis; C/EBP-beta protein;
KW fibrosis-related disease; brain damage; myocardial infarction;
KW arteriosclerosis; ocular fibrosis; fibrotic skin condition; epitope;
KW fibrotic pulmonary disease; wound healing.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
FT Modified-site 7 /note= "Amino acid is phosphorylated"
XX
XX W0200254938-A2.
XX
XX 18-JUL-2002.
XX
XX 26-NOV-2001; 2002WO-US02393.
XX
XX 27-OCT-2000; 2000US-244018P.
XX
XX (REGD ) UNIV CALIFORNIA.
XX
XX Chajkier M. Buck M;
XX
XX WPI; 2002-566736/60.
XX
XX New modified CCAAT/Enhancer binding protein for inducing apoptosis and
XX treating a fibrosis-related disease, and a hepatic disease, brain
XX damage, myocardial infarction, or arteriosclerosis
XX
XX Example 5; Page 52; 79pp; English.
XX
XX The invention comprises modified CCAAT/Enhancer binding proteins that are
XX capable of inducing apoptosis. The invention specifically comprises
XX modified mouse, rat and human C/EBP-beta proteins. The C/EBP-beta
XX proteins of the invention are useful for inducing apoptosis in a cell or
XX tissue. The C/EBP-beta proteins are also useful for treating a fibrosis-
XX related disease, such as: brain damage; myocardial infarction;
XX arteriosclerosis; ocular fibrosis; fibrotic skin conditions; fibrotic
XX pulmonary disease; and to improve wound healing. The present amino acid
XX sequence represents an epitope of the rat C/EBP-beta protein.
XX
SQ Sequence 13 AA;
    Query Match 36.4%; Score 4; 18 21; Length 18;
    Best Local Similarity 100.0%; Pred. No. 6, 8+02;
    Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKKP 5
   1111
LB 4 SKKP 6
  
```

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AM protein - protein search, using sw mode.

Run on: September 30, 2003, 10:13:55 : Search time 21.5 Seconds
(without alignments)
77,413 Million cell updates/sec

Title: US-09-787-443-1

Perfect score: 1

Sequence: 1 ASKPKKNRIKA 11

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Procd. No. is the number of results printed. The search is done a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	11	100.0	11	15	US-10-147-954-28			Sequence 28, Appl
2	4	36.4	9	9	US-09-796-294-45			Sequence 35, Appl
3	4	36.4	9	9	US-09-796-294-54			Sequence 54, Appl
4	4	36.4	9	11	US-09-876-904A-444			Sequence 444, Appl
5	4	36.4	9	12	US-10-291-250-14			Sequence 14, Appl
6	4	36.4	9	12	US-10-348-504-91			Sequence 86, Appl
7	4	36.4	9	12	US-10-348-504-92			Sequence 109, Appl
8	4	36.4	9	12	US-10-348-504-93			Sequence 112, Appl
9	4	36.4	10	11	US-09-572-434B-124			Sequence 921, Appl
10	4	36.4	10	11	US-09-572-434B-124			Sequence 1474, Appl
11	4	36.4	10	11	US-09-572-434B-124			Sequence 2564, Appl
12	4	36.4	10	11	US-09-572-434B-124			Sequence 3221, Appl
13	4	36.4	10	11	US-09-572-434B-124			Sequence 3151, Appl
14	4	36.4	10	11	US-09-572-434B-124			Sequence 597, Appl
15	4	36.4	11	13	US-09-876-904A-597			Sequence 597, Appl

16	4	36.4	12	11	US-09-876-904A-607			Sequence 607, Appl
17	4	36.4	12	15	US-10-185-815-2			Sequence 2, Appl
18	4	36.4	13	10	US-09-897-107-60			Sequence 60, Appl
19	4	36.4	13	12	US-10-291-250-30			Sequence 30, Appl
20	4	36.4	14	11	US-09-992-665-49			Sequence 49, Appl
21	4	36.4	15	9	US-09-884-260A-2			Sequence 2, Appl
22	4	36.4	15	11	US-09-992-665-16			Sequence 16, Appl
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51	3	27.3	8	12	US-09-974-992-18			Sequence 18, Appl
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75	3	27.3	9	9	US-09-224-683-69			Sequence 69, Appl
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94	3	27.3	9	10	US-09-780-053-134	Sequence 224, App	167	3	27.3	9	12	US-10-062-109A-485	Sequence 485, App
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242	3	27.3	US-09-876-904A-573	Sequence 573, App	315	3	27.3	10	12	US-09-572-270A-674	Sequence 672, App
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245	3	27.3	US-09-572-404B-348	Sequence 348, App	318	3	27.3	10	12	US-09-572-270A-889	Sequence 889, App
246	3	27.3	US-09-572-404B-350	Sequence 350, App	319	3	27.3	10	12	US-09-572-270A-957	Sequence 957, App
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249	3	27.3	US-09-572-404B-458	Sequence 458, App	322	3	27.3	10	12	US-10-376-383-10	Sequence 10, Appl
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282	3	27.3	US-09-572-404B-4164	Sequence 4164, App	355	3	27.3	10	12	US-10-239-313A-691	Sequence 691, App
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290	3	27.3	US-09-572-404B-4164	Sequence 781, App	363	3	27.3	10	15	US-10-108-795-6	Sequence 6, Appl
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397	3	27.3	11	10	US-09-872-832-37	Sequence 37, Appl	470	3	27.3	12	11	US-09-954-385-106	Sequence 106, App
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ALIGNMENTS

RESULT 1

US-10-157-954-28

; Sequence 28, Application US/10197954

; Publication No. US20030119021A1

; GENERAL INFORMATION:

; APPLICANT: K*ster, Hubert

; APPLICANT: Siddiqui, Subaib

; APPLICANT: Little, Daniel

; TITLE OF INVENTION: Capture Compounds, Collections Thereof

; TITLE OF INVENTION: And Methods For Analyzing The Proteome And Complex

; TITLE OF INVENTION: Compositions

; FILE REFERENCE: 24743-2305

; CURRENT APPLICATION NUMBER: US/10/197,954

; PRIOR FILING DATE: 2002-07-16

; PRIOR APPLICATION NUMBER: 60/306,019

; PRIOR FILING DATE: 2001-07-16

; PRIOR APPLICATION NUMBER: 60/314,123

; PRIOR FILING DATE: 2001-08-21

; PRIOR APPLICATION NUMBER: 60/363,433

; PRIOR FILING DATE: 2002-03-11

; NUMBER OF SEQ ID NOS: 149

SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 28
? LENGTH: 11
? TYPE: PRT
? ORGANISM: Homo Sapien
US-10-197-954-28

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Best Local Similarity 100.0%; Pred. No. 28-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-09-796-294-35
? Sequence 35, Application US/03796294
? Patent No. US20020037581A1
? GENERAL INFORMATION:
? APPLICANT: Underwood, Lowell J.
? TITLE OF INVENTION: Extracellular Serine Protease
? FILE REFERENCE: D6020CIP3
? CURRENT APPLICATION NUMBER: US/09/796-294
? CURRENT FILING DATE: 2001-02-28
? PRIOR APPLICATION NUMBER: US 09/618-259
? PRIOR FILING DATE: 2000-07-18
? NUMBER OF SEQ ID NOS: 72
? SEQ ID NO 35
? LENGTH: 9
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? OTHER INFORMATION: Residues 71-79 of the IAB14 protein
US-09-796-294-35

Query Match 36.4%; Score 4; DB 9; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 KKPK 6
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DB 5 KKPK 8

RESULT 3

US-09-796-294-54
? Sequence 54, Application US/09796294
? Patent No. US20020037581A1
? GENERAL INFORMATION:
? APPLICANT: Underwood, Lowell J.
? TITLE OF INVENTION: Extracellular Serine Protease
? FILE REFERENCE: D6020CIP3
? CURRENT APPLICATION NUMBER: US/09/796-294
? CURRENT FILING DATE: 2001-02-28
? PRIOR APPLICATION NUMBER: US 09/618-259
? PRIOR FILING DATE: 2000-07-18
? NUMBER OF SEQ ID NOS: 72
? SEQ ID NO 54
? LENGTH: 9
? TYPE: PRT
? ORGANISM: Homo sapiens
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US-09-796-294-54

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Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-09-876-904A-444
? Sequence 444, Application US/09876904A
? Publication No. US20030072794A1
? GENERAL INFORMATION:
? APPLICANT: BCUKAS, TEN;
? TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
? TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
? FILE REFERENCE: TB-2002-00
? CURRENT APPLICATION NUMBER: US/09/876, 904A
? PRIOR APPLICATION NUMBER: US 60/210, 925
? PRIOR FILING DATE: 2001-06-08
? NUMBER OF SEQ ID NOS: 629
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 444
? LENGTH: 9
? TYPE: PRT
? ORGANISM: Saccharomyces cerevisiae
? FEATURE:
? OTHER INFORMATION: Yeast NPS1 transcription protein factor (1359 aa)
? OTHER INFORMATION: Involved in cell growth control at G2 phase.
US-09-876-904A-444

Query Match 36.4%; Score 4; DB 11; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 KKPK 5
||||
DB 5 KKPK 8

RESULT 5

US-10-291-250-14
? Sequence 14, Application US/10291250
? Publication No. US20030133912A1
? GENERAL INFORMATION:
? APPLICANT: University of Iowa Research Foundation
? APPLICANT: Davidson, Beverly L.
? APPLICANT: Xia, Haibin
? APPLICANT: Law, Lane K.
? TITLE OF INVENTION: RECEPTION-TARGETED ADENO VIRAL VECTORS
? FILE REFERENCE: 675,051US1
? CURRENT APPLICATION NUMBER: US/10/291,250
? CURRENT FILING DATE: 2002-11-07
? PRIOR APPLICATION NUMBER: US 60/349,282
? PRIOR FILING DATE: 2001-12-11
? NUMBER OF SEQ ID NOS: 40
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 14
? LENGTH: 9
? TYPE: PRT
? ORGANISM: Adenovirus
US-10-291-250-14

Query Match 36.4%; Score 4; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 3 KKPK 6
||||
DB 5 KKPK 7

RESULT 6

US-10-357-176-57

```

? Sequence 86, Application US/09/557175
? Publication No. US20030170707A1
? GENERAL INFORMATION:
? APPLICANT: G'Brien, Timothy J.
? TITLE OF INVENTION: Transmembrane Serine Protease and Uses Thereof
? FILE REFERENCE: D6192CIP/D/CIP
? CURRENT APPLICATION NUMBER: US/09/557,175
? PRIOR FILING DATE: 2003-02-03
? PRIOR APPLICATION NUMBER: 09/650,371
? PRIOR FILING DATE: 2000-08-28
? NUMBER OF SEQ ID NOS: 158
? SEQ ID NO 86
? LENGTH: 9
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? LOCATION: 294..304
? OTHER INFORMATION: TAG 12 peptide
US-10-357-175-86

```

```

Query Match          36.4%  Score 4;  DB 12;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 5e+05;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

QY 4 KPKR 7

DB 3 KPKR 6

RESULT 7

```

US-10-357-175-109
? Sequence 109, Application US/10/57175
? Publication No. US20030170707A1
? GENERAL INFORMATION:
? APPLICANT: G'Brien, Timothy J.
? TITLE OF INVENTION: Transmembrane Serine Protease and Uses Thereof
? FILE REFERENCE: D6192CIP/D/CIP
? CURRENT APPLICATION NUMBER: US/10/57,175
? CURRENT FILING DATE: 2003-02-03
? PRIOR FILING DATE: 2000-08-28
? NUMBER OF SEQ ID NOS: 158
? SEQ ID NO 109
? LENGTH: 9
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? LOCATION: 298..306
? OTHER INFORMATION: TAGS 12 peptide
US-10-357-175-109

```

```

Query Match          36.4%  Score 4;  DB 12;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 5e+05;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

QY 4 KPKR 7

DB 1 KPKR 4

RESULT 8

```

US-10-357-175-112
? Sequence 112, Application US/10/57175
? Publication No. US20030170707A1
? GENERAL INFORMATION:
? APPLICANT: G'Brien, Timothy J.
? TITLE OF INVENTION: Transmembrane Serine Protease and Uses Thereof
? FILE REFERENCE: D6192CIP/D/CIP
? CURRENT APPLICATION NUMBER: US/10/57,175
? CURRENT FILING DATE: 2003-02-03

```

```

? PRIOR APPLICATION NUMBER: 09/650,371
? PRIOR FILING DATE: 2000-08-28
? NUMBER OF SEQ ID NOS: 158
? SEQ ID NO 112
? LENGTH: 9
? TYPE: PRT
? ORGANISM: Homo sapiens
? FEATURE:
? LOCATION: 294..302
? OTHER INFORMATION: TAG 12 peptide
US-10-357-175-112

```

```

Query Match          36.4%  Score 4;  DB 12;  Length 9;
Best Local Similarity 100.0%;  Pred. No. 5e+05;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

```

QY 4 KPKR 7

DB 5 KPKR 8

RESULT 9

```

US-09-572-404B-921
? Sequence 921, Application US/09572404B
? Publication No. US20030078374A1
? GENERAL INFORMATION:
? APPLICANT: Proteom Ltd
? TITLE OF INVENTION: Complementary peptide ligands from the human genome
? FILE REFERENCE: Humac patent
? CURRENT APPLICATION NUMBER: US/09/572,404B
? CURRENT FILING DATE: 2000-05-17
? NUMBER OF SEQ ID NOS: 4203
? SOFTWARE: ProPatent version 1.0
? SEQ ID NO 921
? LENGTH: 10
? TYPE: PRT
? ORGANISM: Homo Sapiens
? FEATURE:
? OTHER INFORMATION: Sequence located in ADRBK1 OR GRK2 OR BARK1 OR BARK at 22-31
? OTHER INFORMATION: Interact with Sequence 922 in this patent.
US-09-572-404B-921

```

```

Query Match          36.4%  Score 4;  DB 11;  Length 10;
Best Local Similarity 100.0%;  Pred. No. 3.6e+02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Caps 0;

```

QY 1 ASKK 4

DB 7 ASKK 10

RESULT 10

```

US-09-572-404B-1478
? Sequence 1478, Application US/09572404B
? Publication No. US20030079374A1
? GENERAL INFORMATION:
? APPLICANT: Proteom Ltd
? TITLE OF INVENTION: Complementary peptide ligands from the human genome
? FILE REFERENCE: Humac patent
? CURRENT APPLICATION NUMBER: US/09/572,404B
? CURRENT FILING DATE: 2000-05-17
? NUMBER OF SEQ ID NOS: 4203
? SOFTWARE: ProPatent version 1.0
? SEQ ID NO 1478
? LENGTH: 10
? TYPE: PRT
? ORGANISM: Homo Sapiens
? FEATURE:
? OTHER INFORMATION: Sequence located in RGS13 at 50-59 and may interact with Sequ
? OTHER INFORMATION: in this patent.
US-09-572-404B-1478

```

```

Query Match          36.4%  Score 4;  DB 11;  Length 10;

```

```
Best Local Similarity 100.0%; Pred. No. 4 6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 4 KKPK 6
   1 1 1
Db 7 KKPK 10

RESULT 11
US-09-572-404B-2564
: Sequence 2564, Application US/09572404B
: Publication No. US20030078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Complementary peptide ligands from the human genome
: FILE REFERENCE: Human patent
: CURRENT APPLICATION NUMBER: US/09/572.404B
: CURRENT FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 4203
: SOFTWARE: ProPatent version 1.0
: SEQ ID NO 2564
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo Sapiens
: FEATURE:
: OTHER INFORMATION: sequence located in EMBL at 35 64 and may interact with Sequence
: OTHER INFORMATION: this patent.
US-09-572 404B-2564

Query Match 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKPK 7
   1 1 1
Db 5 KKPK 8

RESULT 12
US-09-572 404B-3121
: Sequence 3121, Application US/09572404B
: Publication No. US20030078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Complementary peptide ligands from the human genome
: FILE REFERENCE: Human patent
: CURRENT APPLICATION NUMBER: US/09/572.404B
: CURRENT FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 4203
: SOFTWARE: ProPatent version 1.0
: SEQ ID NO 3121
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo Sapiens
: FEATURE:
: OTHER INFORMATION: sequence located in GUCY2F OR GUC2F OR RETGC2 at 939 945 and may
: OTHER INFORMATION: interact with Sequence 3122 in this patent.
US-09-572 404B-3121

Query Match 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKRN 8
   1 1 1
Db 4 PKRN 7

RESULT 13
US-09-572 404B-3123
: Sequence 3123, Application US/09572404B
: Publication No. US20030078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Complementary peptide ligands from the human genome
: FILE REFERENCE: Human patent
: CURRENT APPLICATION NUMBER: US/09/572.404B
: CURRENT FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 4203
: SOFTWARE: ProPatent version 1.0
: SEQ ID NO 3123
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo Sapiens
: FEATURE:
: OTHER INFORMATION: sequence located in GUCY2F OR GUC2F OR RETGC2 at 942-951 and
: OTHER INFORMATION: interact with Sequence 3154 in this patent.
US-09-572-404B-3153

Query Match 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKRN 8
   1 1 1
Db 1 PKRN 4

RESULT 14
US-09-572-404B-3153
: Sequence 3153, Application US/09572404B
: Publication No. US20030078374A1
: GENERAL INFORMATION:
: APPLICANT: Proteom Ltd
: TITLE OF INVENTION: Complementary peptide ligands from the human genome
: FILE REFERENCE: Human patent
: CURRENT APPLICATION NUMBER: US/09/572.404B
: CURRENT FILING DATE: 2000-05-17
: NUMBER OF SEQ ID NOS: 4203
: SOFTWARE: ProPatent version 1.0
: SEQ ID NO 3153
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Homo Sapiens
: FEATURE:
: OTHER INFORMATION: sequence located in GUCY2F OR GUC2F OR RETGC2 at 942-951 and
: OTHER INFORMATION: interact with Sequence 3154 in this patent.
US-09-572-404B-3153

Query Match 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKRN 8
   1 1 1
Db 1 PKRN 4

RESULT 15
US-09-876-904A 597
: Sequence 597, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TETI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMIID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876.904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR APPLICATION NUMBER: US 60/210,925
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 597
: LENGTH: 11
```



```

: TYPE: PRT
: ORGANISM: Parachinus angulosus
: FEATURE:
: OTHER INFORMATION: Sea urchin Parachinus angulosus sperm H1 (248 aa).
US-09-876-904A-597

Query Match          36.4%; Score 4; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.2e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKKP 6
    III
Db 5 KKKP 8

RESULT 16
US-09-876-904A-607
: Sequence 607, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR APPLICATION NUMBER: US 60/210,925
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 607
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Unknown Organism
: FEATURE:
: OTHER INFORMATION: Description of Unknown Organism: Annealed sperm H1a (119 aa).
US-09-876-904A-607

Query Match          36.4%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.2e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKKP 6
    III
Db 2 KKKP 5

RESULT 17
US 10 185-815-2
: Sequence 2; Application US/10185815
: Publication No. US20030096354A1
: GENERAL INFORMATION:
: APPLICANT: Elan Corporation, plc
: APPLICANT: O'Mahony, Daniel
: APPLICANT: Lambkin, Imelda
: APPLICANT: Higgins, Lisa
: TITLE OF INVENTION: Peyer's Patch And/or M-cell Targeting Ligands
: FILE REFERENCE: E1067-20093
: CURRENT APPLICATION NUMBER: US/10/185,815
: CURRENT FILING DATE: 2002-10-09
: PRIOR APPLICATION NUMBER: 60/302,591
: PRIOR FILING DATE: 2001-07-02
: NUMBER OF SEQ ID NOS: 99
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: polypeptide ligand
US-10-185-815-2
```

```

Query Match          36.4%; Score 4; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.2e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KRNI 9
    III
Db 6 KRNI 9

RESULT 18
US-09-897-107-60
: Sequence 60, Application US/09897107
: Patent No. US20020137094A1
: GENERAL INFORMATION:
: APPLICANT: YAMAGISHI, Akihiko
: TITLE OF INVENTION: METHOD FOR IMPROVING THERMOSTABILITY OF PROTEINS, PROTEINS HA
: TITLE OF INVENTION: THERMOSTABILITY IMPROVED BY THE METHOD AND NUCLEIC ACIDS ENC
: FILE REFERENCE: 2103830S0
: CURRENT APPLICATION NUMBER: US/09/897,107
: CURRENT FILING DATE: 2001-07-03
: PRIOR APPLICATION NUMBER: JP2000-201920
: PRIOR FILING DATE: 2000-07-04
: PRIOR APPLICATION NUMBER: JP2001-164332
: PRIOR FILING DATE: 2001-05-31
: NUMBER OF SEQ ID NOS: 104
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 60
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
: OTHER INFORMATION:
US-09-897-107-60

Query Match          36.4%; Score 4; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.5e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASKK 4
    III
Db 10 ASKK 13

RESULT 19
US-10-291-250-30
: Sequence 30, Application US/10291250
: Publication No. US20030133912A1
: GENERAL INFORMATION:
: APPLICANT: University of Iowa Research Foundation
: APPLICANT: Davidson, Beverly L.
: APPLICANT: Xia, Haibin
: APPLICANT: Law, Lane K.
: TITLE OF INVENTION: RECEPTOR TARGETED ADENO VIRAL VECTORS
: FILE REFERENCE: 875 0510S1
: CURRENT APPLICATION NUMBER: US/10/291,250
: CURRENT FILING DATE: 2002-11-07
: PRIOR APPLICATION NUMBER: US 60/339,282
: PRIOR FILING DATE: 2001-12-11
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 30
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: A protein motif.
US-10-291-250-30

Query Match          36.4%; Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.5e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKKP 6
    III
Db 7 KKKP 10
```

RESULT 20
 US-09-992-665-49
 ? Sequence 49, Application US/09992665
 ? Publication No. US20030092009A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Kaia Palm
 ? TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
 ? TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
 ? FILE REFERENCE: CEMINES.002A
 ? CURRENT APPLICATION NUMBER: US/09/992-665
 ? PRIOR FILING DATE: 2001-11-13
 ? PRIOR APPLICATION NUMBER: 60/249,508
 ? PRIOR FILING DATE: 2000-11-16
 ? NUMBER OF SEQ ID NOS: 380
 ? SOFTWARE: FastSeq for Windows Version 4.0
 ? SEQ ID NO 49
 ? LENGTH: 14
 ? TYPE: PRT
 ? ORGANISM: Artificial Sequence
 ? FEATURE:
 ? OTHER INFORMATION: Probe
 US-09-992-665-49

Query Match 36.4%; Score 4; DB 11; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KKPK 6
 DB 11 KKPK 14

RESULT 21
 US-09-884-260A-2
 ? Sequence 2, Application US/09884260A
 ? Patent No. US20020098570A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Alan Brash
 ? APPLICANT: Nathalie Tiljet
 ? TITLE OF INVENTION: MUSKELON (CUCUMIS MELD) HYDROPEROXIDE
 ? TITLE OF INVENTION: LYSASE AND USES THEREOF
 ? FILE REFERENCE: 06027.000202
 ? CURRENT APPLICATION NUMBER: US/09/884-260A
 ? PRIOR FILING DATE: 2001-06-19
 ? PRIOR APPLICATION NUMBER: C9/537,557
 ? PRIOR FILING DATE: 2000-03-29
 ? NUMBER OF SEQ ID NOS: 56
 ? SOFTWARE: FastSeq for Windows Version 4.0
 ? SEQ ID NO 2
 ? LENGTH: 15
 ? TYPE: PRT
 ? ORGANISM: Cucumis melo
 US-09-884-260A-2

Query Match 36.4%; Score 4; DB 9; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 KRNI 9
 DB 10 KRNI 13

RESULT 22
 US-09-992-665-16
 ? Sequence 16, Application US/09992665
 ? Publication No. US20030092009A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Kaia Palm
 ? TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
 ? TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE

? FILE REFERENCE: CEMINES.002A
 ? CURRENT APPLICATION NUMBER: US/09/992-665
 ? CURRENT FILING DATE: 2001-11-13
 ? PRIOR APPLICATION NUMBER: 60/249,508
 ? PRIOR FILING DATE: 2000-11-16
 ? NUMBER OF SEQ ID NOS: 380
 ? SOFTWARE: FastSeq for Windows Version 4.0
 ? SEQ ID NO 16
 ? LENGTH: 15
 ? TYPE: PRT
 ? ORGANISM: Artificial Sequence
 ? FEATURE:
 ? OTHER INFORMATION: Probe
 US-09-992-665-16

Query Match 36.4%; Score 4; DB 11; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPKR 7
 DB 2 KPKR 5

RESULT 23
 US-10-229-567-17
 ? Sequence 17, Application US/10229567
 ? Publication No. US20030092080A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Braum, Jonathan
 ? APPLICANT: Chahy, Offer
 ? TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
 ? ulcerative Colitis, and Clinical Subtypes Thereof, Usin
 ? Microbial UC PANCA antigens
 ? NUMBER OF SEQUENCES: 41
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Campbell & Flores LLP
 ? STREET: 4370 La Jolla Village Drive, Suite 700
 ? CITY: San Diego
 ? STATE: California
 ? COUNTRY: USA
 ? ZIP: 92122
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Floppy disk
 ? COMPUTER: IBM PC compatible
 ? OPERATING SYSTEM: PC-DOS/MS-DOS
 ? SOFTWARE: PatentIn Release #1.0, Version #1.25
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/10/229,567
 ? FILING DATE: 27-Aug-2002
 ? CLASSIFICATION: <Unknown>
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/417,264
 ? FILING DATE: <Unknown>
 ? APPLICATION NUMBER: US 09/041,889
 ? FILING DATE: <Unknown>
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Campbell, Cathryn A.
 ? REGISTRATION NUMBER: 31,815
 ? REFERENCE/DOCKET NUMBER: P-PM 3006
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (619) 535-9001
 ? TELEFAX: (619) 535-8949
 ? INFORMATION FOR SEQ ID NO: 17:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 15 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 US-10-229-567-17

Query Match 36.4%; Score 4; DB 15; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5e+02;

```

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 3 KKKK 6
   11 1
DB 12 KKKK 15

RESULT 24
US-10-229-567-18
? Sequence 18, Application US/10229567
? Publication No. US20030092080A1
? GENERAL INFORMATION:
? APPLICANT: Braun, Jonathan;
? Cohavy, Giff
? TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
? Ulcerative Colitis, and Related Subtypes Thereof, Using
? Microbial or PANCA antigens
? NUMBER OF SEQUENCES: 41
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Campbell & Flores LLP
? STREET: 4370 La Jolla Village Drive, Suite 700
? CITY: San Diego
? STATE: California
? COUNTRY: USA
? ZIP: 92122
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/10/229,567
? FILING DATE: 27 Aug-2002
? CLASSIFICATION: <unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/09/417,264
? FILING DATE: <unknown>
? APPLICATION NUMBER: US/04/1,499
? FILING DATE: <unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Campbell, Cathryn A.
? REGISTRATION NUMBER: 31,810
? REFERENCE/DOCKET NUMBER: P 1M 400
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (619) 545-9001
? TELEFAX: (619) 545-8949
? INFORMATION FOR SEQ ID NO: 18:
? SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-229-567-18

Query Match 36.4%; Score 4; DR 15; Length 152
Best Local Similarity 100.0%; Pred. No. Gaps 0;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 3 KKKK 6
   11 1
DB 12 KKKK 15

RESULT 25
US-08-817-832B-9
? Sequence 9, Application US/08817832B
? Publication No. US20030104516A1
? GENERAL INFORMATION:
? APPLICANT: MANDELKOW, Eckhard, et al.
? TITLE OF INVENTION: NO. US20030104516A1 Protein Kinase (NPK-110)
? NUMBER OF SEQUENCES: 32
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
? STREET: 233 S. Wacker Drive, 6300 Sears Tower
? CITY: Chicago
? STATE: Illinois
? COUNTRY: US
? ZIP: 60606-6402
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/817,832B
? FILING DATE: 28-APR-1997
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: WO PCT/EP95/04258
? FILING DATE: 30-OCT-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: EP 94 11 7122.5
? FILING DATE: 26-OCT-1994
? INFORMATION FOR SEQ ID NO: 14:
? SEQUENCE CHARACTERISTICS:

```

```

? STREET: 233 S. Wacker Drive, 6300 Sears Tower
? CITY: Chicago
? STATE: Illinois
? COUNTRY: US
? ZIP: 60606-6402
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/817,832B
? FILING DATE: 28-APR-1997
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: WO PCT/EP95/04258
? FILING DATE: 30-OCT-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: EP 94 11 7122.5
? FILING DATE: 28-OCT-1994
? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 8 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? FEATURES:
? NAME/KEY: Peptide
? LOCATION:
? OTHER INFORMATION: /note- "Ser at position 3 is
? OTHER INFORMATION: phosphorylated."
US-08-817-832B-9

Query Match 27.4%; Score 3; DR 8; Length 8;
Best Local Similarity 100.0%; Pred. No. Gaps 0;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 8 NIK 15
   11
DB 6 NIK 8

RESULT 26
US-08-817-832B-14
? Sequence 14, Application US/08817832B
? Publication No. US20030104516A1
? GENERAL INFORMATION:
? APPLICANT: MANDELKOW, Eckhard, et al.
? TITLE OF INVENTION: NO. US20030104516A1 Protein Kinase (NPK-110)
? NUMBER OF SEQUENCES: 32
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
? STREET: 233 S. Wacker Drive, 6300 Sears Tower
? CITY: Chicago
? STATE: Illinois
? COUNTRY: US
? ZIP: 60606-6402
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/817,832B
? FILING DATE: 28-APR-1997
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: WO PCT/EP95/04258
? FILING DATE: 30-OCT-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: EP 94 11 7122.5
? FILING DATE: 26-OCT-1994
? INFORMATION FOR SEQ ID NO: 14:
? SEQUENCE CHARACTERISTICS:

```

? LENGTH: 8 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: peptide
? FEATURE:
? NAME/KEY: Peptide
? LOCATION: 3
? OTHER INFORMATION: /note "Ser at position 3 is
? OTHER INFORMATION: phosphorylated."
US-08-817-832B-14

Query Match: 27.3%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NIK 10
DB 5 NIK 8

RESULT 27
US-09-879-936-19
? Sequence 19, Application US/09879536
? Patent No. US20020045564A1
? GENERAL INFORMATION:
? APPLICANT: Van Eyk, Jennifer E.
? APPLICANT: Mak, Alan S.
? TITLE OF INVENTION: Methods of Modulating Muscle Contraction
? FILE REFERENCE: 1997-021-03US
? CURRENT APPLICATION NUMBER: US/09/879,936
? CURRENT FILING DATE: 2001-06-14
? PRIOR APPLICATION NUMBER: 60/050,474
? PRIOR FILING DATE: 1997-06-23
? PRIOR APPLICATION NUMBER: 60/089,505
? PRIOR FILING DATE: 1998-06-16
? NUMBER OF SEQ ID NOS: 26
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 19
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Unknown
? FEATURE:
? NAME/KEY: PEPTIDE
? LOCATION: (1)-(8)
? OTHER INFORMATION: Site C (catalytic site) and phosphorylation site
? OTHER INFORMATION: PKA1
US-09-879-936-19

Query Match: 27.3%; Score 3; DB 9; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
DB 4 PKR 6

RESULT 28
US-09-854-799-48
? Sequence 48, Application US/09854799
? Patent No. US2002015064A1
? GENERAL INFORMATION:
? APPLICANT: SmithKline Beecham, Corporation
? TITLE OF INVENTION: Recombinant Feline Coronavirus S
? PROTEIN
? NUMBER OF SEQUENCES: 54
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: SmithKline Beecham Corporation
? STREET: 709 Swedeland Road
? CITY: King of Prussia
? STATE: PA

? COUNTRY: USA
? ZIP: 19406-2799
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/854,799
? FILING DATE: 14-May-2001
? CLASSIFICATION: <Unknown>
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/392,459
? FILING DATE: <Unknown>
? APPLICATION NUMBER: US 07/613,066
? FILING DATE: 14-NOV-1990
? ATTORNEY/AGENT INFORMATION:
? NAME: King, William T.
? REGISTRATION NUMBER: 30,954
? REFERENCE/DOCKET NUMBER: SBC 14532B
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (215) 270-5015
? TELEFAX: (215) 270-5090
? INFORMATION FOR SEQ ID NO: 48:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 8 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-854-799-48

Query Match: 27.3%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RNI 9
DB 2 RNI 4

RESULT 29
US-09-984-056-34
? Sequence 34, Application US/09984056
? Patent No. US20020120106A1
? GENERAL INFORMATION:
? APPLICANT: BOGUCH, SAMUEL
? TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICONS AND METHODS OF USE
? FILE REFERENCE: 09425-459C3
? CURRENT APPLICATION NUMBER: US/09/984,056
? CURRENT FILING DATE: 2001-10-26
? PRIOR APPLICATION NUMBER: 60/303,396
? PRIOR FILING DATE: 2001-07-09
? PRIOR APPLICATION NUMBER: 60/278,761
? PRIOR FILING DATE: 2001-03-27
? PRIOR APPLICATION NUMBER: 09/146,755
? PRIOR FILING DATE: 1998-09-04
? PRIOR APPLICATION NUMBER: 09/87,144
? PRIOR FILING DATE: 2001-03-27
? PRIOR APPLICATION NUMBER: 08/198,139
? PRIOR FILING DATE: 1994-02-17
? NUMBER OF SEQ ID NOS: 103
? SOFTWARE: PatentIn 2.1
? SEQ ID NO 34
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Caldothra prolifera
US-09-984-056-34

Query Match: 27.3%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASK 3
1 1
DB 2 ASK 4

RESULT 40

US-09-984-056-79
Sequence 79, Application US/09984056
Patent No. US20020120166A1
GENERAL INFORMATION:
APPLICANT: BOGUCH, ELEMORE S.
TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICINS AND METHODS OF USE
FILE REFERENCE: 09425-46903
CURRENT APPLICATION NUMBER: US/09/984,056
PRIOR FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 60/303,396
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/278,761
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 09/146,755
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 09/817,144
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 08/198,139
PRIOR FILING DATE: 1994-02-17
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn 2.1
SEQ ID NO 79
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-09-984-056-79

Query Match: 27.3%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
1 1
DB 2 KKP 4

RESULT 31

US-09-984-057-44
Sequence 34, Application US/09984057
Patent No. US20020151677A1
GENERAL INFORMATION:
APPLICANT: BOGUCH, ELEMORE S.
TITLE OF INVENTION: REPLICINS AND METHODS OF IDENTIFYING
FILE REFERENCE: 09425-46902
CURRENT APPLICATION NUMBER: US/09/984,057
PRIOR FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 60/303,396
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/278,761
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 09/146,755
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 09/817,144
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 08/198,139
PRIOR FILING DATE: 1994-02-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn 2.1
SEQ ID NO 34
LENGTH: 8
TYPE: PRT
ORGANISM: Calophora prolifera
US-09-984-057-44

Query Match: 27.3%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASK 3
1 1
DB 2 ASK 4

RESULT 32

US-09-984-057-79
Sequence 79, Application US/09984057
Patent No. US20020151677A1
GENERAL INFORMATION:
APPLICANT: BOGUCH, ELEMORE S.
TITLE OF INVENTION: REPLICINS AND METHODS OF IDENTIFYING
FILE REFERENCE: 09425-46902
CURRENT APPLICATION NUMBER: US/09/984,057
PRIOR FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 60/303,396
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/278,761
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 09/146,755
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 09/817,144
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 08/198,139
PRIOR FILING DATE: 1994-02-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn 2.1
SEQ ID NO 79
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-09-984-057-79

Query Match: 27.3%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
1 1
DB 2 KKP 4

RESULT 33

US-09-938-497-6
Sequence 6, Application US/09938497
Patent No. US20020173462A1
GENERAL INFORMATION:
APPLICANT: WASTFALL, Maria K. Boden
TITLE OF INVENTION: FIBRINOGEN BINDING PROTEIN
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/938,497
FILING DATE: 27-Aug-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/276,141
FILING DATE: <Unknown>
APPLICATION NUMBER: SE 9302955-1
FILING DATE: 13-SEP-1993
APPLICATION NUMBER: WO PCT/SE93/30759
FILING DATE: 20-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,400
REFERENCE/DOCKET NUMBER: 012859-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-948-497-6

Query Match 27.3% Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
DB 5 KKP 7

RESULT 34

US-09-726-470A-69
Sequence 69, Application US/09726470A
Publication No. US20030036628A1
GENERAL INFORMATION:
APPLICANT: Zheleva, Dantella I
APPLICANT: Fischer, Peter M
APPLICANT: McInnes, Campbell
APPLICANT: Andrews, Martin JI
APPLICANT: Chan, Weng C
APPLICANT: Atkinson, Gail E
TITLE OF INVENTION: p21 Peptides
FILE REFERENCE: CCI-014
CURRENT APPLICATION NUMBER: US/09/726,470A
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: GB 9928344.6
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 275
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 69
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: p21 derived
OTHER INFORMATION: Synthesised with free amino terminus and as the C-terminal carboxamide
US-09-726-470A-69

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KRN 8
DB 3 KRN 5

RESULT 35
US-09-876-904A-57
Sequence 57, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002-00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 57
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Chicken Ets1
OTHER INFORMATION: core NLS peptide
US-09-876-904A-57

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6
DB 6 KPK 8

RESULT 36

US-09-876-904A-84
Sequence 84, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002-00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 84
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Putative core
OTHER INFORMATION: NLS of yeast TRM1
US-09-876-904A-84

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKK 4
DB 3 SKK 5

RESULT 37

US-09-876-904A-203
Sequence 203, Application US/09876904A
Publication No. US20030072794A1

GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 203
LENGTH: 8
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
FEATURE:
OTHER INFORMATION: Karyophilic peptide
US-09-876-904A-203

Query Match 27.3% Score 3; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
III
DB 2 PKR 4

RESULT 38

US-09-876-904A-258
Sequence 258, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 258
LENGTH: 8
TYPE: PRT
ORGANISM: Bos sp.
FEATURE:
OTHER INFORMATION: Calf thymus HMC 1
US-09-876-904A-258

Query Match 27.3% Score 3; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
III
DB 2 KKP 4

RESULT 39

US-09-876-904A-266
Sequence 266, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A

GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 266
LENGTH: 8
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Redox factor 1 from HeLa cell
US-09-876-904A-266

Query Match 27.3% Score 3; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
III
DB 2 PKR 4

RESULT 40

US-09-876-904A-267
Sequence 267, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 267
LENGTH: 8
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Apurinic/apurimidinic
US-09-876-904A-267

Query Match 27.3% Score 3; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
III
DB 2 PKR 4

RESULT 41

US-09-876-904A-405
Sequence 405, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 405

LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Human TFIIIE beta (general transcription initiation
OTHER INFORMATION: protein factor; forms tetramer; alpha 2 beta 2 with
OTHER INFORMATION: TFIIIE-alpha)
US-09-876-904A-405

Query Match 27.5% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKK 4
III
DB 1 SKK 3

RESULT 42
US-09-876-904A-438
Sequence 438, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 438
LENGTH: 8
TYPE: PRT
ORGANISM: Caenorhabditis elegans
FEATURE:
OTHER INFORMATION: C. elegans sex determining Hra-1 protein.

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
III
DB 2 KKP 4

RESULT 43
US-09-876-904A-536
Sequence 536, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 536
LENGTH: 8
TYPE: PRT
ORGANISM: Xenopus laevis
FEATURE:
OTHER INFORMATION: Xenopus laevis L1 ribosomal protein (homologous to

OTHER INFORMATION: yeast L2).

US-09-876-904A-536

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
III
DB 6 KKP 8

RESULT 44
US-09-876-904A-537
Sequence 537, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 537
LENGTH: 8
TYPE: PRT
ORGANISM: Xenopus laevis
FEATURE:
OTHER INFORMATION: Xenopus laevis L1 ribosomal protein (homologous to
OTHER INFORMATION: yeast L2).

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
III
DB 6 KKP 8

RESULT 45
US-09-876-904A-576
Sequence 576, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 576
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Human H2B variant differentially expressed during
OTHER INFORMATION: the cell cycle.

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 2 SKK 4
111
DB 5 SKK 7

RESULT 46
US-09-876-904A-584
Sequence 584, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 584
LENGTH: 8
TYPE: PRT
ORGANISM: Bos sp.
FEATURE:
OTHER INFORMATION: Calf thymus h2H (125 aa).
US-09-876-904A-584

Query Match: 27.3%, Score 4; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 2 SKK 4
111
DB 5 SKK 7

RESULT 47
US-09-876-904A-599
Sequence 599, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 599
LENGTH: 8
TYPE: PRT
ORGANISM: Parechinus angulosus
FEATURE:
OTHER INFORMATION: Sea urchin Parechinus angulosus sperm H1 (248 aa).
US-09-876-904A-599

Query Match: 27.3%, Score 4; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 3 KKP 5
111
DB 4 KKP 8

RESULT 48
US-09-876-904A-613
Sequence 613, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 613
LENGTH: 8
TYPE: PRT
ORGANISM: Bos sp.
FEATURE:
OTHER INFORMATION: Calf thymus HMG 1 (259 aa).
US-09-876-904A-613

Query Match: 27.3%, Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 3 KKP 5
111
DB 2 KKP 4

RESULT 49
US-09-827-542-12
Sequence 12, Application US/09827542
Publication No. US20030088057A1
GENERAL INFORMATION:
APPLICANT: Traugh, Colinda A.
TITLE OF INVENTION: Peptide Substrates Phosphorylated By P21-Activated
TITLE OF INVENTION: Protein Kinase
FILE REFERENCE: JC Case No. US20030088057A1 1999-035-2/Traugh et al.
CURRENT APPLICATION NUMBER: US/09/827,542
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 09/290,964
PRIOR FILING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 8
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-827-542-12

Query Match: 27.3%, Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 5 PKR 7
111
DB 2 PKR 4

RESULT 50
US-09-791-524-149
Sequence 149, Application US/09791524
Publication No. US2003014209A1
GENERAL INFORMATION:
APPLICANT: Aventis Pharmaceuticals Inc.

TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery of Heterologous Genes

FILE REFERENCE: A3319A
CURRENT APPLICATION NUMBER: US/99/791,524
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/09825
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn version 3.0
SEQ ID NO 149
LENGTH: 8
TYPE: PRT
ORGANISM: Adenovirus
US-09-791-524 149

Query Match 27.3% Score 41 DB 127 Ident 81
Best Local Similarity 100.0% Pval. No. 5e-051
Matches 3: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

QY 5 PKR 7
db 1 PKR 3

Search completed: September 30, 2003, 16:42:47
Job time : 27.5 secs

GenCore version 5.1.6
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OM protein protein search, using sw model

Run on: September 30, 2003, 10:07:04 : Search time 11.333 Seconds
(without alignments)
93.140 Million cell updates/sec

Title: US-09-787-443-1

Perfect score: 11

Sequence: 1 ASKKPRNIKA 11

Scoring table: 0L1G0
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96166682 residues

Word size : 6

Total number of hits satisfying chosen parameters: 2064

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : PIR 76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	27.3	8	2	S4565: probable Na ⁺ trans
2	3	27.3	9	2	J56402: xenopsin-related p
3	3	27.3	9	2	A63320: xenopsin-related p
4	3	27.3	10	2	S76722: 65.4K GTP-binding
5	3	27.3	10	2	F41835: ribosomal protein
6	3	27.3	10	2	PA0116: ferredoxin-NA ⁺ re
7	3	27.3	10	2	PS0220: ferredoxin-NA ⁺ re
8	3	27.3	11	2	S42449: anti protein - pha
9	4	27.3	11	2	B41835: translation c:enga
10	3	27.3	11	2	S19775: wound-induced prot
11	3	27.3	13	2	T08533: hypothetical prote
12	3	27.3	13	2	S22955: hypothetical prote
13	3	27.3	13	2	JQ1350: hypothetical prote
14	3	27.3	13	2	E50396: antiqer 7H8/2 - ma
15	3	27.3	13	2	S52456: hypothetical prote
16	3	27.3	14	2	H64008: hypothetical prote
17	3	27.3	14	2	PA0013: photosystem II oxy
18	3	27.3	14	2	S33803: chaperone, Tcpl-re
19	3	27.3	14	2	H83778: hypothetical prote
20	3	27.3	14	2	A54370: inorganic diphosph
21	3	27.3	15	2	S36889: ribosomal protein
22	3	27.3	15	2	T09463: ribosomal protein
23	3	27.3	15	2	PA0046: protein QA10044 -
24	3	27.3	15	2	PT0082: protein QA60023 -
25	3	27.3	15	2	S71300: ICL3 protein - Par
26	3	27.3	15	2	S77987: cytochrome-c oxida
27	3	27.3	15	2	S03955: acidic fibroblast
28	3	27.3	15	2	PX0031: mixed lymphocyte r
29	2	18.2	8	1	LF5AME: probable msrA lead

30	2	18.2	8	2	A31570: angiotensin-conver
31	2	18.2	8	2	S70727: ipgf protein - Shi
32	2	18.2	8	2	A39308: glycine reductase
33	2	18.2	8	2	T10952: hypothetical prote
34	2	18.2	8	2	S21288: lectin - potato (f
35	2	18.2	8	2	A39892: P element, P cytot
36	2	18.2	8	2	A14683: aspartate transami
37	2	18.2	8	2	A28719: thymic humoral fac
38	2	18.2	8	2	A54823: olfactory receptor
39	2	18.2	8	2	PT0595: T-cell receptor be
40	2	18.2	8	2	PT0827: T-cell receptor be
41	2	18.2	8	2	PT0530: T-cell receptor be
42	2	18.2	8	2	PT0527: T-cell receptor be
43	2	18.2	8	2	PT0522: T-cell receptor be
44	2	18.2	8	2	PT0509: T-cell receptor be
45	2	18.2	8	2	PT0639: T-cell receptor be
46	2	18.2	8	2	PT0631: T-cell receptor be
47	2	18.2	8	2	PT0613: T-cell receptor be
48	2	18.2	8	2	PT0653: T-cell receptor be
49	2	18.2	8	2	PT0547: T-cell receptor be
50	2	18.2	8	2	PT0557: T-cell receptor be
51	2	18.2	8	2	PT0559: T-cell receptor be
52	2	18.2	8	2	PT0554: T-cell receptor be
53	2	18.2	8	2	PT0716: T-cell receptor be
54	2	18.2	8	2	PT0724: T-cell receptor be
55	2	18.2	8	2	PT0725: T-cell receptor be
56	2	18.2	8	2	PT0588: T-cell receptor be
57	2	18.2	8	2	PT0691: T-cell receptor be
58	2	18.2	8	2	A38887: T-cell receptor ga
59	2	18.2	8	2	I48935: apolipoprotein A1
60	2	18.2	8	2	B54823: olfactory receptor
61	2	18.2	8	2	A42889: major postsynaptic
62	2	18.2	8	2	PH0934: T-cell receptor be
63	2	18.2	8	2	I57532: gene Tn150w prote
64	2	18.2	8	4	S66296: Na ⁺ -transporting A
65	2	18.2	8	4	I54017: granulocyte-colony
66	2	18.2	9	2	B28495: conopressin S - co
67	2	18.2	9	2	A28495: conopressin G - co
68	2	18.2	9	2	S35538: ribosomal protein
69	2	18.2	9	2	S30494: cat gene leader pe
70	2	18.2	9	2	B24362: chloramphenicol O-
71	2	18.2	9	2	JQ1202: leader peptide - p
72	2	18.2	9	2	QDRB: delta sleep-induci
73	2	18.2	9	2	C36730: hutU protein - Kle
74	2	18.2	9	2	S19523: orf AB protein - S
75	2	18.2	9	2	JP0073: ribosomal protein
76	2	18.2	9	2	C41170: photosystem II pro
77	2	18.2	9	2	PC2021: oxytocin-related p
78	2	18.2	9	2	D41978: calliFERFamide 4 -
79	2	18.2	9	2	F41978: calliFERFamide 6 -
80	2	18.2	9	2	S10920: venom protein HR-3
81	2	18.2	9	2	A45199: L-lysophorin - Ja
82	2	18.2	9	2	A60356: 118K stomach cance
83	2	18.2	9	2	I54379: gene NF2 protein -
84	2	18.2	9	2	PC2197: zymogen granule me
85	2	18.2	9	2	S66636: alpha-2-macroglobu
86	2	18.2	9	2	B46250: alpha-actinin - bo
87	2	18.2	9	2	PC7076: spectrin alpha cha
88	2	18.2	9	2	PT0670: T-cell receptor be
89	2	18.2	9	2	PT0634: T-cell receptor be
90	2	18.2	9	2	PT0562: T-cell receptor be
91	2	18.2	9	2	PC7078: unidentified 48.7K
92	2	18.2	9	2	I49406: bone gla protein -
93	2	18.2	9	2	PH0943: T-cell receptor be
94	2	18.2	9	2	PH0935: T-cell receptor be
95	2	18.2	9	2	PH0937: T-cell receptor be
96	2	18.2	9	2	PH0902: T-cell receptor be
97	2	18.2	9	2	PH0917: T-cell receptor be
98	2	18.2	9	2	PH0918: T-cell receptor be
99	2	18.2	9	2	PH0921: T-cell receptor be
100	2	18.2	9	2	S78426: 52.5K protein - sp
101	2	18.2	9	2	S56004: glucan 1,3-beta-gl
102	2	18.2	9	2	S39040: lysine-conopressin

103	2	18.2	9	2	PC7073	ab:guano-rytochro	176	11	2	523308	substance p - rain
104	2	18.2	10	1	XASNR3	andiotensis-conver	177	11	2	523306	ranatachykinin A -
105	2	18.2	10	1	RHLMG5	gonadoliberin - se	178	11	2	A61033	ranatachykinin D -
106	2	18.2	10	2	A45491	C3 homolag HX - in	179	11	2	D61033	hypothetical prote
107	2	18.2	10	2	S10526	inhibin beta A cha	180	11	2	QJ0395	beta-glucosidase (
108	2	18.2	10	2	A60410	beta-neoenderphin	181	11	2	P00231	quinoline 2-oxidor
109	2	18.2	10	2	I36834	apolipoprotein A1	182	11	2	S66606	celf protein - Esc
110	2	18.2	10	2	H37110	ornithine decarbox	183	11	2	S42587	acetoactate synth
111	2	18.2	10	2	S39030	lysi-Bradykinin -	184	11	2	S33782	58K heat shock pro
112	2	18.2	10	2	C61033	ranatachykinin C -	185	11	2	PC2172	probable secreted
113	2	18.2	10	2	B33143	proemadin - human	186	11	2	S33519	protein QA300023 -
114	2	18.2	10	2	A33143	proemadin - rat	187	11	2	PT0081	seed protein ws-23
115	2	18.2	10	2	A21617	ecdysteroid UDPglu	188	11	2	G61497	ribosomal protein
116	2	18.2	10	2	S51912	hemagglutinin - in	189	11	2	PC4267	unidentified 5.7/3
117	2	18.2	10	2	G58501	48K Elle/gallblad	190	11	2	P00731	DNA-binding protei
118	2	18.2	10	2	A24407	amicydin - Paraco	191	11	2	A34135	probable substance
119	2	18.2	10	2	S66458	ferredoxin - Rhizo	192	11	2	S33300	talin - chicken (f
120	2	18.2	10	2	S59625	beta-galactosidase	193	11	2	D42965	Rhesus blood group
121	2	18.2	10	2	PC4442	cytochrome c553 -	194	11	2	I54193	T cell receptor V-
122	2	18.2	10	2	S70251	nitrogenase (EC 1.	195	11	2	S57575	T cell receptor V-
123	2	18.2	10	2	S42282	parasporal crystal	196	11	2	S68637	acetylcholinestera
124	2	18.2	10	2	F44644	neurotoxin-associi	197	11	2	S78765	ribosomal protein
125	2	18.2	10	2	JF6072	ribosomal protein	198	11	2	S54347	tubulin beta chain
126	2	18.2	10	2	C39745	sphingomyelinase -	199	11	2	PN0044	protein kinase C 1
127	2	18.2	10	2	PC2044	beta Kirilowin - M	200	11	2	PT0217	T-cell receptor be
128	2	18.2	10	2	PA0050	protegin CA100052 -	201	11	2	C38887	T-cell receptor ga
129	2	18.2	10	2	A59272	peptide-M4 (N-acet	202	11	2	I41946	T-cell receptor ga
130	2	18.2	10	2	H28027	protein p11 - curl	203	11	2	PD0441	translatation elonga
131	2	18.2	10	2	A20489	transcription fact	204	11	2	S65377	cytochrome-c oxida
132	2	18.2	10	2	A59187	gonadotropin-relea	205	11	2	S78422	ribosomal protein
133	2	18.2	10	2	S77580	cytochrome-c oxida	206	11	2	PH0939	T-cell receptor be
134	2	18.2	10	2	H37196	bradykinin-potenti	207	11	2	PH0940	T-cell receptor be
135	2	18.2	10	2	B45482	platelet activatin	208	11	2	PH0941	T-cell receptor be
136	2	18.2	10	2	S23371	T-cell receptor al	209	11	2	PH0929	T-cell receptor be
137	2	18.2	10	2	F49031	T-cell receptor ga	210	11	2	PH0891	T-cell receptor be
138	2	18.2	10	2	S71948	matrix metalloprote	211	11	2	PH0938	T-cell receptor be
139	2	18.2	10	2	C54823	olfactory receptor	212	11	2	PH0947	T-cell receptor be
140	2	18.2	10	2	PT0632	T-cell receptor be	213	11	2	PH0903	T-cell receptor be
141	2	18.2	10	2	PT0664	T-cell receptor be	214	11	2	PH0904	T-cell receptor be
142	2	18.2	10	2	PT0215	T-cell receptor be	215	11	2	PH0924	T-cell receptor be
143	2	18.2	10	2	B38887	T-cell receptor ga	216	11	2	PH0919	T-cell receptor be
144	2	18.2	10	2	D54823	olfactory receptor	217	11	2	PH0914	T-cell receptor be
145	2	18.2	10	2	S65187	cytochrome-c oxida	218	11	2	PH0922	T-cell receptor be
146	2	18.2	10	2	PK0750	lysosome-associate	219	11	2	PH0906	T-cell receptor be
147	2	18.2	10	2	C10572	T-cell receptor be	220	11	2	A61575	Trimeresurus serin
148	2	18.2	10	2	PH0540	T cell receptor be	221	11	2	S60294	tubulin 2 beta-3 c
149	2	18.2	10	2	PH0942	T cell receptor be	222	11	4	PC2390	trichorozin I - fu
150	2	18.2	10	2	PH0944	T cell receptor be	223	11	4	PC2392	trichorozin III -
151	2	18.2	10	2	PH0933	T-cell receptor be	224	11	4	S52252	hypothetical prote
152	2	18.2	10	2	PH0894	T-cell receptor be	225	11	4	I54081	retinoic acid rece
153	2	18.2	10	2	PH0941	T-cell receptor be	226	11	2	C49215	urease (EC 3.5.1.5
154	2	18.2	10	2	PH0925	T-cell receptor be	227	12	2	A28856	fructose-bisphosph
155	2	18.2	10	2	PH0926	T-cell receptor be	228	12	2	C36201	1-aminocyclopropan
156	2	18.2	10	2	PH0916	T-cell receptor be	229	12	2	S25485	transcription fact
157	2	18.2	10	2	PH0923	T-cell receptor be	230	12	2	S26541	T-cell receptor be
158	2	18.2	10	2	PH0895	T-cell receptor be	231	12	2	S26557	T-cell receptor be
159	2	18.2	10	2	PH0948	T-cell receptor be	232	12	2	S26546	T-cell receptor be
160	2	18.2	10	2	C54226	light-harvesting p	233	12	2	S26547	T-cell receptor be
161	2	18.2	10	1	XASNBA	bradykinin-potenti	234	12	2	S26555	T-cell receptor be
162	2	18.2	11	1	SPH03	substance p - hors	235	12	2	S26556	T-cell receptor be
163	2	18.2	11	1	EA0CC	eledoisin - curled	236	12	2	S26553	T-cell receptor be
164	2	18.2	11	1	A60654	substance p - guin	237	12	2	S26558	T-cell receptor be
165	2	18.2	11	1	EXOC	eledoisin - musky	238	12	2	S26552	T-cell receptor be
166	2	18.2	11	2	S32575	ribosomal protein	239	12	2	S26549	T-cell receptor be
167	2	18.2	11	2	A38841	rhodopsin homolog	240	12	2	S26559	T-cell receptor be
168	2	18.2	11	2	C53652	rhIR protein - pse	241	12	2	S26548	T-cell receptor be
169	2	18.2	11	2	A25930	ermC leader peptid	242	12	2	S26554	T-cell receptor be
170	2	18.2	11	2	YHR1	morphogenetic neur	243	12	2	S26544	T-cell receptor be
171	2	18.2	11	2	YHHU	morphogenetic neur	244	12	2	S65409	histone H2B - huma
172	2	18.2	11	2	YHBO	morphogenetic neur	245	12	2	S10122	translatation elonga
173	2	18.2	11	2	YHXA6	morphogenetic neur	246	12	2	S10059	tachykinin - Afric
174	2	18.2	11	2	YHJFYH	morphogenetic neur	247	12	2	S07206	kassinin - Senegal
175	2	18.2	11	2	B26744	medascol-takinin -	248	12	2	A58501	24K kidney and bla

249	2	18.2	12	2	G49215	urease (EC 3.5.1.5)	322	2	18.2	13	1	UNOBT	neurotensin - brus
250	2	18.2	12	2	E54573	hypothetical prote	323	2	18.2	13	1	MTOMAD	melanotropin alpha
251	2	18.2	12	2	S71034	patB protein - Sal	324	2	18.2	13	1	MTOMAD	cytochrome P450 CW
252	2	18.2	12	2	S43013	hypothetical prote	325	2	18.2	13	2	S16874	neurotensin [valid
253	2	18.2	12	2	B28551	hypothetical prote	326	2	18.2	13	2	A28505	neurotensin - comm
254	2	18.2	12	2	T44420	hypothetical prote	327	2	18.2	13	2	A61067	enkephalin precurs
255	2	18.2	12	2	S18722	mark protein - lee	328	2	18.2	13	2	A32734	alpha-conotoxin SI
256	2	18.2	12	2	S7540	agglutinin-III lec	329	2	18.2	13	2	A28953	histone H1.c - mou
257	2	18.2	12	2	P00596	1,4-alpha-glucan b	330	2	18.2	13	2	H35245	histone H1.c - mou
258	2	18.2	12	2	P00098	ribosomal protein	331	2	18.2	13	2	A35245	ribosomal protein
259	2	18.2	12	2	C60629	hemocyanin 1 - gre	332	2	18.2	13	2	S78519	ribosomal protein
260	2	18.2	12	2	E61408	hemocyanin chain 5	333	2	18.2	13	2	S39413	tubulin beta chain
261	2	18.2	12	2	A33500	hydrol 1 - African	334	2	18.2	13	2	A60336	outer membrane pro
262	2	18.2	12	2	S10626	lipovitellin - Afr	335	2	18.2	13	2	E37390	traA protein - Esc
263	2	18.2	12	2	A34859	proteinase E - bla	336	2	18.2	13	2	E39778	lactose phosphotra
264	2	18.2	12	2	A55837	5-aminimidazole r	337	2	18.2	13	2	P01022	OLL protein - vacc
265	2	18.2	12	2	A61504	sterol carrier pro	338	2	18.2	13	2	S21152	tryptophyllin-rela
266	2	18.2	12	2	S29830	dimethylalanine mo	339	2	18.2	13	2	A05174	tryptophyllin-13 -
267	2	18.2	12	2	T77529	estrogen receptor	340	2	18.2	13	2	A60458	protocatechuate 3,
268	2	18.2	12	2	S47463	T-cell antigen rec	341	2	18.2	13	2	S12388	argA protein - Sal
269	2	18.2	12	2	S47491	T-cell antigen rec	342	2	18.2	13	2	S70723	lipamide dehydrog
270	2	18.2	12	2	S47393	T-cell antigen rec	343	2	18.2	13	2	B26093	microbial collagen
271	2	18.2	12	2	S47394	T-cell antigen rec	344	2	18.2	13	2	PC1008	40K extracellular
272	2	18.2	12	2	S47395	T-cell antigen rec	345	2	18.2	13	2	S63492	dissimilatory sulf
273	2	18.2	12	2	PH1180	T-cell receptor a1	346	2	18.2	13	2	S36668	hypothetical prote
274	2	18.2	12	2	PH1187	T-cell receptor a1	347	2	18.2	13	2	A46463	predorsal antio
275	2	18.2	12	2	PH1189	T-cell receptor a1	348	2	18.2	13	2	S08575	botulinum neurotox
276	2	18.2	12	2	PH1182	T-cell receptor a1	349	2	18.2	13	2	G44644	neurotoxin-associa
277	2	18.2	12	2	PH1185	T-cell receptor a1	350	2	18.2	13	2	S36887	ribosomal protein
278	2	18.2	12	2	PH1180	T-cell receptor a1	351	2	18.2	13	2	S23103	erythronolide synt
279	2	18.2	12	2	PH1183	T-cell receptor a1	352	2	18.2	13	2	S14316	photosystem I 9K c
280	2	18.2	12	2	PH1188	T-cell receptor a1	353	2	18.2	13	2	PA0049	protein QA100046 -
281	2	18.2	12	2	PH1172	T-cell receptor a1	354	2	18.2	13	2	S28425	20K protein - rape
282	2	18.2	12	2	PH1171	T-cell receptor a1	355	2	18.2	13	2	S00316	photosystem I 13K
283	2	18.2	12	2	PH1175	T-cell receptor a1	356	2	18.2	13	2	B44957	protein L7 - commo
284	2	18.2	12	2	PH1174	T-cell receptor a1	357	2	18.2	13	2	PC1149	equinatoxin 1A - s
285	2	18.2	12	2	PH1179	T-cell receptor a1	358	2	18.2	13	2	A61514	glutathione transf
286	2	18.2	12	2	PH1181	T-cell receptor a1	359	2	18.2	13	2	PS0443	potassium channel
287	2	18.2	12	2	S51737	T-cell receptor be	360	2	18.2	13	2	B55533	CD61 homolog - cha
288	2	18.2	12	2	P00554	glytrophin-associa	361	2	18.2	13	2	B57789	galbladder stone
289	2	18.2	12	2	A20407	Ig kappa chain J1	362	2	18.2	13	2	B28810	glutathione transf
290	2	18.2	12	2	G20407	Ig kappa-1 chain J	363	2	18.2	13	2	S23638	Ig kappa chain J s
291	2	18.2	12	2	D20407	Ig kappa-1 chain J	364	2	18.2	13	2	S23640	Ig kappa chain J s
292	2	18.2	12	2	E20907	Ig kappa 2 chain J	365	2	18.2	13	2	S47356	T-cell antigen rec
293	2	18.2	12	2	PH0743	T-cell receptor be	366	2	18.2	13	2	S47357	T-cell antigen rec
294	2	18.2	12	2	PH1467	T-cell receptor be	367	2	18.2	13	2	S47358	T-cell antigen rec
295	2	18.2	12	2	PH1468	T-cell receptor be	368	2	18.2	13	2	S47359	T-cell antigen rec
296	2	18.2	12	2	PH1467	T-cell receptor be	369	2	18.2	13	2	S47362	T-cell antigen rec
297	2	18.2	12	2	PH1467	T-cell receptor be	370	2	18.2	13	2	S47365	T-cell antigen rec
298	2	18.2	12	2	PH1470	T-cell receptor be	371	2	18.2	13	2	S47368	T-cell antigen rec
299	2	18.2	12	2	PH1464	T-cell receptor be	372	2	18.2	13	2	S47371	T-cell antigen rec
300	2	18.2	12	2	PH1466	T-cell receptor be	373	2	18.2	13	2	S47372	T-cell antigen rec
301	2	18.2	12	2	PH1461	T-cell receptor be	374	2	18.2	13	2	S47373	T-cell antigen rec
302	2	18.2	12	2	PH1469	T-cell receptor be	375	2	18.2	13	2	S47376	T-cell antigen rec
303	2	18.2	12	2	PH1457	T-cell receptor be	376	2	18.2	13	2	S47377	T-cell antigen rec
304	2	18.2	12	2	PH1459	T-cell receptor be	377	2	18.2	13	2	S47378	T-cell antigen rec
305	2	18.2	12	2	PH0771	T-cell receptor be	378	2	18.2	13	2	S47380	T-cell antigen rec
306	2	18.2	12	2	PH1463	T-cell receptor be	379	2	18.2	13	2	S47381	T-cell antigen rec
307	2	18.2	12	2	PT0216	T-cell receptor be	380	2	18.2	13	2	S47382	T-cell antigen rec
308	2	18.2	12	2	H41946	T-cell receptor ga	381	2	18.2	13	2	S47383	T-cell antigen rec
309	2	18.2	12	2	B32521	hexokinase (EC 2.7	382	2	18.2	13	2	S47384	T-cell antigen rec
310	2	18.2	12	2	PH0930	T-cell receptor be	383	2	18.2	13	2	S47385	T-cell antigen rec
311	2	18.2	12	2	PH0931	T-cell receptor be	384	2	18.2	13	2	S47386	T-cell antigen rec
312	2	18.2	12	2	PH0936	T-cell receptor be	385	2	18.2	13	2	S47389	T-cell antigen rec
313	2	18.2	12	2	PH0920	T-cell receptor be	386	2	18.2	13	2	S47390	T-cell antigen rec
314	2	18.2	12	2	PC4377	telomeric and tetr	387	2	18.2	13	2	S47392	T-cell antigen rec
315	2	18.2	12	2	S71380	lebetin 1 isoform	388	2	18.2	13	2	S47400	T-cell antigen rec
316	2	18.2	12	2	B56049	urinary tract ston	389	2	18.2	13	2	S47474	T-cell antigen rec
317	2	18.2	12	2	S27624	Na+/K+-exchanging	390	2	18.2	13	2	PH0138	T-cell receptor be
318	2	18.2	12	2	S27623	Na+/K+-exchanging	391	2	18.2	13	2	S61798	T-cell-specific tr
319	2	18.2	12	2	A51332	Na+/K+-exchanging	392	2	18.2	13	2	A39846	agrecan - bovine
320	2	18.2	12	2	S49677	frame shifted cyto	393	2	18.2	13	2	S78766	ribosomal protein
321	2	18.2	13	1	UNB5	neurotensin - bovi	394	2	18.2	13	2	C53275	Ig kappa-1 chain J

395	2	18.2	13	2	E53275	lg kappa chain J	468	2	18.2	14	2	PH1448	T-cell receptor al
396	2	18.2	13	2	B25448	lg kappa chain J	469	2	18.2	14	2	PH0792	T-cell receptor al
397	2	18.2	13	2	B34932	lg kappa chain J	470	2	18.2	14	2	PH0801	T-cell receptor al
398	2	18.2	13	2	A33333	lg kappa chain J	471	2	18.2	14	2	PH1450	T-cell receptor be
399	2	18.2	13	2	B26406	lg kappa chain J	472	2	18.2	14	2	PH1471	T-cell receptor be
400	2	18.2	13	2	B08035	T-cell receptor al	473	2	18.2	14	2	PH0765	T-cell receptor be
401	2	18.2	13	2	PH1473	T-cell receptor be	474	2	18.2	14	2	PH0753	T-cell receptor be
402	2	18.2	13	2	PH0754	T-cell receptor be	475	2	18.2	14	2	PH0762	T-cell receptor be
403	2	18.2	13	2	PH0928	T-cell receptor be	476	2	18.2	14	2	PH0755	T-cell receptor be
404	2	18.2	13	2	A47635	lg kappa chain J	477	2	18.2	14	2	PH0774	T-cell receptor de
405	2	18.2	13	2	B47630	lg kappa chain J	478	2	18.2	14	2	D35141	T-cell receptor de
406	2	18.2	13	2	B47630	lg kappa chain J	479	2	18.2	14	2	C35141	T-cell receptor de
407	2	18.2	13	2	B47630	lg kappa chain J	480	2	18.2	14	2	E35141	T-cell receptor de
408	2	18.2	13	2	B47630	lg kappa chain J	481	2	18.2	14	2	PC7079	unidentified 27.2K
409	2	18.2	13	2	C131905	collecting duct wa	482	2	18.2	14	2	S65392	cytochrome c oxid
410	2	18.2	13	2	G33488	hypothetical prote	483	2	18.2	14	2	A37789	heat shock cognate
411	2	18.2	13	2	C61576	ribosomal protein	484	2	18.2	14	2	PH0945	T-cell receptor be
412	2	18.2	13	2	A86126	hypothetical prote	485	2	18.2	14	2	PH0915	T-cell receptor be
413	2	18.2	13	2	H85575	hypothetical prote	486	2	18.2	14	2	PC4382	dehydrin 4.5K poly
414	2	18.2	13	2	S01534	H+-transporting tw	487	2	18.2	14	2	B83836	hypothetical prote
415	2	18.2	13	2	L70075	glycophorin B (mis	488	2	18.2	14	2	B85761	trp operon leader
416	2	18.2	13	1	QWAVV	mastoparan B (mis	489	2	18.2	14	2	B81280	probable proteolys
417	2	18.2	14	1	QWVHM	mastoparan B - hor	490	2	18.2	14	2	C39170	acyl-(acyl)-carrier
418	2	18.2	14	1	QWVHX	mastoparan X - hor	491	2	18.2	14	2	G33160	H+-transporting tw
419	2	18.2	14	1	QWVHP	mastoparan C - hor	492	2	18.2	14	2	A17150	glucose 1-dehydrog
420	2	18.2	14	1	QWAPP	pollistes mastopara	493	2	18.2	14	4	S00843	hypothetical prote
421	2	18.2	14	1	LPEZW	trp operon leader	494	2	18.2	15	2	B26597	unspecific monooxy
422	2	18.2	14	1	LPEWZ	trp operon leader	495	2	18.2	15	2	B61243	dimethylalaniline mo
423	2	18.2	14	2	PC2373	probable EMP dehyd	496	2	18.2	15	2	PA0003	nucleoside-diphosp
424	2	18.2	14	2	JN0489	histamine release	497	2	18.2	15	2	PC0195	SflII-glycoprotein
425	2	18.2	14	2	PH1705	lg heavy chain V r	498	2	18.2	15	2	S21240	alpha-glucosidase
426	2	18.2	14	2	E15332	histone H4.1 prece	499	2	18.2	15	2	S21202	glucan 1,4-alpha-g
427	2	18.2	14	2	B29743	translation initia	500	2	18.2	15	2	PC2215	fibrinogenolytic p
428	2	18.2	14	2	A44513	trp 55 leader pep							
429	2	18.2	14	2	A61562	bradykinin-like pe							
430	2	18.2	14	2	JH032E	probable tetraose							
431	2	18.2	14	2	E70858	trp operon leader							
432	2	18.2	14	2	S29632	xylin 1,4 beta-xy							
433	2	18.2	14	2	A63503	kidney and bladder							
434	2	18.2	14	2	L39753	nitronease (EC 1.							
435	2	18.2	14	2	FL0142	carbon monoxide de							
436	2	18.2	14	2	S59495	borate dehydrogen							
437	2	18.2	14	2	E49445	gene C protein - E							
438	2	18.2	14	2	B48544	1,2,4 diaminobuty							
439	2	18.2	14	2	B64863	phot system I reac							
440	2	18.2	14	2	S60354	amyl-mallolamide -							
441	2	18.2	14	2	S36842	ribosomal protein							
442	2	18.2	14	2	S13863	acetyl coenzyme M							
443	2	18.2	14	2	S29789	hypothetical prote							
444	2	18.2	14	2	PA0169	porin por 13 - Ara							
445	2	18.2	14	2	PA0045	porin por1 - Arabi							
446	2	18.2	14	2	S09721	2S allomann snail c							
447	2	18.2	14	2	G44957	photosystem II oxy							
448	2	18.2	14	2	PS0249	porin - rice (stra							
449	2	18.2	14	2	S35267	acetyl CoA carboxy							
450	2	18.2	14	2	A61306	ribonuclease M (EC							
451	2	18.2	14	2	B34135	DNA binding protein							
452	2	18.2	14	2	PC1215	homeotic protein E							
453	2	18.2	14	2	G61408	hemocyanin chain 3							
454	2	18.2	14	2	S14336	mastoparan B - hor							
455	2	18.2	14	2	S12504	protein kinase (EC							
456	2	18.2	14	2	S62374	alpha-1-acetichmot							
457	2	18.2	14	2	I64815	carbonic anhydrase							
458	2	18.2	14	2	S23639	lg kappa chain J s							
459	2	18.2	14	2	S41601	interferon alpha r							
460	2	18.2	14	2	PH1769	T cell receptor al							
461	2	18.2	14	2	PH0135	T cell receptor be							
462	2	18.2	14	2	E49039	T-cell receptor be							
463	2	18.2	14	2	A47421	leukotriene B4 12							
464	2	18.2	14	2	F46394	glycoprotein cospo							
465	2	18.2	14	2	A39704	tabulin beta-1 cha							
466	2	18.2	14	2	PC7075	guanylate cyclase							
467	2	18.2	14	2	PH1601	lg B chain V D-J r							

ALIGNMENTS

RESULT 1
 S45651
 Probable Na+-transporting ATP synthase (EC 3.6.1.-) - Acetobacterium woodii (fragmen
 C:Species: Acetobacterium woodii
 C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 07-May-1999
 C:Accession: S45651
 K:Reidinger, C.; Mueller, V.
 Eur J Biochem 223: 275-284, 1994
 A:Title: Purification of ATP synthase from Acetobacterium woodii and identification
 A:Reference number: S45648; M01D:94307271; PMID:8033902
 A:Accession: S45651
 A:Molecule type: protein
 A:Residues: 18 <RE1>
 A:Experimental source: DSM 1030
 C:Keywords: hydrolase

Query Match 27.38; Score 3; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASK 3

DB 4 ASK 6

RESULT 2

J50302

Xenopsin-related peptide 2 - turkey

N:Contains: xenopsin-related peptide 1

C:Species: Meleagris gallopavo (common turkey)

C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Aug-2000

C:Accession: J50302

R:Caraway, R.E.; Cochran, D.E.; Mitra, S.P.

Regul. Pept. 22: 403-414, 1988

A:Title: Xenopsin related peptide generated in avian gastric extracts.

A:Reference number: J50302; MUID:89042995; PMID:2465902

A:Accession: J50302

A:Molecule type: protein

A:Residues: 1-9 <CA>

C:Comment: The peptides are present within several tissues primarily in large molecular

C:Superfamily: yeast coatomer complex alpha chain; WB repeat homology

C:Keywords: neuropeptide

F:1-9/Product: xenopsin-related peptide 2 #status experimental <XP2>

F:2-9/Product: xenopsin-related peptide 1 #status experimental <XP1>

Query Match 27.3% Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7

DB 1 PKR 5

RESULT 3

A60320

xenopsin-related peptide 2 - rat

N:Contains: xenopsin-related peptide 1

C:Species: Rattus norvegicus (Norway rat)

C>Date: 10-Nov-1992 #sequence_revision 10 Nov 1992 #text_change 18-Aug-2000

C:Accession: A60320

R:Caraway, R.E.; Mitra, S.P.; Muraki, K.

Regul. Pept. 29, 229-239, 1990

A:Title: Isolation and structures of xenopsin related peptides from rat stomach, liver a

A:Reference number: A60320; MUID:91018491; PMID:2217944

A:Accession: A60320

A:Molecule type: protein

A:Residues: 1-9 <CA>

A:Note: the authors purified these peptides from pepsin-treated extracts of stomach, liv

C:Comment: Xenopsin and xenopsin-related peptides are similar to neurotensin in sequence

C:Superfamily: yeast coatomer complex alpha chain; WB repeat homology

C:Keywords: neuropeptide

F:1-9/Product: xenopsin-related peptide 2 #status experimental <XP1>

F:2-9/Product: xenopsin-related peptide 1 #status experimental <XP2>

Query Match 27.3% Score 3; DB 2; Length 9;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7

DB 3 PKR 5

RESULT 4

S70722

65.4K GTP-binding protein (glnA tdkE intergenic region) homolog - Salmonella typhimurium

N:Alternate names: yihK protein homolog

C:Species: Salmonella typhimurium

C>Date: 11-Mar-1998 #sequence_revision 17 Apr 1998 #text_change 24-Apr-1998

C:Accession: S70722

R:Qi, S.Y.; Li, Y.; Szynski, A.; Gilles, L.G.; Weir, A.; Connor, C.D.

Mol. Microbiol. 17, 523-531, 1995

A:Title: Salmonella typhimurium responses to a bacteriophageal protein from human neutrophil

A:Reference number: S70719; MUID:96100451; PMID:8559071

A:Accession: S70722

A:Molecule type: protein

A:Residues: 1-10 <QIS>

A:Experimental source: strain SL1344

Query Match 27.3% Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RNI 9

DB 6 RNI 8

RESULT 5

F41839

ribosomal protein L16 - Achleplasma laidlawii (fragment)

C:Species: Achleplasma laidlawii

C>Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 18-Nov-1994

C:Accession: F41839

R:Lim, P.O.; Sears, B.B.

J. Bacteriol. 174, 2606-2611, 1992

A:Title: Evolutionary relationships of a plant-pathogenic mycoplasma-like organism a

A:Reference number: F41839; MUID:92210505; PMID:1556079

A:Accession: F41839

A>Status: preliminary; translation not shown

A:Molecule type: DNA

A:Residues: 1-10 <LIM>

A:Cross-references: GB:M74471

C:Genetics:

A:Gene: rpl16

C:Keywords: protein biosynthesis; ribosome

Query Match 27.3% Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7

DB 4 PKR 6

RESULT 6

PA0116

ferredoxin:NADP reductase (EC 1.18.1.2) - rice (fragment)

C:Species: Oryza sativa (rice)

C>Date: 07-Apr-1995 #sequence_revision 26-May-1995 #text_change 03-Jun-2002

C:Accession: PA0116

R:Kamo, M.; Tsugita, A.

submitted to JIPID, March 1995

A:Reference number: PA0114

A:Accession: PA0116

A:Molecule type: protein

A:Residues: 1-10 <KAM>

A:Experimental source: ieat

C:Keywords: NADP; oxidoreductase

Query Match 27.3% Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKK 4

DB 5 SKK 7

RESULT 7

PS0220

ferredoxin:NADP reductase (EC 1.18.1.2) - rice (fragment)

C:Species: Oryza sativa (rice)

C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002

C:Accession: PS0220

R:Uchiyama, Y.; Tsugita, A.

submitted to JIPID, August 1991

A:Reference number: PS0205

A:Accession: PS0220

A:Molecule type: protein

A:Residues: 1-10 <UCH>

C:Keywords: NADP; oxidoreductase

Query Match 27.3% Score 3; DB 2; Length 10;

Best Local Similarity 100.0%; Pred. No. 2.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKK 4

DB 11

```

Db          5 SKK 7

RESULT 8
S4249
C:Species: anti1 protein, phage P7
C:Date: 07-Sep-1994 #sequence_revision: 26 May 1995 #text_change: 08-Oct-1999
C:Accession: S42449
R:Clifton, M.; Schuster, H.
Cell 62, 591-598, 1990
A:Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.
A:Reference number: S42448; MUID:90335568; PMID:1696181
A:Accession: S42449
A>Status: preliminary; translation: not shown
A:Molecule type: DNA
A:Residues: 1-11 <CIT>
A:Cross-references: EMBL:M35139; NID:g215705; PIDN:AAA32437.1; PID:g215707

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3 KKP 5
           III
Db          2 KKP 4

RESULT 9
B41835
C:Species: translation elongation factor EF-G homolog - Bacillus subtilis (fragment)
C:Date: 30-Sep-1993 #sequence_revision: 30 Sep 1994 #text_change: 05-Dec-1997
C:Accession: B41835
R:Mitchell, C.; Morris, P.W.; Vary, J.C.
J. Bacteriol. 174, 2474-2477, 1992
A:Title: Identification of proteins phosphorylated by ATP during sporulation of Bacillus
A:Reference number: B41835; MUID:92210469; PMID:1556567
A:Accession: B41835
A:Molecule type: protein
A:Residues: 1-11 <MIT>
A:Note: this protein is phosphorylated during stationary phase but not during exponential
C:Keywords: phosphoprotein

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          7 RNI 9
           III
Db          7 RNI 9

RESULT 10
S19775
C:Species: wound-induced protein - tomato (fragment)
C:Date: 30-Jun-1992 #sequence_revision: 30 Jun-1992 #text_change: 09-Sep-1997
C:Accession: S19775
R:Parsons, B.L.
submitted to the EMBL Data Library, May 1991
A:Reference number: S19773
A:Accession: S19775
A:Molecule type: mRNA
A:Residues: 1-11 <PAR>
A:Cross-references: EMBL:X59884; NID:g19124; PID:g19124

Query Match          27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 SKK 4
           III

Db          4 SKK 6

RESULT 11
T08533
C:Species: hypothetical protein X - Enterobacter aerogenes plasmid R751
C:Date: 11-Jun-1999 #sequence_revision: 11-Jun-1999 #text_change: 21-Jul-2000
C:Accession: T08533
R:Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.
Plasmid 36, 95-111, 1996
A:Title: Conservation of the genetic switch between replication and transfer genes (
A:Reference number: T16434; MUID:97118926; PMID:8954881
A:Accession: T08533
A>Status: preliminary; translated from GB/EMBL/DDBB
A:Molecule type: DNA
A:Residues: 1-13 <THO>
A:Cross-references: EMBL:U67194; NID:g1572520; PIDN:AAC64477.1; PID:g1572582
C:Genetics:
A:Genome: plasmid R751

Query Match          27.3%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3 KKP 5
           III
Db          7 KKP 9

RESULT 12
S22995
C:Species: hypothetical protein X (traJ 5' region) - Escherichia coli plasmid R751
C:Date: 31-Dec-1993 #sequence_revision: 02-Aug-1994 #text_change: 08-Oct-1999
C:Accession: S22995
R:Ziegelin, G.; Pansegrau, W.; Strack, B.; Balzer, D.; Kroeger, M.; Kruff, V.; Lank
DNA Seq. 1, 303-327, 1991
A:Title: Nucleotide sequence and organization of genes flanking the transfer origin
A:Reference number: S22992; MUID:92190548; PMID:1665997
A:Accession: S22995
A:Molecule type: DNA
A:Residues: 1-13 <ZIE>
A:Cross-references: EMBL:X54458; NID:g42656; PIDN:CAA38330.1; PID:g581211
C:Genetics:
A:Genome: plasmid
A:Start codon: TTG

Query Match          27.3%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          3 KKP 5
           III
Db          7 KKP 9

RESULT 13
JQ1350
C:Species: hypothetical protein, 1.3K (rps16 5' region) - Emericella nidulans
C:Date: 30-Jun-1992 #sequence_revision: 30-Jun-1992 #text_change: 09-Sep-1997
C:Accession: JQ1350
R:Bradshaw, R.E.; Pillar, T.M.
Gene 108, 157-162, 1991
A:Title: Isolation and nucleotide sequence of the ribosomal protein S16-encoding gen
A:Reference number: JQ1349; MUID:92104500; PMID:1761226
A:Accession: JQ1350
A:Molecule type: DNA
A:Residues: 1-13 <BRA>
A:Cross-references: GB:M65259; NID:g168087; PID:g168089
A:Experimental source: strain R153

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Query Match 27.3% Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
 DB 10 KKP 12

RESULT 14
 E60396
 antigen 7H8/2 - malaria parasite (Plasmodium falciparum) (fragments)
 C:Species: Plasmodium falciparum
 C:Date: 10-Sep-1993 #sequence_revision 30 Sep-1993 #text_change 09-Jun-2000
 C:Accession: E60396
 R:Limpaiboon, T.; Taylor, D.W.; Jones, G.; Geyse, H.M.; Saul, A.
 Southeast Asian J. Trop. Med. Public Health 21, 458-496, 1990
 A:Title: Characterization of a Plasmodium falciparum epitope recognized by a monoclonal
 A:Reference number: A60396; MUID:91164876; PMID:1706114
 A:Accession: E60396
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-13 <LIM>
 A:Cross-references: GB:M31305

Query Match 27.3% Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKP 9
 DB 11 KKP 13

RESULT 15
 S52456
 hypothetical protein - human
 C:Species: Homo sapiens (man)
 C:Date: 08-May-1995 #sequence_revision 21-Jun-1995 #text_change 05-Nov-1999
 C:Accession: S52456
 R:Agarokastritis, A.; Leversha, M.A.; Ferguson-Smith, M.; Moschonas, M.K.
 submitted to the EMBL Data Library, March 1995
 A:Description: A cosmid clone mapped to human chromosome 11p15 detects a lag 1 restriction
 A:Reference number: S52355
 A:Accession: S52356
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-13 <AGR>
 A:Cross-references: EMBL:X72861; NID:9567002; EMBL:AA51342 1; PID:q557003

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASK 3
 DB 6 ASK 8

RESULT 16
 H64008
 hypothetical protein H10492 - Haemophilus influenzae (strain Rd Kw20)
 C:Species: Haemophilus influenzae
 C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 30-Jun-1998
 C:Accession: H64008
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kiehlavag, A.
 ; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.; Glodek, A.; Kelley, J.M.; Weidman, J.
 D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fahrman, J.L.; Geoghagen, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:Accession: H64008

A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-14 <TIOR>
 A:Cross-references: GB:U32731; GB:I42023; NID:gi573465; PID:gl573478; TIGR:H10492

Query Match 27.3% Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKP 6
 DB 2 KKP 4

RESULT 17
 PA0013
 photosystem II oxygen-evolving complex protein 2 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
 C:Accession: PA0013
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JIPID, July 1994
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimen-
 A:Reference number: PA0001
 A:Accession: PA0013
 A:Molecule type: protein
 A:Residues: 1-14 <KAM>
 A:Experimental source: leaf
 C:Keywords: photosynthesis; photosystem II

Query Match 27.3% Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKP 6
 DB 11 KKP 13

RESULT 18
 S33803
 chaperone, TCPI-related - oat
 C:Species: Avena sativa (oat)
 C:Date: 02-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 17-Mar-1999
 C:Accession: S33803
 R:Mumert, E.; Grimm, K.; Speth, V.; Eckerskorn, C.; Schiltz, E.; Gatenby, A.A.; Sch
 Nature 453, 644-648, 1993
 A:Title: A TCPI-related molecular chaperone from plants refolds phytochrome to its I
 A:Reference number: S33800; MUID:93288140; PMID:8099715
 A:Accession: S33803
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <NUM>

Query Match 27.3% Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
 DB 8 KKP 10

RESULT 19
 H83778
 hypothetical protein BH1032 [imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: H83778
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.;
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
 A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: H83778
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-14 <STO>
 A:Cross-references: GB:AP001510; GB:BA000004; NID:430174440; PIDN:5AR04751.1; GSUB:GN00
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BHI032

Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
 DB 4 PKR 6

RESULT 20
 A54370

inorganic diphosphatase (EC 3.6.1.1) cucumber (fragment)
 C:Species: Cucurbita sp. (cucurbit)
 C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 04-Jun-2002
 C:Accession: A54370
 R:Sato, M.H.; Kasahara, M.; Ishii, N.; Hamareta, H.; Matsui, H.; Yoshida, M.
 J. Biol. Chem. 269, 6725-6728, 1994
 A:Title: Purified vacuolar inorganic pyrophosphatase consisting of a 75-kDa polypeptide
 A:Reference number: A54370; MUID:94.65068; PMID:7120031
 A:Accession: A54370
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-14 <SAT>
 C:Keywords: hydrolase

Query Match 27.3% Score 3; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RNI 9
 DB 4 RNI 5

RESULT 21

S3889
 ribosomal protein S26 - Mycobacterium bovis (fragment)
 C:Species: Mycobacterium bovis
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
 C:Accession: S3889
 Richard, N.; Kimura, M.; Higashi, Y.; Yamada, T.
 FEBS Lett. 331, 9-14, 1993
 A:Title: Isolation and amino acid sequence of the 16S ribosomal protein S19 from Mycobac
 A:Reference number: S3889; MUID:9400965; PMID:8404418
 A:Accession: S3889
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <GNA>
 C:Keywords: protein biosynthesis; ribosome

Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NIK 10
 DB 2 NIK 4

RESULT 22

T09463
 ribosomal protein S14 - brown alga (Pylaiella littoralis) mitochondrion (fragment)
 C:Species: mitochondrion Pylaiella littoralis
 C:Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999

C:Accession: T09463
 R:Rousvold, S.; Oudot, M.; Fontaine, J.; Kloareg, B.; Goer, S.L.
 J. Mol. Biol. 277, 1047-1057, 1998
 A:Title: Witnessing the evolution of transcription in mitochondria: The mitochondria
 A:Reference number: 21668; MUID:98239704; PMID:9571021
 A:Accession: T09463
 A:Status: translated from GB/EMBL/DDHJ
 A:Molecule type: DNA
 A:Residues: 1-15 <ROU>
 A:Cross-references: EMBL:AF04976; NID:q3243103; PID:q3243104
 A:Experimental source: strain Roscoff
 C:Genetics:
 A:Gene: rps14
 A:Genome: mitochondrion
 C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASK 3
 DB 2 ASK 4

RESULT 23

PA0046
 protein GAI00044 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
 C:Accession: PA0046; PA0042
 R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
 submitted to JPIB, July 1994
 A:Description: Separation and characterization of Arabidopsis proteins by two-dimens
 A:Reference number: PA0001
 A:Accession: PA0046
 A:Molecule type: protein
 A:Residues: 1-15 <KAM>
 A:Experimental source: stem

Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKK 4
 DB 3 SKK 5

RESULT 24

PT0082
 protein QA00023 - Arabidopsis thaliana (fragment)
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 06-Jun-1997
 C:Accession: PT0082
 R:Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
 submitted to JPIB, December 1995
 A:Description: Two dimensional electrophoresis of plant proteins and standardization
 A:Reference number: PN0173
 A:Accession: PT0082
 A:Molecule type: protein
 A:Residues: 1-15 <TSU>
 A:Experimental source: leaf

Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6
 DB 4 KPK 6

RESULT 25

S71300
ICL1 protein - Paramoecium tetraurelia (fragment)
C:Species: Paramoecium tetraurelia
C>Date: 11-Mar-1998 #sequence_revision 17 Apr 1998 #text_change 32 Dec-1999
C:Accession: S71300
R:Madecdu, L.; Klotz, G.; le Caer, J.P.; Boissac, J.
Eur. J. Biochem. 238, 121-128, 1996

A:Title: Characterization of centrin spots in Paramoecium
A:Reference number: S71298; MUID:96248429; PMID:8566529
A:Accession: S71300
A:Molecule type: protein
A:Residues: 1-15 <MAD>
A:Experimental source: strain d4-2
C:Genetics:
A:Genetic code: SGC5

Query Match 27.3% Score 3; DB 2; Length 15;

Best Local Similarity 100.0% Pred. No. 3.7e-04; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7

DB 10 PKR 12

RESULT 26

S77987
cytochrome-c oxidase (EC 1.9.3.1) chain V10.2 - bovine tuna (fragments)
C:Species: Thunnus obesus (bigeye tuna)
C>Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 04-Sep-1998
C:Accession: S77987
R:Arnold, S.; Lee, J.; Kim, M.; Sund, E.; Linder, B.; Lottspächer, F.; Kadenbach, B.

submitted to the Protein Sequence Database, June 1997

A:Reference number: S77980

A:Accession: S77987

A:Molecule type: protein

A:Residues: 18-9-15 <ARN>

A:Experimental source: heart

C:Genetics:

A:Genome: nuclear

C:Function:

A:Putway: oxidative phosphorylation; respiratory chain

C:Keywords: electron transfer; membrane associated complex; mitochondrial inner membrane

Query Match 27.3% Score 3; DB 2; Length 15;

Best Local Similarity 100.0% Pred. No. 3.7e-04; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5

DB 8 KKP 10

RESULT 27

S03955
acidic fibroblast growth factor - dog (fragment)
N:Alternate names: alpha-endothelial cell growth factor
C:Species: Canis lupus familiaris (dog)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993
C:Accession: S03955
R:Quinkler, W.; Maasberg, M.; Bernotat-Gambacossi, S.; Luethe, N.; Sharma, H.S.; Schape

Eur. J. Biochem. 181, 67-75, 1989

A:Title: Isolation of heparin-binding growth factors from bovine, porcine and canine hea

A:Reference number: S03953; MUID:8921204; PMID:2714282

A:Accession: S03955

A:Molecule type: protein

A:Residues: 1-15 <QUI>

C:Keywords: growth factor

Query Match 27.3% Score 3; DB 2; Length 15;

Best Local Similarity 100.0% Pred. No. 3.7e-04; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6

DB 4 KPK 5

RESULT 28

PX0031
mixed lymphocyte reaction inhibitor rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 24-Feb-1995
C:Accession: PX0031
R:Shinomiya, T.; Chhara, T.; Wada, N.; Omori, A.; Kamada, N.
J. Biochem. 107, 435-449, 1990

A:Title: Rat liver arginase suppresses mixed lymphocyte reaction.

A:Reference number: PX0031; MUID:90256720; PMID:2140355

A:Accession: PX0031

A:Molecule type: protein

A:Residues: 1-15 <SHI>

A:Experimental source: liver

C:Keywords: lymphocyte

Query Match 27.3% Score 3; DB 2; Length 15;

Best Local Similarity 100.0% Pred. No. 3.7e-03; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6

DB 10 KPK 12

RESULT 29

LFSAME

probable msrA leader peptide - Staphylococcus epidermidis

C:Species: Staphylococcus epidermidis

C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999

C:Accession: S11157

R:Ross, J.L.; Eady, E.A.; Cove, J.H.; Cunliffe, W.J.; Baumberg, S.; Wootton, J.C.

Mol. Microbiol. 4, 1207-1214, 1990

A:Title: Inducible erythromycin resistance in staphylococci is encoded by a member c

A:Reference number: S11157; MUID:91041730; PMID:2233255

A:Accession: S11157

A:Molecule type: DNA

A:Residues: 1-8 <ROS>

A:Cross-references: EXPL.X52085; NID:947000; PIDN:CAA36303.1; PID:9581653

C:Superfamily: probable msrA leader peptide

Query Match 18.2% Score 2; DB 1; Length 8;

Best Local Similarity 100.0% Pred. No. 2.8e+05; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

DB 3 AS 4

RESULT 30

A31570

angiotensin-converting enzyme inhibitor - yellowfin tuna

C:Species: Thunnus albacares (yellowfin tuna)

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Aug-2000

C:Accession: A31570

R:Kohama, Y.; Matsumoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.

Biochem. Biophys. Res. Commun. 155, 332-337, 1988

A:Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.

A:Reference number: A31570; MUID:88326322; PMID:3415688

A:Accession: A31570

A:Molecule type: protein

A:Residues: 1-8 <ROH>

A>Note: The source is designated as Neothunnus macropterus

C:Superfamily: unassigned animal peptides

C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 PK 10
 II
 4 PK 5

DB

RESULT 31
 S70727
 IpaF protein - Shigella flexneri (fragment)
 C:Species: Shigella flexneri
 C:Date: 15-Feb-1997 #sequence_revision 15-Mar-1997 #text_change 05-Oct-1999
 C:Accession: S70727
 K:Allaoui, A.; Sansonetti, P.J.; Menard, R.; Ratzu, S.; Mounier, J.; Phalipon, A.; Parso
 Mol. Microbiol. 17, 461-470, 1995
 A:Title: MxiG, a membrane protein required for secretion of Shigella spp. Ipa invasins:
 A:Reference number: S70727; MUID:96100445; PMID:8559665
 A:Accession: S70727
 A:Status: Preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-8 <ALL>
 A:CROSS-references: EMBL:Z48957; NID:q429880; PDB:CAA8821.1; PID:3929881
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995
 C:Genetics:
 A:Gene: IpaF

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SK 3
 II
 1 SK 2

DB

RESULT 32
 A39308
 Glycine reductase (EC 1.4.99.1) sulfolipyl protein of alpha chain - Clostridium sticklandii
 C:Species: Clostridium sticklandii
 C:Date: 19-Jan-1992 #sequence_revision 19-Jun-1992 #text_change 15-Aug-1997
 C:Accession: A39308
 R:Stadman, T.C.; Davis, J.N.
 J. Biol. Chem. 265, 22147-22154, 1991
 A:Title: Glycine reductase protein of Clostridium sticklandii: characterization of its role in the
 A:Reference number: A39308; MUID:9294143; PMID:1972192
 A:Accession: A39308
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <STA>
 C:Function:
 A:Description: glycine reductase complex catalyzes the reductive decarboxylation of glycine
 C:Keywords: ALP; oxidoreductase

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KP 5
 II
 2 KP 3

DB

RESULT 33
 T10952
 Hypothetical protein 1 - spring vetch
 C:Species: Vicia sativa (spring vetch, faba)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C:Accession: T10952
 R:Christianson, A.; Hansen, A.C.; Villemann, R.; Rasmussen, K.; Yan, W.; Biss
 submitted to the EMBL Data Library, December 1997
 A:Description: A novel type of DNA binding protein interacts with a conserved sequence

A:Reference number: Z17228
 A:Accession: T10952
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-8 <CHR>
 A:CROSS-references: EMBL:X5995; NID:q1360633; PID:e225824

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SK 4
 II
 7 SK 8

DB

RESULT 34
 S21288
 Lectin - potato (fragment)
 C:Species: Solanum tuberosum (potato)
 C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 05-Dec-1998
 C:Accession: S21288
 R:Miller, D.J.; Allen, A.K.; Smith, C.G.; Sidebottom, C.; Siabas, A.R.; Bolwell, G.P
 Biochem. J. 283, 813-821, 1992
 A:Title: Chitin-binding proteins in potato (Solanum tuberosum L.) tuber. Characteriz
 A:Reference number: S21288; MUID:92272683; PMID:1590771
 A:Accession: S21288
 A:Molecule type: protein
 A:Residues: 1-8 <MIL>
 A:Experimental source: var. Ulster Sceptre
 C:Function:
 A:Description: may be involved in defence mechanism of the plant
 C:Keywords: hydroxyproline; lectin

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
 II
 2 AS 3

DB

RESULT 35
 A39832
 Element, P cytotypic-determining - fruit fly (Drosophila melanogaster) (fragment)
 C:Species: Drosophila melanogaster
 C:Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 16-Feb-1997
 C:Accession: A39832
 R:Nitakaka, E.; Mukai, T.; Yamazaki, T.
 Proc. Natl. Acad. Sci. U.S.A. 84, 7605-7608, 1987
 A:Title: Repressor of P elements in Drosophila melanogaster: cytotypic determination
 A:Reference number: A39832
 A:Accession: A39832
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-8 <NIT>
 C:Genetics:
 A:Gene: FlyBase:P-element
 A:CROSS-references: FlyBase:FBgn0003055

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6
 II
 2 PK 3

DB

RESULT 36
 A14983
 aspartate transaminase (EC 2.6.1.1), mitochondrial - chicken (tentative sequence) (f

N:Alternate names: aspartate aminotransferase, mitochondrial
 C:Species: Gallus gallus (chicken)
 C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Mar-2000

R:Accession: A14683
 R:Wilson, K.J.; Hunziker, P.; Hughes, G.J.
 FEBS Lett. 108, 98-102, 1979

A:Title: Microsequence analysis. IV. Automatic liquid-phase sequencing using DABITC.
 A:Reference number: A14683; MUID:80092116; PMID:520566

A:Accession: A14683

A:Molecule type: protein

A:Residues: 1-8 <WIL>

C:Keywords: aminotransferase; mitochondrion

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6

DB 7 PK 8

RESULT 37

A28719 Thymic humoral factor gamma-2 bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1993

C:Accession: A28719

R:Burstein, Y.; Buchner, V.; Pecht, M.; Trainor, N.

Biochemistry 27, 4066-4071, 1988

A:Title: Thymic humoral factor gamma-2: purification and amino acid sequence of an immunoreactive protein

A:Reference number: A28719; MUID:88126920; PMID:3261954

A:Accession: A28719

A:Molecule type: protein

A:Residues: 1-8 <BUK>

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6

DB 5 PK 6

RESULT 38

A54823 Olfactory receptor 17 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 28-Apr-1995 #sequence_revision 24-Apr-1995 #text_change 17-Mar-1999

C:Accession: A54823

R:Chess, A.; Simon, I.; Cedar, H.; Axel, R.

Cell 78, 823-834, 1994

A:Title: Allelic inactivation regulates olfactory receptor gene expression.

A:Reference number: A54823; MUID:94373818; PMID:808245

A:Accession: A54823

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-8 <CHE>

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RN 8

DB 4 RN 5

RESULT 39

PT0595

T-cell receptor beta chain V-D-J region (100-2AA) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0595
 R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N region

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0595

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

DB 1 AS 2

RESULT 40

PT0627

T-cell receptor beta chain V-D-J region (100-2H) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0627

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N region

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0627

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FEE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

DB 1 AS 2

RESULT 41

PT0530

T-cell receptor beta chain V-D-J region (100-4AK) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0530

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N region

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0530

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FEE>

A:Experimental source: adult thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

DB 1 AS 2

RESULT 42

PT0527

T-cell receptor beta chain V-D-J region (100-40) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0527

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0527

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FE>

A:Experimental source: adult thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

II

DB 1 AS 2

RESULT 43

PT0522

T-cell receptor beta chain V-D-J region (100-40) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0522

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0522

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FE>

A:Experimental source: adult thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

II

DB 1 AS 2

RESULT 44

PT0509

T-cell receptor beta chain V-D-J region (100-4N) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0509

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0509

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FE>

A:Experimental source: adult thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

II

DB 1 AS 2

RESULT 45

PT0639

T-cell receptor beta chain V-D-J region (111-1AA) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0639

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N region

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0639

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

II

DB 1 AS 2

RESULT 46

PT0631

T-cell receptor beta chain V-D-J region (111-1I) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0631

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N region

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0631

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2

II

DB 1 AS 2

RESULT 47

PT0613

T-cell receptor beta chain V-D-J region (111-1L) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0613

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have few N region

A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0613

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FE>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
DB 1 AS 2

RESULT 48

PT0557

T-cell receptor beta chain V-D-J region (126-141) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0553

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Functional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711556

A:Accession: PT0553

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <PEE>

A:Experimental source: day 4 postnatal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.9e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
DB 1 AS 2

RESULT 49

PT0547

T-cell receptor beta chain V-D-J region (126-141) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0547

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Functional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711556

A:Accession: PT0547

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <PEE>

A:Experimental source: day 18 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
DB 1 AS 2

RESULT 50

PT0557

T-cell receptor beta chain V-D-J region (126-141) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0557

R:Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A:Title: Functional sequences of fetal T cell receptor beta chains have few N regions.

A:Reference number: PT0509; MUID:91277601; PMID:1711556

A:Accession: PT0557
A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <PEE>

A:Experimental source: day 18 fetal thymus, strain BALB/c

C:Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
DB 1 AS 2

Search completed: September 30, 2003, 10:09:37

Job time : 20.4167 secs

GenCore version 5.1.6
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OM protein - protein search, using SW mode

Run on: September 30, 2003, 11:07:04 : Search time 6.25 Seconds

(without alignment)
82.767 Million cell updates/sec

Title: US-09-787-443-1

Perfect score: 11

Sequence: : ASKKPRNIKA 11

Scoring table: SLIGO

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 707

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	8	B44K_PORGI	P61886 porphyromon
2	4	36.4	11	CS15_BACSU	P61095 bacillus su
3	3	27.3	10	R416_ACHIA	P29421 achioleplasm
4	3	27.3	12	RS19_ELVEI	P47681 elm yellows
5	3	27.3	14	RS19_PEWPI	P42091 piceon pea
6	3	27.3	15	FX41_THRUP	P08278 thymus ooc
7	3	27.3	15	FGF1_CARRA	P18651 carnis fami
8	3	27.3	15	PSKH_PETVA	P30059 physocystis
9	3	27.3	15	RS2C_PAVSI	P59681 bacillus st
10	2	18.2	8	AP11_HUAL	P18691 thymus alb
11	2	18.2	8	ALL7_CANMA	P41809 carinus ma
12	2	18.2	8	FAK1_PENNO	P43166 penaeus aca
13	2	18.2	8	FAK3_HUMAN	P41486 homarus ame
14	2	18.2	8	FAK4_HUMAN	P41487 homarus ame
15	2	18.2	8	LCK4_LETMA	P41143 leucophaea
16	2	18.2	8	LPMS_STAPP	P24211 staphylococ
17	2	18.2	8	RS7_MYCCT	P43564 mycobacteri
18	2	18.2	9	QONO_CUNGL	P05486 conus geogr
19	2	18.2	9	QONO_CONST	P05487 conus stria
20	2	18.2	9	COM_CONVE	P03047 conus ventr
21	2	18.2	9	DSIP_RABIT	P01158 oryctolagus
22	2	18.2	9	FAK4_CALAVI	P41859 calliphora
23	2	18.2	9	FAK5_ASSSU	P43170 ascaris suu
24	2	18.2	9	FAK5_PANRE	P82651 panagrellus
25	2	18.2	9	FAK6_CALAV	P41861 calliphora
26	2	18.2	9	FAK6_MALAS	P84279 macrobrachi
27	2	18.2	9	HUTU_KLEAF	P22381 klebsiella
28	2	18.2	9	LECA_STAPH	P36684 staphylococ
29	2	18.2	9	NEF_HV128	P12451 human rhin
30	2	18.2	9	NEUG_FAVIN	P49456 ravia porce
31	2	18.2	9	OXYT_ELESP	P42945 eleuthera toe
32	2	18.2	9	OXYT_CACTUI	P80027 cactodes val
33	2	18.2	9	CLAD_HUMAN	P41929 clad. sapie

34	2	18.2	10	1	AH3_PRUSE	P29261 prunus sero
35	2	18.2	10	1	BPP6_BOTIN	P30426 bothrops in
36	2	18.2	10	1	BRK_VIPAS	P31351 vipera aspi
37	2	18.2	10	1	BRK_ONCMY	P99731 oncorhynch
38	2	18.2	10	1	COXM_RAT	P80431 rattus norv
39	2	18.2	10	1	COXO_RABIT	P80336 oryctolagus
40	2	18.2	10	1	COXO_SHEEP	P80337 ovis aries
41	2	18.2	10	1	FAR7_MACRS	P83280 macrobrachi
42	2	18.2	10	1	FIBB_CERS1	P14537 ceratotheri
43	2	18.2	10	1	GONI_CHEPR	P80677 chelyosoma
44	2	18.2	10	1	GONI_PETMA	P04378 petromyzon
45	2	18.2	10	1	GONI_PETMA	P30946 petromyzon
46	2	18.2	10	1	GOF2_BOVIN	P11180 bos taurus
47	2	18.2	10	1	PNEU_HUMAN	P22103 homo sapien
48	2	18.2	10	1	PNEU_RAT	P21996 rattus norv
49	2	18.2	10	1	SPI_HALRO	Q10997 halocynthia
50	2	18.2	10	1	TKNC_RANCA	P22690 rana catesb
51	2	18.2	10	1	TRP7_LEUMA	P81739 leucophaea
52	2	18.2	10	1	UPA5_HUMAN	P30091 homo sapien
53	2	18.2	10	1	UPA8_HUMAN	P30094 homo sapien
54	2	18.2	10	1	URA6_HUMAN	P32080 homo sapien
55	2	18.2	10	1	UXA2_CHLTR	P38003 chlamydia t
56	2	18.2	10	1	UXA6_CHLTR	P38007 chlamydia t
57	2	18.2	10	1	XYNB_DICB4	P80717 dictyoglomu
58	2	18.2	11	1	BPPB_AKCHA	P01021 agkistrodon
59	2	18.2	11	1	BRK_MESFL	P12797 megascolla
60	2	18.2	11	1	EFG_CLOPA	P81350 clostridium
61	2	18.2	11	1	LAOD_ONCMY	P81018 oncorhynch
62	2	18.2	11	1	MORN_HUMAN	P01163 homo sapien
63	2	18.2	11	1	PVK1_PERAM	P41837 periplaneta
64	2	18.2	11	1	Q2QA_COMTE	P80464 comamonas t
65	2	18.2	11	1	RR2_CONAM	P42341 conopholis
66	2	18.2	11	1	TKN7_UPERU	P08616 uperoletia r
67	2	18.2	11	1	TKNA_GADMO	P28498 gadus morhu
68	2	18.2	11	1	TKNA_HORSE	P01290 equus cabal
69	2	18.2	11	1	TKNA_HORSE	P28499 oncorhynch
70	2	18.2	11	1	TKNA_RANCA	P22688 rana catesb
71	2	18.2	11	1	TKNA_RANCI	P29207 rana ridibu
72	2	18.2	11	1	TKNA_SCYCA	P41333 scyllorhinu
73	2	18.2	11	1	TKND_RANCA	P22891 rana catesb
74	2	18.2	11	1	TKN_ELEMO	P01293 eleodon mos
75	2	18.2	12	1	FAR7_PENMO	P83322 penaeus mon
76	2	18.2	12	1	GRAK_RANRU	P40754 rana rugosa
77	2	18.2	12	1	HCYL_CARMA	P83176 carcinus ma
78	2	18.2	12	1	LOSK_LOCOMI	P47733 locustua mlg
79	2	18.2	12	1	GPS3_DROVI	P17845 drosophila
80	2	18.2	12	1	RR16_GNBI	P36207 ginkgo bilio
81	2	18.2	12	1	RS19_CLYEP	Q46490 clover yell
82	2	18.2	12	1	RS19_TOBBP	Q56251 tomato big
83	2	18.2	12	1	SO15_BACSU	P80863 bacillus su
84	2	18.2	12	1	TKN1_KASMA	P08613 kassina mac
85	2	18.2	12	1	TKN_KASSE	P08611 kassina sen
86	2	18.2	12	1	UHO3_RAT	P56372 rattus norv
87	2	18.2	13	1	ADFB_TENMO	P83109 tenebrio mo
88	2	18.2	13	1	AH4_PRUSE	P29262 prunus sero
89	2	18.2	13	1	AU11_LITRA	P82386 litoria ran
90	2	18.2	13	1	AU12_LITRA	P82387 litoria ran
91	2	18.2	13	1	BRK_PARDI	P42717 parapolybia
92	2	18.2	13	1	EP65_HUMAN	P54963 homo sapien
93	2	18.2	13	1	IDHP_RAT	P56574 rattus norv
94	2	18.2	13	1	ITB5_BOVIN	P80747 bos taurus
95	2	18.2	13	1	MLA_ANOCA	P41589 anolis caro
96	2	18.2	13	1	MLA_CANDR	P01198 camelus dro
97	2	18.2	13	1	NEUT_BUFMA	P81796 bufo marinu
98	2	18.2	13	1	NEUT_CHICK	P13724 gallus gall
99	2	18.2	13	1	NEUT_RANTE	P41536 rana tempor
100	2	18.2	13	1	NEUT_TRIVU	P31745 trichosurus
101	2	18.2	13	1	ODPA_CANFA	P49823 canis fami
102	2	18.2	13	1	PSAE_PEA	P20118 pisum sativ
103	2	18.2	13	1	PSBP_PINPS	P81668 pinus pinas
104	2	18.2	13	1	RPOC_MYCPA	P47716 mycoplasma
105	2	18.2	13	1	RS19_ASHYG	Q44592 ash yellows
106	2	18.2	13	1	TEML_RANTE	P57104 rana tempor

107	2	18.2	13	1	TV13_HYBR	P04096 phyllorhizus	180	1	9.1	8	1	ALL1_CYDPO	P82152 cydia pomon
108	2	18.2	13	1	UBT1_LITWR	P82050 litoria ewi	181	1	9.1	8	1	ALL3_CYDPO	P82154 cydia pomon
109	2	18.2	14	1	EFTU_CANF	P54835 canis fami	182	1	9.1	8	1	ALL4_CALVO	P41840 calliphora
110	2	18.2	14	1	IF2G_RAT	P81795 rattus norv	183	1	9.1	8	1	ALL4_CYDPO	P82155 cydia pomon
111	2	18.2	14	1	KLP5_SCAR	P58396 scaptoessa	184	1	9.1	8	1	ALL5_CALVO	P41841 calliphora
112	2	18.2	14	1	LHW_ELFPR	P30056 catrobacter	185	1	9.1	8	1	ALL5_CYDPO	P82156 cydia pomon
113	2	18.2	14	1	LHW_EF011	P03053 escherichia	186	1	9.1	8	1	ALL6_CYDPO	P82157 cydia pomon
114	2	18.2	14	1	LHW_EHIME	P18854 Elizabethia m	187	1	9.1	8	1	ALL8_CARMA	P81811 carcinus ma
115	2	18.2	14	1	MAST_PALJO	P42716 parapolybia	188	1	9.1	8	1	ALL9_CARMA	P81812 carcinus ma
116	2	18.2	14	1	MAST_PALJA	P41517 polistes ja	189	1	9.1	8	1	ANG2_BOTJA	Q10582 bothrops ja
117	2	18.2	14	1	MAST_VESBA	P21694 vespa basal	190	1	9.1	8	1	CAD1_ENTFA	P13268 enterococcu
118	2	18.2	14	1	MAST_VESCR	P41516 vespa crabr	191	1	9.1	8	1	CLP_THICU	P80488 thobacillu
119	2	18.2	14	1	MAST_VESLE	P41514 vespa lew	192	1	9.1	8	1	COM2_CONPU	P58785 conus purpu
120	2	18.2	14	1	MAST_VESMA	P42205 vespa manda	193	1	9.1	8	1	COXG_RAT	P80430 rattus norv
121	2	18.2	14	1	MAST_VESOR	P17238 vespa orien	194	1	9.1	8	1	CPD1_ENTFA	P13269 enterococcu
122	2	18.2	14	1	MAST_VESXA	P01515 vespa xanth	195	1	9.1	8	1	FAR1_PANRE	P41872 panagrellus
123	2	18.2	14	1	MGRX_METIM	P56815 methanobact	196	1	9.1	8	1	FAR2_MACRS	P83275 macrobrachi
124	2	18.2	14	1	MGR2_METIM	P56816 methanobact	197	1	9.1	8	1	FAR4_MACRS	P83277 macrobrachi
125	2	18.2	14	1	RS19_CLOPP	P46228 clover prot	198	1	9.1	8	1	FAR7_ASCSU	P43171 ascaris suu
126	2	18.2	14	1	RS19_COWRP	P46878 clover witc	199	1	9.1	8	1	FAR8_CALVO	P41863 calliphora
127	2	18.2	14	1	RS19_FROAP	Q44160 prunus arme	200	1	9.1	8	1	FUSS_FUSSO	P81010 fusarium so
128	2	18.2	14	1	FAT_RV1W2	P12509 human immun	201	1	9.1	8	1	GLUR_HUMAN	P02729 homo sapien
129	2	18.2	14	1	FAT_RV1W4	P12511 human immun	202	1	9.1	8	1	HIF1_PERAM	P04549 periplaneta
130	2	18.2	14	1	TKN1_SCHCK	P42470 schistocerc	203	1	9.1	8	1	HIF2_PERAM	P04549 periplaneta
131	2	18.2	14	1	TKNM_KARMA	P40951 ratia margar	204	1	9.1	8	1	HIF_TENNO	P25419 tenebrio mo
132	2	18.2	14	1	UC04_MALZE	P36610 zea mays (m	205	1	9.1	8	1	ICK1_LEUMA	P21140 leucophaea
133	2	18.2	14	1	UN46_CU4FA	P41362 cecrostidum	206	1	9.1	8	1	ICK2_LEUMA	P21141 leucophaea
134	2	18.2	15	1	ACEA_ACTCA	P28467 acinetobact	207	1	9.1	8	1	ICK3_LEUMA	P21142 leucophaea
135	2	18.2	15	1	ACT_PINGS	P81085 pinus pinas	208	1	9.1	8	1	LCK5_LEUMA	P19987 leucophaea
136	2	18.2	15	1	AH2_PMSK	P49260 prunus sero	209	1	9.1	8	1	LCK6_LEUMA	P19988 leucophaea
137	2	18.2	15	1	ASFL_LACSN	P82648 lactobacilli	210	1	9.1	8	1	LCK7_LEUMA	P19989 leucophaea
138	2	18.2	15	1	ATP2_PINGS	P81653 pinus pinas	211	1	9.1	8	1	LCK8_LEUMA	P19990 leucophaea
139	2	18.2	15	1	ATP2_SPLIC	P36993 spinacia ol	212	1	9.1	8	1	LCK9_LEUMA	P22396 locusta mag
140	2	18.2	15	1	CXX_WHEAT	P38763 tritium ae	213	1	9.1	8	1	LPK_LEUMA	P13049 leucophaea
141	2	18.2	15	1	DEMM_PSECH	P19917 pseudomonas	214	1	9.1	8	1	NPB_BOVIN	P15507 bos taurus
142	2	18.2	15	1	G10H_PSECH	P80721 pseudomonas	215	1	9.1	8	1	NS3_MYCTU	P81152 mycobacteri
143	2	18.2	15	1	ELFA_MIGCK	P82466 macroplatis	216	1	9.1	8	1	ORMY_ORCLI	P82455 orconectes
144	2	18.2	15	1	GR78_HORSE	P76392 equus cabal	217	1	9.1	8	1	PLP_BRANA	P81707 brassica na
145	2	18.2	15	1	LEP1_LACTIO	P28588 aximelia po	218	1	9.1	8	1	PKK2_PERAM	P82692 periplaneta
146	2	18.2	15	1	MAL1_BACTO	P80072 bacillus th	219	1	9.1	8	1	PKK3_PERAM	P82618 periplaneta
147	2	18.2	15	1	MAGX_CHICK	Q42060 gallus gall	220	1	9.1	8	1	RPCH_PANBO	P08939 pandalus bo
148	2	18.2	15	1	MILL_MCKKE	P41037 oncorhynch	221	1	9.1	8	1	RS1_ERWCH	P37985 erwinia chr
149	2	18.2	15	1	MK1_PALPR	P64408 palomedia pr	222	1	9.1	8	1	RT34_BOVIN	P82929 bos taurus
150	2	18.2	15	1	MK2A_PALPR	P64409 palomedia pr	223	1	9.1	8	1	UC26_MALZE	P80632 zea mays (m
151	2	18.2	15	1	NK05_PSELE	P63743 sorghum tub	224	1	9.1	8	1	UCG6_MOUSE	P38644 mus muscultu
152	2	18.2	15	1	NK05_PSELE	P63743 pseudomaja	225	1	9.1	8	1	UH09_RAT	P56575 rattus norv
153	2	18.2	15	1	ORPA_MARBP	P41285 mamestra tr	226	1	9.1	8	1	UPA1_HUMAN	P30087 homo sapien
154	2	18.2	15	1	ORPA_MARBP	P41287 oenothera	227	1	9.1	8	1	UPAA_HUMAN	P30096 herpes simp
155	2	18.2	15	1	RTVA_SCHIC	P64454 spinacia ol	228	1	9.1	8	1	VGLG_HSV2B	P81780 herpes simp
156	2	18.2	15	1	R05_PSELE	P63657 physcomitro	229	1	9.1	8	1	WPL_PERAT	P83195 perkinsus a
157	2	18.2	15	1	RS10_SAVIN	P55041 lactobacilli	230	1	9.1	8	1	WPL_PERAT	P83195 perkinsus a
158	2	18.2	15	1	RT32_BOVIN	P62927 bos taurus	231	1	9.1	8	1	ALC0_CARMA	P81813 carcinus ma
159	2	18.2	15	1	SOUP_PINGS	P81082 pinus pinas	232	1	9.1	8	1	ALC1_CARMA	P81814 carcinus ma
160	2	18.2	15	1	TAT1_FERR	P34070 tremella br	233	1	9.1	8	1	ALC2_CARMA	P82678 chlamydomon
161	2	18.2	15	1	THE_CLOPA	P81347 clostridium	234	1	9.1	8	1	BS43_SERPL	P81337 serratia pl
162	2	18.2	15	1	UBL1_MONIA	P50103 monodiphis	235	1	9.1	8	1	BUK_CLOPA	P81337 clostridium
163	2	18.2	15	1	UC01_MALZE	P80607 zea mays (m	236	1	9.1	8	1	CCAP_CARMA	P38556 carcinus ma
164	2	18.2	15	1	UC08_MALZE	P80614 zea mays (m	237	1	9.1	8	1	COXE_THUOB	P80975 thunnus obe
165	2	18.2	15	1	UC13_MALZE	P80619 zea mays (m	238	1	9.1	8	1	DI_NEPNO	P24816 nephrops no
166	2	18.2	15	1	UC17_MALZE	P80623 zea mays (m	239	1	9.1	8	1	DNF1_LOOMI	P16339 locusta mig
167	2	18.2	15	1	UC23_MALZE	P80629 zea mays (m	240	1	9.1	8	1	FAR1_CALVO	P41856 calliphora
168	2	18.2	15	1	UNC4_FINDS	P81673 pinus pinas	241	1	9.1	8	1	FAR2_CALVO	P41857 calliphora
169	2	18.2	15	1	VORA_METIM	P80907 methanobact	242	1	9.1	8	1	FAR2_PANRE	P41873 panagrellus
170	1	9.1	8	1	ACT_CARMA	P80709 carcinus ma	243	1	9.1	8	1	FAR3_CALVO	P41868 calliphora
171	1	9.1	8	1	AKHG_GRYIC	P14086 gryllus bim	244	1	9.1	8	1	FAR3_MACRS	P83276 macrobrachi
172	1	9.1	8	1	AKH_LILISAU	P25418 libellula a	245	1	9.1	8	1	FAR3_PENMO	P83319 penaeus mon
173	1	9.1	8	1	AKH_MELML	P25423 melolontha	246	1	9.1	8	1	FAR5_CALVO	P41860 calliphora
174	1	9.1	8	1	AKH_TASAL	P14595 tabanus atr	247	1	9.1	8	1	FAR5_PENMO	P83320 penaeus mon
175	1	9.1	8	1	ALI2_CARMA	P81815 carcinus ma	248	1	9.1	8	1	FAR7_CALVO	P41862 calliphora
176	1	9.1	8	1	ALI5_CARMA	P81818 carcinus ma	249	1	9.1	8	1	FAR8_MACRS	P83281 macrobrachi
177	1	9.1	8	1	ALI6_CARMA	P81819 carcinus ma	250	1	9.1	8	1	FAR9_ASCSU	P43172 ascaris suu
178	1	9.1	8	1	ALI7_CARMA	P81820 carcinus ma	251	1	9.1	8	1	FARA_CALVO	P41865 calliphora
179	1	9.1	8	1	ALI8_CARMA	P81821 carcinus ma	252	1	9.1	8	1	FARD_CALVO	P41868 calliphora

253	1	9.1	9	1	FARP_CALSI	P18495	callinectes	326	1	9.1	10	1	FARP_PANRE	P82660	panagrellus
254	1	9.1	9	1	FIBB_ERIPA	P19346	erythrocebu	327	1	9.1	10	1	FARP_CALVO	P41867	calliphora
255	1	9.1	9	1	FIBB_MACFI	P19345	macaca fusc	328	1	9.1	10	1	FARP_LOCHI	P38553	locusta mig
256	1	9.1	9	1	FIBB_PAPNA	P19344	papio anubi	329	1	9.1	10	1	FARP_MANSE	P18523	manduca sex
257	1	9.1	9	1	FIBB_PAPNA	P19343	papio hamad	330	1	9.1	10	1	FARP_MYTED	P42560	mytilus edu
258	1	9.1	9	1	FIBB_THERF	P19342	theropithec	331	1	9.1	10	1	GAJU_HUMAN	P01358	homo sapien
259	1	9.1	9	1	FLA2_TREHY	P80159	treponema h	332	1	9.1	10	1	GLEM_HUMAN	P02728	homo sapien
260	1	9.1	9	1	FRT1_SARBU	P83350	sarcophaga	333	1	9.1	10	1	GONI_ALLMI	P37041	alligator m
261	1	9.1	9	1	IPR_RHOVI	P82992	rhodopsendo	334	1	9.1	10	1	GONI_CLUPA	P81749	clupea pall
262	1	9.1	9	1	ISOI_CYPCA	P42993	cyprinus ca	335	1	9.1	10	1	GONI_CHEPR	P80678	chelyosoma
263	1	9.1	9	1	KNL3_BOMVA	P83058	bombina var	336	1	9.1	10	1	GON2_CHICK	P37043	gallus gall
264	1	9.1	9	1	LITO_LITAU	P88945	litoria aur	337	1	9.1	10	1	GON3_ONCKE	P20367	oncorhynch
265	1	9.1	9	1	LITR_PHYHO	P88946	phyllomedus	338	1	9.1	10	1	GONL_SQUAC	P27429	squalus aca
266	1	9.1	9	1	LMP3_LOCHI	P11799	locusta mig	339	1	9.1	10	1	GRP_RANKI	P23260	rana ridibu
267	1	9.1	9	1	LMP3_LOCHI	P11799	locusta mig	340	1	9.1	10	1	GS09_BACSU	P80243	bacillus su
268	1	9.1	9	1	MMT1_BOVIN	P29177	bos taurus	341	1	9.1	10	1	HTF1_ROMMI	P18110	romalea mic
269	1	9.1	9	1	MOSF_CLYJA	P19853	clypeaster	342	1	9.1	10	1	HTF2_CARMO	P11385	carausius m
270	1	9.1	9	1	MOSH_CLYJA	P19852	clypeaster	343	1	9.1	10	1	HTF_HELZE	P16353	heliobhis z
271	1	9.1	9	1	NEUX_HUMAN	P04277	homo sapien	344	1	9.1	10	1	HTF_NAUCI	P10939	nauphoeta c
272	1	9.1	9	1	NSK1_SARBU	P41492	sarcophaga	345	1	9.1	10	1	HTF_TABAT	P14596	tabanus atr
273	1	9.1	9	1	OXYA_SCYCA	P42996	scytorhinu	346	1	9.1	10	1	LABA_JATMU	P13270	jatropha mu
274	1	9.1	9	1	OXYA_SQUAC	P42999	squalus aca	347	1	9.1	10	1	LCMS_LEUMA	P21144	leucophaea
275	1	9.1	9	1	OXYE_SCYCA	P42997	scytorhinu	348	1	9.1	10	1	LPK2_LOCHI	P41488	locusta mig
276	1	9.1	9	1	OXYT_BUPFE	P42995	bufo regula	349	1	9.1	10	1	LSK2_LEUMA	P09039	leucophaea
277	1	9.1	9	1	OXYT_CYPCA	P23879	cyprinus ca	350	1	9.1	10	1	MALE_KLEPN	O05564	klebsiella
278	1	9.1	9	1	OXYT_RAB'T	P32878	oryctolagus	351	1	9.1	10	1	MOSQ_CLYJA	P19962	clypeaster
279	1	9.1	9	1	OXYT_RAJCL	P42994	rajia clavat	352	1	9.1	10	1	MP2_MICOC	P81533	microplitis
280	1	9.1	9	1	OXYV_SQUAC	P43000	squalus aca	353	1	9.1	10	1	NO40_TOBAC	P55962	nicotiana t
281	1	9.1	9	1	PGLR_DIAAB	P81179	diaprepes a	354	1	9.1	10	1	NS1_MYCTU	P81135	mycobacteri
282	1	9.1	9	1	PHH1_LYCES	P83380	lycopersico	355	1	9.1	10	1	PAP1_PARMA	P81863	pardachirus
283	1	9.1	9	1	PKK1_PERAM	P82691	periplaneta	356	1	9.1	10	1	PORB_METIM	P80901	methanobact
284	1	9.1	9	1	PSP_BOMBO	P82003	bombyx mori	357	1	9.1	10	1	PPCK_FASHE	P80525	fasciola he
285	1	9.1	9	1	R842_LITREJ	P82075	litoria fub	358	1	9.1	10	1	PSBF_CAPAN	Q03367	capsicum an
286	1	9.1	9	1	RS10_SERMA	O66936	serriatia ma	359	1	9.1	10	1	PVK_LOCHI	P83382	locusta mig
287	1	9.1	9	1	R733_BOVIN	P82526	bos taurus	360	1	9.1	10	1	Q2OB_COMTE	P80465	comamonas t
288	1	9.1	9	1	SAMP_MUSTA	P19095	mustelus ca	361	1	9.1	10	1	Q2OG_COMTE	P80466	comamonas t
289	1	9.1	9	1	SAP_STOVA	P24047	stomopneute	362	1	9.1	10	1	RCA_PINPS	P81084	pinus pinas
290	1	9.1	9	1	TALI_PICJA	P17440	pichia jadi	363	1	9.1	10	1	RRPL_PHODV	P35946	phocine dis
291	1	9.1	9	1	TAL3_PICJA	P17441	pichia jadi	364	1	9.1	10	1	RT02_BOVIN	P82923	bos taurus
292	1	9.1	9	1	THVF_PIG	P01255	sus scrofa	365	1	9.1	10	1	SLAP_BACTG	P49325	bacillus th
293	1	9.1	9	1	TKCL_CALVO	P41527	calliphora	366	1	9.1	10	1	SP34_DICMO	P81545	dictyostell
294	1	9.1	9	1	TKL1_LOCHI	P16223	locusta mig	367	1	9.1	10	1	SYK_CAMP	O56923	campylobact
295	1	9.1	9	1	TRP4_LEUMA	P81736	leucophaea	368	1	9.1	10	1	TEMK_RANTE	P46464	rana tempor
296	1	9.1	9	1	UF02_MOUSE	P18640	mus musculu	369	1	9.1	10	1	TKL2_LOCHI	P16224	locusta mig
297	1	9.1	9	1	UJAR_HUMAN	P11931	homo sapien	370	1	9.1	10	1	TKL3_LOCHI	P30249	locusta mig
298	1	9.1	9	1	ULAH_HUMAN	P1934	homo sapien	371	1	9.1	10	1	TKL4_LOCHI	P30250	locusta mig
299	1	9.1	9	1	ULAK_MOUSE	P99031	mus musculu	372	1	9.1	10	1	TKN1_SCYCA	P08608	scytorhinu
300	1	9.1	9	1	UN19_PAPA	P81355	clostridium	373	1	9.1	10	1	TKNB_CHICK	P19851	gallus gall
301	1	9.1	9	1	UPA6_HUMAN	P30089	homo sapien	374	1	9.1	10	1	TKNB_ONCMY	P22689	oncorhynch
302	1	9.1	9	1	UPA7_HUMAN	P30092	homo sapien	375	1	9.1	10	1	TKNB_RANCA	P22689	rana catesb
303	1	9.1	9	1	UPA7_HUMAN	P30093	homo sapien	376	1	9.1	10	1	TKNB_RANRI	P29135	rana ridibu
304	1	9.1	9	1	XYLA_STERSU	P19149	streptomyce	377	1	9.1	10	1	TKN1_PHYBI	P08610	phyllomedus
305	1	9.1	9	1	YHFR_AZOV1	P25825	azotobacter	378	1	9.1	10	1	TKS1_AEDAE	P42634	aedes aegypt
306	1	9.1	10	1	AGE1_AGRAE	P83465	agroclybe ae	379	1	9.1	10	1	TKS2_AEDAE	P42635	aedes aegypt
307	1	9.1	10	1	AKHX_LOCHI	P81626	locusta mig	380	1	9.1	10	1	TKU1_UREUN	P40751	urechis uni
308	1	9.1	10	1	AL19_CARMA	P81822	carcinus ma	381	1	9.1	10	1	TKU2_UREUN	P40752	urechis uni
309	1	9.1	10	1	AMPN_HE'AM	P81731	helicoverpa	382	1	9.1	10	1	TMOF_AEDAE	P19425	aedes aegypt
310	1	9.1	10	1	ANG1_BOLJA	Q10581	bothrops ja	383	1	9.1	10	1	TPIS_NICPL	P19118	nicotiana p
311	1	9.1	10	1	ANG1_BOVIN	P01017	bos taurus	384	1	9.1	10	1	TRP5_LEUMA	P81737	leucophaea
312	1	9.1	10	1	ANGT_CHICK	P01018	gallus gall	385	1	9.1	10	1	TRP6_LEUMA	P81738	leucophaea
313	1	9.1	10	1	APET_CAPSI	P80474	capnocytoph	386	1	9.1	10	1	TRP8_LEUMA	P81740	leucophaea
314	1	9.1	10	1	BPP2_PCTIN	P30422	bothrops in	387	1	9.1	10	1	TRP9_LEUMA	P81741	leucophaea
315	1	9.1	10	1	BPP2_PCTJA	P01022	bothrops ja	388	1	9.1	10	1	UH05_RAT	P56573	rattus norv
316	1	9.1	10	1	CATB_SHEEP	P83205	ovis aries	389	1	9.1	10	1	UPA3_HUMAN	P40930	homo sapien
317	1	9.1	10	1	COXA_ONCMY	P80328	oncorhynch	390	1	9.1	10	1	UPA2_HUMAN	P30088	homo sapien
318	1	9.1	10	1	COXH_ONCMY	P80331	oncorhynch	391	1	9.1	10	1	UPA4_HUMAN	P30090	homo sapien
319	1	9.1	10	1	COXK_ONCMY	P80332	oncorhynch	392	1	9.1	10	1	UPA9_HUMAN	P30095	homo sapien
320	1	9.1	10	1	COXO_RAT	P80432	rattus norv	393	1	9.1	10	1	UR11_HUMAN	P32118	homo sapien
321	1	9.1	10	1	COXO2_HUCKB	P80982	thinusus obe	394	1	9.1	10	1	UR17_HUMAN	P34990	homo sapien
322	1	9.1	10	1	EST_LACCA	P81758	lactobacill	395	1	9.1	10	1	URES_MORMO	P17339	morganella
323	1	9.1	10	1	ESTA_SCHGA	P81012	schizaphis	396	1	9.1	10	1	UXBI_YEAST	P99012	saccharomyc
324	1	9.1	10	1	FAR2_PENMO	P81317	penaeus mon	397	1	9.1	10	1	VEG6_BACSU	P80699	bacillus su
325	1	9.1	10	1	FAR5_MACKS	P83278	macrobrachi	398	1	9.1	11	1	ANGT_CRIGE	P09037	crinia geor

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399 1 9.1 11 1 ASL1_BACSE
400 1 9.1 11 1 ASL2_BACSE
401 1 9.1 11 1 BPP3_BOTIN
402 1 9.1 11 1 BPP4_BOTIN
403 1 9.1 11 1 BPP4_BOTIN
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470 1 9.1 11 1 BPP4_BOTIN
471 1 9.1 11 1 BPP4_BOTIN

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us-09-787-443-1-oli.rsp

ALIGNMENTS

RESULT 1

B44K_PORGI

ID B44K_PORGI STANDARD: PRT: 8 AA.

AC P81886:

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE 44 kDa immunogenic protein (Fragment).

OS Porphyromonas gingivalis (Bacteroides fragilis).

OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;

OC Porphyromonadaceae; Porphyromonas.

OX NCBI_TaxID=837:

FN 11

RP SEQUENCE:

RC SIRALIN-VPB 3492:

RX MEDLINE-20198497: PubMed=10731616:

RA Norris J.M., Love D.N.:

RI "Serum antibody responses of cats to soluble whole cell antigens of

RT feline Porphyromonas gingivalis";

RL Vet. Microbiol. 73:37-49(2000).

CC -!- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.

KW Antigen.

FT NON_TER

SQ SEQUENCE 8 AA: 989 MW; 9554540326CB476D CRC64;

Query Match 36.4%; Score 4; DB 1; Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 6 KRNI 9

Db 5 KRNI 8

RESULT 2

CS15_BACSU

ID CS15_BACSU STANDARD: PRT: 11 AA.

AC P81095;

DT 15-JUL-1998 (Rel. 36, Created)

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DT 15 JUL-1998 (Rel. 36, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cold shock protein CS15 (11 kDa cold shock protein) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID:1423;
RN [1];
RP SEQUENCE.
RC STRAIN:168 / JH642;
RA Graumann P.L., Schmid R., Marahleh M.A.;
RL Submitted (OCT-1997) to the SWISS-PROT data bank.
RN [2];
RP CHARACTERIZATION.
RC STRAIN:168 / JH642;
RX MEDLINE:96345629; PubMed-8755922;
RA Graumann P., Schroeder K., Schmid R., Marahleh M.A.;
RT "Cold shock stress-induced proteins in Bacillus subtilis.";
RL J. Bacteriol. 178:4611-4619(1996).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- INDUCTION: In response to low temperature.
CC -!- CAUTION: Could not be found in the genome of B. subtilis 168.
FT NON_TER 11
SQ SEQUENCE 11 AA: 1360 MW: 156683.63 kDa CRC64:
Query Match 36.48; Score 4; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RNK 10
DB 2 RNK 5
RESULT 3
RLC:ACHLA
ID R016_ACHLA STANDARD: PRI: 10 AA.
AC P29221;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01 NOV-1995 (Rel. 32, Last annotation update)
DE 50S ribosomal protein L16 (Fragment).
GN RPL16;
OS Acholeplasma laidlawii.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OC Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID:2148;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE:12213505; PubMed 1554679;
RA Lim P.C., Sears B.B.;
RT "Evolutionary relationships of a plant ribonucleoprotein-like organism and Acholeplasma laidlawii deduced from two ribosomal protein gene sequences.";
RL J. Bacteriol. 174:2606-2611(1992).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS LOCATED AT THE A SITE OF THE PEPTIDYLTRANSFERASE CENTER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC
DR EMBL: M74771; AAA21914.1;
DR PIR: F41839; F41839;
DR InterPro: IPR000114; Ribosomal_L16;
DR PROSITE: PS00586; RIBOSOMAL_L16_1; Partial.
DR PRSITE: PS00701; RIBOSOMAL_L16_2; Partial.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 10
SQ SEQUENCE 10 AA: 1324 MW: 15386.62 kDa CRC64:
Query Match 27.3%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SKK 4
DB 10 SKK 12
RESULT 5
RLS19_PPWPB
ID R519_PPWPB STANDARD: PRI: 14 AA.
AC Q52693;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19 (Fragment).
GN RPS19 OR RPS19;
OS Pigeon pea 'watches' from phytoplasma.
OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
OX Acholeplasmataceae; Phytoplasma.
FT NON_TER 10
SQ SEQUENCE 10 AA: 1324 MW: 15386.62 kDa CRC64:
Query Match 27.3%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 SKK 4
DB 10 SKK 12

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RT plastid enzymes.*;
OC Planta 201:261-272(1997).
OX NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
KX MEDLINE=88326322; PubMed 3415688;
KA Kohama Y., Matsunoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
KT "Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.*";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR: A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 IK 10
DB 4 IK 5

RESULT 11
ALL7_CARMA STANDARD: PRT: 8 AA.
ID P81809; P81810;
AC 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Carcinustatin 7 (Contains: Carcinustatin 6; Carcinustatin 1).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed-9461295;
KA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas.*";
RL Eur. J. Biochem. 250:727-734(1997).
CC -- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
OC -- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT PEPTIDE 1 6 CARCINUSTATIN 7.
FT PEPTIDE 2 8 CARCINUSTATIN 6.
FT PEPTIDE 4 8 CARCINUSTATIN 1.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA; 825 MW; 922879DCB4775BD CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
DB 1 AS 2

RESULT 12
FAR1_PENMO STANDARD: PRT: 8 AA.
ID P83316;
AC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLPL (GDRNFLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;

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RT plastid enzymes.*;
OC Planta 201:261-272(1997).
OX NCBI_TaxID=8236;
RN [1]
RP SEQUENCE.
RC TISSUE=Muscle;
KX MEDLINE=88326322; PubMed 3415688;
KA Kohama Y., Matsunoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
KT "Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.*";
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR: A31570; A31570.
SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASK 3
DB 6 ASK 8

RESULT 9
RS20_PACST STANDARD: PRT: 15 AA.
ID RS20_PACST
AC P59681;
DT 15-SEP-2003 (Rel. 42, Created)
DI 15-SEP-2003 (Rel. 42, Last sequence update)
DE 30S ribosomal protein S20 (BS20) (Flagtagent).
GN RPST.
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE.
RC STRAIN=10;
RX PubMed-4507606;
KA Yaguchi M., Matheson A.T., Visentin L.P.;
RT "Prokaryotic ribosomal proteins: N-terminal sequence homologues and structural correspondence of 30 S ribosomal proteins from Escherichia coli and Bacillus stearothermophilus.*";
RL FEBS Lett. 46:296-300(1974).
CC -- FUNCTION: Binds directly to 16S ribosomal RNA (by similarity).
OC -- SIMILARITY: BELONGS TO THE S20 FAMILY OF RIBOSOMAL PROTEINS.
DR HAMAP; MF-00560; ?; 1.
KW Ribosomal protein; rRNA-binding
FT INIT_MET 0
FT NON_TER 15
SQ SEQUENCE 15 AA; 1645 MW; 4F64620E470206064 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 NIK 10
DB 2 NIK 4

RESULT 10
ACLTHUAL STANDARD: PRT: 8 AA.
AC P18691;
DI 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DI 01-NOV-1990 (Rel. 16, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacares (Yellowfin tuna) (Neohannus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Perciformes; Strombroides;

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CC Penaeidae; Penaeus.
 OX NCBI_TaxID:6687;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE-Eyestalk;
 RX MEDLINE-21956277; PubMed-11959015;
 RA Sithigorndul P., Pupem J., Krunkasom C., Lomyant S.,
 Chaisuthangkura P., Sithigorndul W., Pitsom A.,
 RT *Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
 of the giant tiger prawn Penaeus monodon.*
 RL Comp. Biochem. Physiol. 131B:125-137(2002).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 OX -1- MASS SPECTROMETRY: MW-1024.8; MEDIAN MASS:
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 8
 FT MOD_RES 8
 SQ SEQUENCE 8 AA: 1024 MW: 7204.729C4540A8 CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RN 8
 DB 3 RN 4
 RESULT 13
 ID FAR3_HOMAM STANDARD: PRT; 8 AA.
 AC P41487;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE FMRFamide-like neuropeptide 3 (Fli 3) (F2).
 OS Homarus americanus (American lobster).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 CC Nephropoidea; Nephropidae; Homarus.
 OX NCBI_TaxID:6706;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Pericardial organs;
 RX MEDLINE-88116164; PubMed-3429714;
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
 RT *Purification and characterization of FMRFamide-like immunoreactive
 substances from the lobster nervous system: Isolation and sequence
 analysis of two closely related peptides.*
 RL J. Comp. Neurol. 266:16-26(1987).
 CC -1- FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC
 NEUROMUSCULAR JUNCTIONS.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 8
 FT MOD_RES 8
 SQ SEQUENCE 8 AA: 1067 MW: DDD40729C4540451 CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RN 8
 DB 3 RN 4
 RESULT 14
 ID FAR4_HOMAM STANDARD: PRT; 8 AA.
 AC P41487;
 DT 01-NOV-1995 (Rel. 32, Created)
 DE FMRFamide-like neuropeptide 4 (Fli 4) (F1).
 OS Homarus americanus (American lobster).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 CC Nephropoidea; Nephropidae; Homarus.
 OX NCBI_TaxID:6706;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Pericardial organs;
 RX MEDLINE-88116164; PubMed-3429714;
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
 RT *Purification and characterization of FMRFamide-like immunoreactive
 substances from the lobster nervous system: Isolation and sequence
 analysis of two closely related peptides.*
 RL J. Comp. Neurol. 266:16-26(1987).
 CC -1- MISCELLANEOUS: PERICARDIAL ORGANS RELEASE THIS PEPTIDE WITH 100 NM
 POTASSIUM IN THE PRESENCE OF CALCIUM.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 8
 FT MOD_RES 8
 SQ SEQUENCE 8 AA: 1054 MW: C6D4J729C4540AB5 CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RN 8
 DB 3 RN 4
 RESULT 15
 ID LCK4_LEUMA STANDARD: PRT; 8 AA.
 AC P21143;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DE Leucokinin IV (L-IV).
 OS Leucophaea maderae (Madeira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;
 CC Blaberidae; Leucophaea.
 OX NCBI_TaxID:5988;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT *Primary structure and synthesis of two additional neuropeptides
 from Leucophaea maderae: members of a new family of
 cephalomyotropins.*
 RL Comp. Biochem. Physiol. 84C:271-276(1986).
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 ACTIVITY OF COCKROACH PROTHODIUM (HINDGUT).
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
 CC Neuropeptide; Amidation.
 KW MOD_RES 8
 FT MOD_RES 8
 SQ SEQUENCE 8 AA: 906 MW: DC6365B1E9D5BDDA CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AS 2
 DB 2 AS 3
 RESULT 16
 ID LPMS_STAEP STANDARD: PRT; 8 AA.
 AC P41487;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide 4 (Fli 4) (F1).
 OS Homarus americanus (American lobster).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
 CC Nephropoidea; Nephropidae; Homarus.
 OX NCBI_TaxID:6706;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Pericardial organs;
 RX MEDLINE-88116164; PubMed-3429714;
 RA Trimmer B.A., Kobierski L.A., Kravitz E.A.;
 RT *Purification and characterization of FMRFamide-like immunoreactive
 substances from the lobster nervous system: Isolation and sequence
 analysis of two closely related peptides.*
 RL J. Comp. Neurol. 266:16-26(1987).
 CC -1- FUNCTION: CAN ACT AS A MODULATOR OF EXOSKELETAL AND CARDIAC
 NEUROMUSCULAR JUNCTIONS.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 FAMILY.
 CC Neuropeptide; Amidation.
 KW MOD_RES 8
 FT MOD_RES 8
 SQ SEQUENCE 8 AA: 1067 MW: DDD40729C4540451 CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RN 8
 DB 3 RN 4
 RESULT 15
 ID LCK4_LEUMA STANDARD: PRT; 8 AA.
 AC P21143;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DE Leucokinin IV (L-IV).
 OS Leucophaea maderae (Madeira cockroach).
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;
 CC Blaberidae; Leucophaea.
 OX NCBI_TaxID:5988;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE-Head;
 RA Holman G.M., Cook B.J., Nachman R.J.;
 RT *Primary structure and synthesis of two additional neuropeptides
 from Leucophaea maderae: members of a new family of
 cephalomyotropins.*
 RL Comp. Biochem. Physiol. 84C:271-276(1986).
 CC -1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
 ACTIVITY OF COCKROACH PROTHODIUM (HINDGUT).
 CC -1- SIMILARITY: TO THE OTHER LEUCOKININS.
 CC Neuropeptide; Amidation.
 KW MOD_RES 8
 FT MOD_RES 8
 SQ SEQUENCE 8 AA: 906 MW: DC6365B1E9D5BDDA CRC64;
 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AS 2
 DB 2 AS 3
 RESULT 16
 ID LPMS_STAEP STANDARD: PRT; 8 AA.
 AC P41487;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)


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RESULT 19
CONG_CONST          STANDARD:          PRT:          9 AA.
AC  P05487:
DT  01-NOV-1988 (Rel. 09, Created)
DT  01-NOV-1988 (Rel. 09, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Arg-conopressin S.
OS  Conus striatus (Striated cone).
OC  Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC  Apogastropoda; Caenogastropoda; Sordariata; Hypsogastropoda;
OC  Neogastropoda; Conoidea; Conidae; Conus
OX  NCBI_TaxID=6493;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=89058532; PubMed=3680228;
RA  Cruz L.J., de Santos V., Zataralia G.G., Kamilo C.A., Zeikos R.D.,
RA  Gray W.R., Olivera B.M.;
*Invertebrate vasopressin/oxytocin homologs. Characterization of
*peptides from Conus geographus and Conus striatus venoms."
NL  J. Biol. Chem. 262:15821-15824 (1987);
RN  [2]
RP  REVIEW.
RX  MEDLINE=89024586; PubMed=3052286;
RA  Gray W.R., Olivera B.M., Cruz L.J.;
*Peptide toxins from venomous Conus snails."
RL  Annu. Rev. Biochem. 57:665-700 (1988);
OC  1- FUNCTION: Targets vasopressin-oxytocin related receptors.
CC  1- SUBCELLULAR LOCATION: Secreted.
CC  1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC  1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR  EIR: B28495; B28495.
DR  InterPro: IPR000981; Neurohyp_born.
DR  Pfam: PF00220; hormone_1.
LP  PROSITE: PS00264; NEUROHYPOPHYS_HORM.
KW  Hormone; Amidation.
FT  DISULFID 1 6
FT  MOD_RES 9 9  AMIDATION
SQ  SEQUENCE 9 AA: 1031 MW: 178376454.656 CRC64:

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RN 8
DB 11
   4 RN 5

RESULT 20
CONG_CONST          STANDARD:          PRT:          9 AA.
AC  P84047:
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Contryphan Vn.
OS  Conus ventricosus (Mediterranean cone).
OC  Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC  Apogastropoda; Caenogastropoda; Sordariata; Hypsogastropoda;
OC  Neogastropoda; Conoidea; Conidae; Conus.
OX  NCBI_TaxID=117992;
RN  [1]
RP  SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RX  TISSUE-Venom;
RA  Massilia G.R., Schinina M.E., Asgenzi P., Pedicelli F.;
*Contryphan-Vn: a novel peptide from the venom of the Mediterranean
*snail Conus ventricosus."
RL  Biochem. Biophys. Res. Commun. 289:906-913 (2001);
OC  1- SUBCELLULAR LOCATION: Secreted
CC  1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC  1- MASS SPECTROMETRY: MW=1088.6; METHOD MAINT.

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CC  1- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW  Toxin; Amidation; D-amino acid.
FT  DISULFID 3 9
FT  MOD_RES 5 5  D-TRYPTOPHAN.
FT  MOD_RES 9 9  AMIDATION.
SQ  SEQUENCE 9 AA: 1091 MW: 8038676323676EBA CRC64:

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KP 5
DB 6 KP 7

RESULT 21
DISIP_RABBIT          STANDARD:          PRT:          9 AA.
AC  P01158:
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Delta sleep-inducing peptide (DSIP).
OS  Oryctolagus cuniculus (Rabbit).
OC  Eukaryota; Metazoa; Chordata; Cniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX  NCBI_TaxID=9986;
RN  [1]
RP  SEQUENCE.
RX  MEDLINE=77185324; PubMed=862769;
RA  Monnier M., Daudier L., Gachter R., Maier P.F., Tobler H.J.,
RA  Schoenenberger G.A.;
*The delta sleep inducing peptide (DSIP). Comparative properties of
*the original and synthetic nonapeptide."
RL  Experientia 33:548-552 (1977);
RN  [2]
RP  SEQUENCE AND SYNTHESIS.
RX  MEDLINE=79054421; PubMed=568769;
RA  Schoenenberger G.A., Maier P.F., Tobler H.J., Wilson K., Monnier M.;
*The delta EEG (sleep)-inducing peptide (DSIP). XI. Amino-acid
*analysis, sequence, synthesis and activity of the nonapeptide."
RL  Pflugers Arch. 376:119-129 (1978);
RN  [3]
RP  REVIEW.
PX  MEDLINE 87175129; PubMed=3550726;
RA  Gray M.V., Kastin A.J.;
*Delta-sleep-inducing peptide (DSIP): an update."
RL  Peptides 7:1165-1187 (1986);
CC  1- FUNCTION: WHEN INFUSED INTO THE MESODIENCEPHALIC VENTRICLE OF
CC  RECIPIENT RABBITS INDUCES SPINDLE AND DELTA EEG ACTIVITY AND
CC  REDUCED MOTOR ACTIVITIES.
CC  1- MISCELLANEOUS: THIS PEPTIDE WAS OBTAINED FROM DIALYSATES OF
CC  OCCIPITAL VENOUS SINUS BLOOD FROM RABBITS KEPT ASLEEP BY ELECTRIC
CC  STIMULATION OF THE THALAMUS.
CC  1- DATABASE: NAME-Protein Spotlight;
CC  NOTE-Issue 8 of March 2001;
CC  WWW="http://www.expasy.org/spotlight/articles/sptlt008.html".
DR  PIR: A01422; QDRB.
SQ  SEQUENCE 9 AA: 849 MW: DDD365BDDAA8787D CRC64:

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
DB 11
   6 AS 7

RESULT 22
FAR4_CALVO
1D  FAR4_CALVO          STANDARD:          PRT:          9 AA.

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13  FAP6_MACRS          STANDARD:          PRI:          9 AA
14  AC PB1279,
15  DT 28-FEB-2003 (Rel. 41, Last sequence update)
16  DT 26-FEB-2003 (Rel. 41, Last annotation update)
17  DT 26-FEB-2003 (Rel. 41, Last annotation update)
18  DE PMSFamide-like neuropeptide FLP6 (EGSRNHLRF-amide).
19  OS Macrobrachium rosenbergii (Giant Fresh Water Prawn).
20  CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
21  CC Eumalacostraca; Eucarida; Decapoda; Pteryopoda; Caridea;
22  CC Palaemonoidea; Palaemonidae; Macrobrachium.
23  GX NCBI_TaxID=79674;
24  RN
25  RP SEQUENCE, AND MASS SPECTROMETRY.
26  RC TISSUE: Eyestalk.
27  RA MEDLINE=22107394; PubMed=11179812;
28  RA Sithigorakul P., Sarathchokum W., Lonsyant S., Panchat N.,
29  RA Sithigorakul W., Petson A.;
30  RT "Three more novel PMSFamide-like neuropeptide sequences from the
31  RT eyestalk of the giant freshwater prawn Macrobrachium rosenbergii."
32  RL Peptides 22:191-197(2001).
33  CC -1- MASS SPECTROMETRY: MH=1080.7; METHOD=MALDI.
34  CC -1- SIMILARITY: BELONGS TO THE FAP6 (PMSFAMIDE-RELATED PEPTIDE)
35  CC FAMILY.
36  CR GO: GO:0007218; P:neuropeptide signaling pathway; IDA;
37  CR Neuropeptide; Amidation.
38  KW Neuropeptide; Amidation.
39  FT Mol. Res. 9 AM:tail-N.
40  SQ SEQUENCE 9 AA: 1081 MW: 2680072954545878 (55.64);
41
42  Query Match 18.2% Score 2; DB 1; Length 9;
43  Best Local Similarity 100.0%; Pred. No. 1.3e-05;
44  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
45
46  QY 7 RN 8
47  DB 4 RN 5
48
49  RESULT 27
50  HUIU_KLEAE
51  ID HUIU_KLEAE          STANDARD:          PRI:          9 AA.
52  AC P12381,
53  DT 01-OCT-1989 (Rel. 12, Created)
54  DT 01-OCT-1989 (Rel. 12, Last sequence update)
55  DT 28-FEB-2003 (Rel. 41, Last annotation update)
56  DE Urocanate hydratase (EC 4.2.1.49) (Urocanase) (indole-3-pyruvate
57  DE hydratase) (fragment).
58  OS Klebsiella aerogenes.
59  CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;
60  CC Enterobacteriaceae; Klebsiella.
61  GX NCBI_TaxID=28451;
62  RN
63  RP SEQUENCE FROM N.A.
64  RA MEDLINE=86198618; PubMed=2834335;
65  RA Nieuwkoop A.J., Baldauf S.A., Hudspett M.E.S., Bender R.A.;
66  RT "Bidirectional promoter in the huc(p) region: 1 The histidine
67  RT utilization (hut) operons from Klebsiella aerogenes."
68  RL J. Bacteriol. 170:2240-2246(1988).
69  RN
70  RP SEQUENCE FROM N.A.
71  RA MEDLINE=90368611; PubMed=2203754;
72  RA Schwacha A., Bender R.A.;
73  RT "Nucleotide sequence of the gene encoding the repressor for the
74  RT histidine utilization genes of Klebsiella aerogenes."
75  RL J. Bacteriol. 172:5477-5481(1990).
76  CC -1- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydro-4-imidazol-4-yl)propanoate + urocanate -> H(2)O
77  CC -1- COFACTOR: Binds 1 NAD per subunit (5% similarity).
78  CC -1- PATHWAY: Histidine degradation; Serine Syn.
79  CC -1- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).
80  CC -1- SIMILARITY: BELONGS TO THE UROCANASE FAMILY
81  CC
82  CC This SWISS-PROT entry is copyrighted through a collaboration

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CC
CC -----
CC EMBL: M19665; AAA25078.1;
CC EXHL: M34604; AAA25076.1;
CC HAMAP: MF_00577; 1.
CC InterPro: IPR00193; Grotadase.
CC PROSITE: PS01233; UROCANASE; PARTIAL.
CC Histidine metabolism; Lyase; NAD.
CC Non-Ter 9
CC SEQUENCE 9 AA: 1140 MW: 970FC41B5325A6C5 CRC64:
41
42  Query Match 18.2% Score 2; DB 1; Length 9;
43  Best Local Similarity 100.0%; Pred. No. 1.3e-05;
44  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
45
46  QY 2 SK 3
47  DB 4 SK 5
48
49  RESULT 28
50  LPCA_STAAU
51  ID LPCA_STAAU          STANDARD:          PRI:          9 AA.
52  AC P36884;
53  DT 01-JUN-1994 (Rel. 29, Created)
54  DT 01-JUN-1994 (Rel. 29, Last sequence update)
55  DT 01-OCT-1994 (Rel. 30, Last annotation update)
56  DE Chloramphenicol resistance leader peptide.
57  OS Staphylococcus aureus, and
58  OS Streptococcus agalactiae.
59  CC Plasmid pSCS6. Plasmid pSCS7, Plasmid pUB112, and Plasmid pIP501.
60  CC Bacteria; Firmicutes; Bacillales; Staphylococcus.
61  GX NCBI_TaxID=1280, 1311;
62  RN
63  RP SEQUENCE FROM N.A.
64  KC SPECIES STRAIN: STRAIN-415; PLASMID=pSCS7;
65  RX MEDLINE=9207652; PubMed=1929326;
66  RA Schwarz S., Cardoso M.;
67  RT "Nucleotide sequence and phylogeny of a chloramphenicol
68  RT acetyltransferase encoded by the plasmid pSCS7 from Staphylococcus
69  RT aureus."
70  RL Antimicrob. Agents Chemother. 35:1551-1556(1991).
71  RN
72  RP SEQUENCE FROM N.A.
73  KC SPECIES STRAIN: STRAIN-415; PLASMID=pSCS6;
74  RX MEDLINE=92388047; PubMed=1517170;
75  RA Cardoso M., Schwarz S.;
76  RT "Nucleotide sequence and structural relationships of a
77  RT chloramphenicol acetyltransferase encoded by the plasmid pSCS6 from
78  RT Staphylococcus aureus."
79  RL J. Appl. Bacteriol. 72:289-293(1992).
80  RN
81  RP SEQUENCE FROM N.A.
82  KC SPECIES STRAIN: STRAIN-415; PLASMID=pUB112;
83  RX MEDLINE=86081739; PubMed=3865770;
84  RA Brueckner R., Matzura H.;
85  RT "Regulation of the inducible chloramphenicol acetyltransferase gene
86  RT of the Staphylococcus aureus plasmid pUB112."
87  RL EMBO J. 4:2295-2300(1985).
88  RN
89  RP SEQUENCE FROM N.A.
90  KC SPECIES STRAIN: STRAIN-415; PLASMID=pIP501;
91  RX MEDLINE=93096867; PubMed=1461942;
92  RA Trica-Cuot P., de Cespedes G., Horaud T.;
93  RT "Nucleotide sequence of the chloramphenicol resistance determinant of
94  RT the streptococcal plasmid pIP501."
95  RL Plasmid 28:272-276(1992).
96  CC

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CC
 DR EMBL: M58155; AAA26612.1; -
 DR EMBL: M58156; AAA16528.1; -
 DR EMBL: X02872; CAA26630.1; -
 DR EMBL: X60827; CAA43217.1; -
 DR EMBL: X65462; CAA46454.1; -
 DR PIR: B24362; B24362.
 DR PIR: S30494; S30494.
 KW Leader peptide; Antibiotic resistance; Plasmid.
 SQ SEQUENCE 9 AA: 1074 MW: 509CAB5AAR05B33 CRC64;

Query Match 18.2% Score 2: 25 1: Length: 9;
 Best Local Similarity 100.0% Pred. No. 1.3e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KK 4
 II
 DB 2 KK 3

RESULT: 29
 NEF_HV128
 ID NEF_HV128 STANDARD; PRT; 9 AA.
 AC P12481.
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Negative factor (F-protein) (27 kDa protein) (FusF) (Fragment).
 GN NEF.
 OS Human immunodeficiency virus type 1 (Z-84 isolate) (HIV-1).
 OC Viruses; Retroviral viruses; Retroviridae; Lentiviruses.
 OX NCBI_TaxID=11681;
 RN II
 RP SEQUENCE FROM N.A.
 RX MEDLINE 88281278; PubMed=3395517;
 RA Youniss J., Josephs S.F., Reitz M.S. Jr., Zagury D., Wong-Staal F.,
 RA Gallo R.C.;
 RT "Nucleotide sequence analysis of the env gene of a new Zairian
 RT isolate of HIV-1.";
 RL AIDS Res. Hum. Retroviruses 4:165-174(1988).
 CC -!- FUNCTION: NEF has GTPase, GTP-binding and a tyrosine phosphorylating
 CC activities. It seems to downregulate the CD4(55) antigen.
 CC -!- MISCELLANEOUS: THE Z-84 ISOLATE WAS TAKEN FROM A 54 YEAR OLD
 CC ZAIREAN MALE.

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CC
 DR EMBL: J03653; AAA44687.1; -
 DR HIV; J03653; NEFSJY1.
 KW AIDS; Myristate; GTP-binding.
 FT LIPID 2
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA: 967 MW: 319CB335A734876 CRC64;

Query Match 18.2% Score 2: DB 1: Length: 9;
 Best Local Similarity 100.0% Pred. No. 1.3e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 SK 3
 II

DB 6 SK 7

RESULT 30
 NEUU_CAVPO
 ID NEUU_CAVPO STANDARD; PRT; 9 AA.
 AC P34966;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuromedin U-9 (NMU-9).
 GN NMU.

OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN II
 RP SEQUENCE.

PC TISSUE=Small intestine;
 RX MEDLINE=90341105; PubMed=2381877;
 RA Murphy R., Turner C.A., Furness J.B., Parker L., Giraud A.;
 RT "Isolation and microsequence analysis of a novel form of neuromedin U
 RT from guinea pig small intestine.";
 RL Peptides 11:613-617(1990).

CC -!- FUNCTION: STIMULATES UTERINE SMOOTH MUSCLE CONTRACTION AND CAUSES
 CC SELECTIVE VASOCONSTRICTION.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE NMU FAMILY.

DR InterPro: IPR001942; NMU.
 DR Pfam: PF02070; NMU; 1.
 DR PROSITE: PS00967; NMU; 1.
 KW Amidation; Hormone.
 FT MOD_RES 5 9 AMIDATION.
 SQ SEQUENCE 9 AA: 1169 MW: 1ECF177409C729DB CRC64;

Query Match 18.2% Score 2: DB 1: Length: 9;
 Best Local Similarity 100.0% Pred. No. 1.3e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 RN 8
 II
 DB 8 RN 9

RESULT 31
 OXYT_EISFO
 ID OXYT_EISFO STANDARD; PRT; 9 AA.
 AC P42994;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Annetocin.

OS Eisenia foetida (Common brandling worm) (Common dung-worm).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
 OC Lumbricina; Lumbricidae; Eisenia.
 OX NCBI_TaxID=6396;
 RN II

RP SEQUENCE.
 RC TISSUE=Pituitary;
 RX MEDLINE=94121660; PubMed=8292046;

RA Oumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
 RA Nomoto K.;
 RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
 RT Eisenia foetida.";
 RL Biochem. Biophys. Res. Commun. 198:393-399(1994).

CC -!- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
 CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE ANIMAL THROUGH
 CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
 CC NEPHRIDIAL FUNCTION.

CC -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
 CC PIR: PC2021; PC2021.
 DR InterPro: IPR000981; Neuhyp_horm.
 DR Pfam: PF00220; Hormone4; 1.

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DR PROSITE: PS00264: NEUROHYPOPHYS_HORM: FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 5 9 AMIDATION.
SQ SEQUENCE 9 AA: 996 MW: 145874541209 CRC64:
Query Match: 18.2%: Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RN 8
DB 4 RN 5

RESULT 32
OXYT_OCTVU
ID OXYT_OCTVU STANDARD: PRT: 9 AA.
AC P80027;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Cephalotoxin.
OS Octopus vulgaris (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidae; Naucoroidea;
OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopas.
OX NCBI_TaxID=6645;
RN [1]
RP SEQUENCE.
RC TISSUE Nerve endings.
RX MEDLINE=92270139; PubMed=159145;
RA Reich G.;
RT "A new peptide of the oxytocin/vasopressin family isolated from
RT nerves of the cephalopod Octopus vulgaris."
RA Neurosci. Lett. 134:191-194(1992).
CC -! FUNCTION: HAS A ROLE IN THE NEUROSECRETORY SYSTEM OF THE VENA
CC CAVA.
CC -! SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro: IPR000981; Neurohyp-form.
DR Pfam: PF00220; Hormone4.1.
DR PROSITE: PS00264: NEUROHYPOPHYS_HORM. 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 5 9 AMIDATION.
SQ SEQUENCE 9 AA: 1072 MW: 177474541209 CRC64:
Query Match: 18.2%: Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RN 8
DB 4 RN 5

RESULT 33
ULAB_HUMAN
ID ULAB_HUMAN STANDARD: PRT: 9 AA.
AC P31929;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Unknown protein from 2D-page of liver tissue (Spot 106) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94114369; PubMed=813870;
RA Hughes G.J., Frutiger S., Paguet N., Pasquati C., Sanchez J.-C.,
RA Tissot J.-D., Balroch A., Appel R.D., Hochstrasser D.F.;
DR PROSITE: PS00264: NEUROHYPOPHYS_HORM: FALSE_NEG.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 5 9 AMIDATION.
SQ SEQUENCE 9 AA: 996 MW: 145874541209 CRC64:
Query Match: 18.2%: Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 RN 8
DB 4 RN 5

RESULT 34
AH3_PROSE
ID AH3_PROSE STANDARD: PRT: 10 AA.
AC P29261;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
DE isozyme II) (AH 11) (Fragment).
OS Prunus serotina (Black cherry).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids 1; Rosales; Rosaceae; Amygdaloideae; Prunus.
OX NCBI_TaxID=23207;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
KA Li C.P., Swain E., Poulton J.E.;
RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase."
RL Plant Physiol. 100:282-290(1992).
CC -! CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O -> (R)-prunasin + D-
CC glucose.
CC -! SUBUNIT: Monomer.
CC -! DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COVLEDON
CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
CC EMBRYONAL TISSUES.
CC -! PTM: GLYCOSYLATED.
KW Glucosidase; Hydrolase; Glycoprotein; Multigene family.
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1033 MW: 333188051E04777 CRC64:
Query Match: 18.2%: Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AS 2
DB 8 AS 9

RESULT 35
BPP8_BOTIN
ID BPP8_BOTIN STANDARD: PRT: 10 AA.
AC P30426;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island Jararaca) (Queimada Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroqlossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]

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RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE-90351557; PubMed-2386615;
RA Cintra A.C.O., Vieira C.A., Gaglioli J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
  peptides from Bothrops insularis snake venom."
RL J. Protein Chem. 9:221-227(1990);
CC -!- FUNCTION: This peptide both inhibits the activity of the
  angiotensin-converting enzyme and enhances the action of
  bradykinin by inhibiting the kinases that inactivate it.
  It acts as an indirect hypotensive agent.
DR PIR: H37196; H37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1173 MW; 2FFB3545761F6B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KI 9
DB 7 NI 8

RESULT 35
BRP_VIPAS
ID APP_VIPAS STANDARD; PRT: 10 AA.
AC P31351;
DI 01-JUL-1993 (Rel. 26, Created)
DI 01-FEB-1994 (Rel. 28, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin converting
  enzyme inhibitor).
OS Vipera aspis (Aspic viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Vipridae; Viperinae; Vipera.
OX NCBI_TaxID=8706;
RN [1]
RP SEQUENCE.
RX MEDLINE-90382616; PubMed-2169439;
RA Komori Y., Sugihara H.;
RT "Characterization of a new inhibitor for angiotensin converting
  enzyme from the venom of Vipera aspis aspic."
RL Int. J. Biochem. 22:767-771(1990).
CC -!- FUNCTION: This peptide both inhibits the activity of the
  angiotensin-converting enzyme and enhances the action of
  bradykinin by inhibiting the kinases that inactivate it.
  It acts as an indirect hypotensive agent.
DR PIR: A60377; XASNPC.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 10 AA; 1062 MW; 3DAB27C427636734 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6
DB 6 PK 7

RESULT 37
BRK_ONCMY
ID BRK_ONCMY STANDARD; PRT: 10 AA.
AC Q9PRZ1;
DI 16-OCT-2001 (Rel. 40, Created)
DI 16-OCT-2001 (Rel. 40, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lysyl-bradykinin-like.

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OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OX Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
RN NCBI_TaxID=8022;
RN [1]
RP SEQUENCE.
RX MEDLINE-94039817; PubMed-8224232;
RA Conlon J.M., Olson K.R.;
RT "Purification of a vasoactive peptide related to lysyl-bradykinin from
  trout plasma."
RL FEBS Lett. 334:75-78(1993).
CC -!- FUNCTION: SMOOTH MUSCLE CONTRACTION. PROBABLY PLAYS A ROLE FOR
  THIS SYSTEM IN CARDIOVASCULAR REGULATION IN FISH.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DR PIR: S39030; S39030.
KW Bradykinin; Vasodilator.
SQ SEQUENCE 10 AA; 1193 MW; 33C59075A3786777 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KR 7
DB 1 KR 2

RESULT 38
COXM_RAT
ID COXM_RAT STANDARD; PRT: 10 AA.
AC P80431;
DI 01-NOV-1995 (Rel. 32, Created)
DI 01-NOV-1995 (Rel. 32, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIb, mitochondrial (EC 1.9.3.1)
  (Fragment).
GN COX7B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RX STRAIN=Wistar; TISSUE=Liver;
RX MEDLINE-95324529; PubMed-7601105;
RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
  amino-terminal sequences suggest identity of the fetal heart and the
  adult liver isoform."
RL Eur. J. Biochem. 230:235-241(1995).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
  CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
  MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) -> 4 ferricyclochrome
  c + 2 H(2)O.
DR PIR: S65387; S65387.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1210 MW; CFC70EB771A33326 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KK 4
DB 4 KK 5

RESULT 39

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SQ SEQUENCE 10 AA; 1097 MW; 940282620000033A CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KA 11
 II
 4 KA 5

DB

RESULT 43

GON1_PETMA STANDARD; PRT; 10 AA;

AC P80677; 1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH I)

DE (Luliberin I)

OS Chelyosoma productum

CC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogena;

CC Phlebobranchia; Corellidae; Chelyosoma

OX NCBI_TaxID-71177;

RN 11

RN SEQUENCE

KX MEDLINE-95413669; PubMed-8816823;

RA Powell J.E.F., Reska-Skinner S.M., Prakash M., Fischer W.H., Park M., Rivier J.E., Craig A.G., Mackie G.D., Sherwood N.M.;

RT "Two new forms of gonadotropin releasing hormone in a protochordate and the evolutionary implications."

RL Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464 (1996).

CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the GNRH family.

DR InterPro: IPR002012; GNRH.

DR Pfam: PF00446; GNRH; 1.

DR PROSITE: PS00473; GNRH; 1.

KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.

FT MOD_RES 10 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1264 MW; 2846363937APAA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KP 5
 II
 6 KP 9

DB

RESULT 44

GON1_PETMA STANDARD; PRT; 10 AA;

AC P04378;

DT 20-MAR-1987 (Rel. 04, Created)

DT 28-MAR-1987 (Rel. 04, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH I)

DE (Luliberin I)

OS Petromyzon marinus (Sea lamprey).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;

CC Petromyzontiformes; Petromyzontidae; Petromyzon.

OX NCBI_TaxID-7757;

RN 11

RN SEQUENCE

KX MEDLINE-95413669; PubMed-8816823;

RA Powell J.E.F., Reska-Skinner S.M., Prakash M., Fischer W.H., Park M., Rivier J.E., Craig A.G., Mackie G.D., Sherwood N.M.;

RT "Two new forms of gonadotropin releasing hormone in a protochordate and the evolutionary implications."

RL Proc. Natl. Acad. Sci. U.S.A. 93:10461-10464 (1996).

CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the GNRH family.

DR InterPro: IPR002012; GNRH.

DR Pfam: PF00446; GNRH; 1.

DR PROSITE: PS00473; GNRH; 1.

KW Hormone; Amidation; Pyrrolidone carboxylic acid.

FT MOD_RES 10 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1264 MW; 2846363937APAA CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KP 5
 II
 6 KP 9

DB

RESULT 45

GON3_PETMA STANDARD; PRT; 10 AA;

AC P30948; 1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GNRH-III)

DE (Luliberin III)

OS Petromyzon marinus (Sea lamprey).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;

CC Petromyzontiformes; Petromyzontidae; Petromyzon.

OX NCBI_TaxID-7757;

RN 11

RN SEQUENCE

KX MEDLINE-94178316; PubMed-8440174;

RA Sower S.A., Chiana Y.C., Iovas S., Conlon J.M.;

RT "Primary structure and biological activity of a third gonadotropin-releasing hormone from lamprey brain."

PL Endocrinology 132:1125-1131 (1993).

CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the GNRH family.

DR InterPro: IPR002012; GNRH.

DR Pfam: PF00446; GNRH; 1.

DR PROSITE: PS00473; GNRH; 1.

KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.

FT MOD_RES 10 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1277 MW; 284836237AA1F5A3 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KP 5
 II
 8 KP 9

DB

TISSUE=Brain;

MEDLINE-86168142; PubMed-3514603;

Sherwood N.M., Sower S.A., Marshak D.R., Fraser B.A., Brownstein M.J.;

RT "Primary structure of gonadotropin-releasing hormone from lamprey brain."

RL J. Biol. Chem. 261:4812-4819 (1986).

CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the GNRH family.

DR PIR: A01412; RHLMGS.

DR InterPro: IPR002012; GNRH.

DR Pfam: PF00446; GNRH; 1.

DR PROSITE: PS00473; GNRH; 1.

KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.

FT MOD_RES 10 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1244 MW; 1E4B36237B1735AB CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KP 5
 II
 6 KP 9

DB

RESULT 45

GON3_PETMA STANDARD; PRT; 10 AA;

AC P30948; 1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Gonadoliberin III (Gonadotropin-releasing hormone III) (GNRH-III)

DE (Luliberin III)

OS Petromyzon marinus (Sea lamprey).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;

CC Petromyzontiformes; Petromyzontidae; Petromyzon.

OX NCBI_TaxID-7757;

RN 11

RN SEQUENCE

KX MEDLINE-94178316; PubMed-8440174;

RA Sower S.A., Chiana Y.C., Iovas S., Conlon J.M.;

RT "Primary structure and biological activity of a third gonadotropin-releasing hormone from lamprey brain."

PL Endocrinology 132:1125-1131 (1993).

CC -1- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates the secretion of both luteinizing and follicle-stimulating hormones.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the GNRH family.

DR InterPro: IPR002012; GNRH.

DR Pfam: PF00446; GNRH; 1.

DR PROSITE: PS00473; GNRH; 1.

KW Hormone; Amidation; Hypothalamus; Pyrrolidone carboxylic acid.

FT MOD_RES 10 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA; 1277 MW; 284836237AA1F5A3 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KP 5
 II
 8 KP 9

DB


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GDP2_BOVIN
ID QDP2_BOVIN STANDARD PRT 10 AA.
AC P11180;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dihydropyrimidine acetyltransferase component of pyruvate dehydrogenase
DE complex (EC 2.3.1.12) (E2) (Fragment).
GN DLAI.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Proboscidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=88024154; PubMed=3117054;
RA Bradford A.P., Howell S., Aitken A., James E.A., Yeaman S.J.
RI "Primary structure around the lipoyl-attachment site on the E2
RI component of bovine heart pyruvate dehydrogenase complex.";
RL Biochem. J. 245:919-922(1987).
CC -!- FUNCTION: The pyruvate dehydrogenase complex catalyzes the overall
CC conversion of pyruvate to acetyl-CoA and CO(2). It contains
CC multiple copies of three enzymatic components: pyruvate
CC dehydrogenase (E1), dihydrolipoamide acetyltransferase (E2) and
CC lipoamide dehydrogenase (E3).
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + dihydrolipoamide -> CoA + S-
CC acetyldihydrolipoamide.
CC -!- COFACTOR: THE E2 COMPONENT CONTAINS TWO COVALENTLY-BOUND LIPYL
CC COFACTOR.
CC -!- SUBUNIT: FORMS A 24-POLYPEPTIDE STRUCTURAL CORE WITH AN INTERNAL
CC SYMMETRY.
CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -!- SIMILARITY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
CC -!- SIMILARITY: Contains 2 lipoyl-binding domains.
DR InterPro: IPR004016; Lipoyl.
DR PROSITE: PS00189; LIPOYL PARTIAL.
KW Glycolysis; Transferrase; Acyltransferase; Repeat; Mitochondrion;
KW Lipoyl.
FT N-TER 1 10 10
FT BINDING 5 5 LIPYL.
FT N-TER 5 5
SQ SEQUENCE 10 AA; 1066 MW; 889BEDA033AB1 (GenBank)

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e-04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KA 11
LB 5 KA 6

RESULT 47
PNEU_HUMAN STANDARD PRT 10 AA.
AC P22103;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNN).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=91110910; PubMed=2274581;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RI "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: ANTIDIURETIC PEPTIDE THAT TRIGGERS THE RELEASE OF ADH.

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DR PIR: B33143; B33143;
DR CO: G03030103; Pivasopressin secretion; NAS.
KW Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 956 MW; 640378DAA723276B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e-04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6
LB 4 PK 5

RESULT 48
PNEU_RAT STANDARD PRT 10 AA.
AC P21936;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pneumadin (PNN).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID:10116;
RN [1]
RP SEQUENCE AND SYNTHESIS.
RC TISSUE=Lung;
RX MEDLINE=91110910; PubMed=2274681;
RA Batra V.K., Mathur M., Mir S.A., Kapoor R., Kumar M.A.;
RI "Pneumadin: a new lung peptide which triggers antidiuresis.";
RL Regul. Pept. 30:77-87(1990).
CC -!- FUNCTION: THIS ANTIDIURETIC PEPTIDE TRIGGERS THE RELEASE OF ADH.
DR PIR: A33143; A33143;
KW Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1048 MW; 641D00DAA723276B CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e-04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 6
LB 4 PK 5

RESULT 49
SPI_HAIRO STANDARD PRT 10 AA.
AC G10947;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Serine proteinase inhibitor (Fragment).
OS Haicynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Haicynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE.
RX TISSUE=Hemolymph; PubMed=8759245;
RA Shishikura F., Abe T., Ohtake S.-I., Tanaka K.;
RI "Purification and characterization of a 58,000-Da proteinase
RI inhibitor from the hemolymph of a solitary ascidian, Haicynthia
RI roretzi.";
RL Comp. Biochem. Physiol. 114B:1-9(1996).
CC -!- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

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DR InterPro: IPR000215; Serpin.
 DR PROSITE: PS00284; SERPIN; PARTIAL.
 KW Serpin; Serine protease inhibitor; Glycoprotein; Plasma.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA: 1104 MW: 4225073B1B187AA; CR664;

Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1; 20-04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KK 4
 II
 DB 2 KK 3

RESULT 50

TKNC_RANCA
 ID TKNC_RANCA STANDARD; PRI; 10 AA.
 AC P22690;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ranatachykinin C (RTK C).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE AND SYNTHESIS.
 RC TISSUE: Intestine;
 RX MEDLINE=91254337; PubMed=2043143;
 RA Kozawa H., Hino J., Minamino N., Kanagawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (Rana catesbeiana) brain and intestine.";
 RL Biochem. Biophys. Res. Commun. 177:588-594(1991).
 RN [2]
 RP SEQUENCE
 RC TISSUE=Intestine;
 RX MEDLINE=94523216; PubMed=8212506;
 RA Kanagawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RT "Four novel tachykinins in frog (Rana catesbeiana) brain and intestine.";
 RL Regul. Pept. 46:81-88(1993).
 CC !- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS, EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH MUSCLES.
 CC !- SUBCELLULAR LOCATION: Secreted.
 CC !- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: C61033; C61033.
 DR InterPro: IPR002040; Tachykinin.
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 10 10
 SQ SEQUENCE 10 AA: 1086 MW: 3A3A40705905BDC; CR664;

Query Match 18.2%; Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1; 20-04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AS 2
 II
 DB 4 AS 5

Search completed: September 30, 2003, 10:25:56
 Job time : 20.25 secs

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OM protein - protein search, using SW method

Run on: September 30, 2003, 10:07:04 : Search time 31.6617 seconds
(without alignments)
89.639 Million cell updates/sec

Title: US-09-787-443-1

Perfect score: 11

Sequence: 1 ASKKPKRNIKA 11

Scoring table: OLICO

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3459

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database:

- 1: SPTREMBL_231**
- 2: sp_archaea**
- 3: sp_bacteria**
- 4: sp_fungi**
- 5: sp_human**
- 6: sp_invertebrate**
- 7: sp_mammal**
- 8: sp_mhc**
- 9: sp_organelle**
- 10: sp_plant**
- 11: sp_rodent**
- 12: sp_virus**
- 13: sp_vertebrate**
- 14: sp_unclassified**
- 15: sp_virus**
- 16: sp_bacteriophage**
- 17: sp_archaeop**

Ercof. No. is the number of records per 1000 hits chosen to have a score greater than or equal to the given value. Results being printed, and is derived by analysis of the database distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	8	8	Q900W5 gossypium
2	4	36.4	9	4	Q8X14 homo sapien
3	4	36.4	10	12	Q900W6 gossypium
4	4	36.4	10	12	Q81V76 polyomaviru
5	4	36.4	10	12	Q900W1 gossypium
6	4	36.4	10	12	Q81V76 polyomaviru
7	4	36.4	10	12	Q900W6 gossypium
8	4	36.4	10	12	Q81V76 polyomaviru
9	4	36.4	10	12	Q900W7 gossypium
10	4	36.4	10	12	Q81V76 polyomaviru
11	4	36.4	10	12	Q900W7 gossypium
12	4	36.4	10	12	Q81V76 polyomaviru
13	4	36.4	10	12	Q81V76 polyomaviru
14	4	36.4	10	12	Q81V76 polyomaviru
15	4	36.4	10	12	Q900W7 gossypium
16	4	36.4	10	12	Q81V76 polyomaviru

17	4	36.4	10	12	Q900W5
18	4	36.4	10	12	Q900X3
19	4	36.4	10	12	Q900X5
20	4	36.4	10	12	Q900M3
21	4	36.4	10	12	Q8JV80
22	4	36.4	10	12	Q900X1
23	4	36.4	10	12	Q900X9
24	4	36.4	10	12	Q8JV72
25	3	27.3	8	2	Q91S80
26	3	27.3	8	2	Q56759
27	3	27.3	8	2	Q921H9
28	3	27.3	8	8	Q19561
29	3	27.3	8	8	Q19558
30	3	27.3	8	8	Q19560
31	3	27.3	8	8	Q19559
32	3	27.3	8	8	Q19556
33	3	27.3	8	4	Q16605
34	3	27.3	9	4	Q900W0
35	3	27.3	9	8	Q9T2L0
36	3	27.3	9	8	Q9T2L1
37	3	27.3	9	12	Q71067
38	3	27.3	9	12	Q71068
39	3	27.3	10	2	Q9JN49
40	3	27.3	10	4	Q81Z82
41	3	27.3	10	8	Q8H0B4
42	3	27.3	10	10	Q8LPT7
43	3	27.3	10	13	Q73594
44	3	27.3	11	2	Q95618
45	3	27.3	11	5	Q95PX6
46	3	27.3	11	5	Q25916
47	3	27.3	11	6	Q9TQ50
48	3	27.3	11	9	Q38415
49	3	27.3	11	10	Q04131
50	3	27.3	11	12	Q86866
51	3	27.3	11	12	Q86864
52	3	27.3	11	12	Q86868
53	3	27.3	12	2	Q8VLX8
54	3	27.3	12	4	Q9HB04
55	3	27.3	12	5	Q61574
56	3	27.3	12	8	Q8MEM1
57	3	27.3	12	8	Q8HU93
58	3	27.3	12	10	Q8LPT6
59	3	27.3	12	10	Q8LPT6
60	3	27.3	13	2	Q9R3R6
61	3	27.3	13	6	Q9GJ02
62	3	27.3	13	11	Q8CIW3
63	3	27.3	13	13	Q83338
64	3	27.3	14	2	Q50268
65	3	27.3	14	3	Q8J1G2
66	3	27.3	14	4	Q16232
67	3	27.3	14	10	Q8LAP5
68	3	27.3	14	11	Q99PB8
69	3	27.3	14	11	Q8CFB6
70	3	27.3	14	12	Q8VJ06
71	3	27.3	14	16	Q9KE26
72	3	27.3	15	2	Q9R546
73	3	27.3	15	2	Q9ZF32
74	3	27.3	15	2	Q9R4T2
75	3	27.3	15	4	Q81ZK4
76	3	27.3	15	6	Q83444
77	3	27.3	15	8	Q9T2Q2
78	3	27.3	15	8	Q78794
79	2	18.2	8	2	Q9AGP4
80	2	18.2	8	2	Q8KJ10
81	2	18.2	8	2	Q44463
82	2	18.2	8	2	Q77556
83	2	18.2	8	2	Q6R8R3
84	2	18.2	8	2	Q87471
85	2	18.2	8	2	Q56429
86	2	18.2	8	2	Q9R9E0
87	2	18.2	8	2	Q9R5R0
88	2	18.2	8	2	Q8C940
89	2	18.2	8	4	Q15889

Q90W5 polyomaviru
Q90X3 polyomaviru
Q90X5 polyomaviru
Q90W3 polyomaviru
Q8JV80 polyomaviru
Q90X1 polyomaviru
Q90X9 polyomaviru
Q8JV72 polyomaviru
Q93R0 staphylococ
Q56759 xanthobacte
Q921H9 neisseria m
Q19561 gossypium d
Q19558 gossypium b
Q19560 gossypium m
Q19559 gossypium t
Q19556 gossypium a
Q16605 homo sapien
Q90W0 homo sapien
Q9T2L0 spinacia ol
Q9T2L1 spinacia ol
Q71067 canine dist
Q71068 canine dist
Q9JN49 staphylococ
Q81Z82 homo sapien
Q8H0B4 anomobryum
Q8LPT7 zea mays (m
Q73594 gallus gall
Q95618 prochloroco
Q95PX6 caenorhabdi
Q25916 plasmodium
Q9TQ50 bos taurus
Q38415 bacterioph
Q04131 lycopersico
Q86866 lymphocytic
Q86864 lymphocytic
Q86868 lymphocytic
Q8VLX8 thermus the
Q9HB04 homo sapien
Q61574 osteriadia
Q8MEM1 maiva neqle
Q8HU93 bryum donia
Q8LPT6 zea mays (m
Q8LPT6 pisum sativ
Q9R3R6 prochloroco
Q9GJ02 ovis aries
Q8CIW3 mus musculu
Q83338 oncorhynch
Q50268 phytoplasma
Q8J1G2 ashbya goss
Q16232 homo sapien
Q8LAP5 zea mays (m
Q99PB8 mus musculu
Q8CFB6 mus musculu
Q8VJ06 tomato yell
Q9KE26 bacillus ha
Q9R546 mycobacteri
Q9ZF32 salmonella
Q9R4T2 bacillus in
Q81ZK4 homo sapien
Q83444 ovis aries
Q9T2Q2 chlamydomon
Q78794 pylaella l
Q9AGP4 arthroacte
Q8KJ10 streptomyce
Q44463 rhizobiales
Q77556 escherichia
Q8R8R3 lactobacilli
Q87471 haemophilus
Q56429 thermus the
Q9R9E0 bacillus su
Q9R5R0 shigella dy
Q8C940 borrelia bu
Q15889 homo sapien

90	2	18.2	8	4	Q15900	Q15900 homo sapien	163	2	18.2	8	9	Q8H9H6	Q8H9H6 bacterioph
91	2	18.2	8	4	Q9JHK1	Q9JHK1 homo sapien	164	2	18.2	8	9	Q8H9H5	Q8H9H5 bacterioph
92	2	18.2	8	4	Q15888	Q15888 homo sapien	165	2	18.2	8	9	Q8H9H3	Q8H9H3 bacterioph
93	2	18.2	8	4	Q9JJS5	Q9JJS5 homo sapien	166	2	18.2	8	10	Q42507	Q42507 lriticum ae
94	2	18.2	8	4	Q16468	Q16468 homo sapien	167	2	18.2	8	10	Q8G135	Q8G135 lycopersico
95	2	18.2	8	4	Q9JCN4	Q9JCN4 homo sapien	168	2	18.2	8	11	Q99NT0	Q99NT0 pedetes cap
96	2	18.2	8	4	Q9JZ85	Q9JZ85 homo sapien	169	2	18.2	8	11	Q99NT1	Q99NT1 castor cana
97	2	18.2	8	4	Q8TVK3	Q8TVK3 homo sapien	170	2	18.2	8	11	Q99NS6	Q99NS6 erethizon d
98	2	18.2	8	5	Q9K6M5	Q9K6M5 toxof-asma	171	2	18.2	8	11	Q99NS8	Q99NS8 rattus norv
99	2	18.2	8	5	Q8Z686	Q8Z686 perip-facula	172	2	18.2	8	11	Q99NS5	Q99NS5 dipodomys h
100	2	18.2	8	6	Q9HFA7	Q9HFA7 macroscellid	173	2	18.2	8	11	Q99NS2	Q99NS2 myocastor c
101	2	18.2	8	6	Q9HFB2	Q9HFB2 ursus arcto	174	2	18.2	8	11	Q99NS3	Q99NS3 hydrochoeru
102	2	18.2	8	6	Q9HFC2	Q9HFC2 macropus eu	175	2	18.2	8	11	Q99NT2	Q99NT2 tamias stri
103	2	18.2	8	6	Q9HFC9	Q9HFC9 tiagetaphus	176	2	18.2	8	11	Q99ND2	Q99ND2 mus musculu
104	2	18.2	8	6	Q9HFX8	Q9HFX8 bos tauru	177	2	18.2	8	11	Q99NS1	Q99NS1 dinomys bra
105	2	18.2	8	6	Q9HFR1	Q9HFR1 echinops te	178	2	18.2	8	11	Q9K1U6	Q9K1U6 mus musculu
106	2	18.2	8	6	Q18654	Q18654 canis fami	179	2	18.2	8	11	Q99NS7	Q99NS7 cricetus
107	2	18.2	8	6	Q9HFA7	Q9HFA7 acelus tusc	180	2	18.2	8	11	Q99NS0	Q99NS0 agouti taer
108	2	18.2	8	6	Q9HFB7	Q9HFB7 capirus tad	181	2	18.2	8	11	Q99NS9	Q99NS9 mus musculu
109	2	18.2	8	6	Q9HFB9	Q9HFB9 euphractus	182	2	18.2	8	11	Q99NS4	Q99NS4 cavia tschu
110	2	18.2	8	6	Q9HFB8	Q9HFB8 chaetophrac	183	2	18.2	8	11	Q99NS4	Q99NS4 mus spretus
111	2	18.2	8	6	Q9HFA8	Q9HFA8 toxodonta a	184	2	18.2	8	12	Q83977	Q83977 influenzavi
112	2	18.2	8	6	Q9HFX1	Q9HFX1 canis fami	185	2	18.2	8	12	Q84271	Q84271 human papil
113	2	18.2	8	6	Q9HFA9	Q9HFA9 procavia ca	186	2	18.2	8	12	Q84273	Q84273 human papil
114	2	18.2	8	6	Q9HFB2	Q9HFB2 sorex arane	187	2	18.2	8	13	Q902V5	Q902V5 fulica leuc
115	2	18.2	8	6	Q9HFB5	Q9HFB5 erinaceus e	188	2	18.2	8	13	Q8JFN8	Q8JFN8 gallus gall
116	2	18.2	8	6	Q9HFB6	Q9HFB6 myrmecophag	189	2	18.2	9	2	Q9K3T0	Q9K3T0 borrelia af
117	2	18.2	8	6	Q9HFB3	Q9HFB3 condylura c	190	2	18.2	9	2	Q9E214	Q9E214 sodalis glo
118	2	18.2	8	6	Q9HFB4	Q9HFB4 equus cabal	191	2	18.2	9	2	Q9R5R1	Q9R5R1 shigella dy
119	2	18.2	8	6	Q9HFB5	Q9HFB5 reusettus l	192	2	18.2	9	2	Q45852	Q45852 clostridium
120	2	18.2	8	6	Q9HFB4	Q9HFB4 panthera on	193	2	18.2	9	2	Q9JN16	Q9JN16 streptococ
121	2	18.2	8	6	Q9HFB3	Q9HFB3 didelphis m	194	2	18.2	9	2	Q13363	Q13363 borrelia ga
122	2	18.2	8	6	Q9HFA4	Q9HFA4 tupia aiuro	195	2	18.2	9	2	Q51349	Q51349 pseudomonas
123	2	18.2	8	6	Q9HFA2	Q9HFA2 tarsius lat	196	2	18.2	9	2	Q9K735	Q9K735 streptomyce
124	2	18.2	8	6	Q9HFA2	Q9HFA2 tarsius p	197	2	18.2	9	2	Q9K792	Q9K792 borrelia bu
125	2	18.2	8	6	Q9HFB1	Q9HFB1 chaetoeopus h	198	2	18.2	9	2	Q30790	Q30790 erwinia amy
126	2	18.2	8	6	Q9HFB4	Q9HFB4 oxapia fahu	199	2	18.2	9	2	Q9K4M6	Q9K4M6 streptococ
127	2	18.2	8	6	Q9HFB6	Q9HFB6 pteropus gi	200	2	18.2	9	2	Q93E20	Q93E20 streptococ
128	2	18.2	8	6	Q9HFB7	Q9HFB7 linchechus	201	2	18.2	9	2	Q9K9C4	Q9K9C4 borrelia bu
129	2	18.2	8	6	Q9HFB5	Q9HFB5 felis silve	202	2	18.2	9	2	Q8GL26	Q8GL26 borrelia bu
130	2	18.2	8	6	Q9HFB2	Q9HFB2 tarsius tr	203	2	18.2	9	3	Q9UR18	Q9UR18 sclerotium
131	2	18.2	8	6	Q9HFB7	Q9HFB7 tasandua te	204	2	18.2	9	4	Q16276	Q16276 homo sapien
132	2	18.2	8	6	Q9HFB1	Q9HFB1 hippopotamu	205	2	18.2	9	4	Q9BQQ2	Q9BQQ2 homo sapien
133	2	18.2	8	6	Q9HFB4	Q9HFB4 taipia alta	206	2	18.2	9	4	Q9H4B1	Q9H4B1 homo sapien
134	2	18.2	8	6	Q9HFC0	Q9HFC0 choloepus d	207	2	18.2	9	4	Q15896	Q15896 homo sapien
135	2	18.2	8	6	Q9HFA4	Q9HFA4 callimico a	208	2	18.2	9	4	Q9H326	Q9H326 homo sapien
136	2	18.2	8	6	Q9HFA4	Q9HFA4 lemur catia	209	2	18.2	9	4	Q9UMA0	Q9UMA0 homo sapien
137	2	18.2	8	6	Q9HFA7	Q9HFA7 oryctolopus	210	2	18.2	9	4	Q9UCN5	Q9UCN5 homo sapien
138	2	18.2	8	6	Q9HFA7	Q9HFA7 canis fami	211	2	18.2	9	5	Q28112	Q28112 bos taurus
139	2	18.2	8	6	Q9HFA7	Q9HFA7 a. filipes fa	212	2	18.2	9	5	Q9TUY0	Q9TUY0 monodelphis
140	2	18.2	8	6	Q9HFA7	Q9HFA7 cynocephalu	213	2	18.2	9	6	Q9TT77	Q9TT77 bos taurus
141	2	18.2	8	6	Q9HFB4	Q9HFB4 cyrtelis th	214	2	18.2	9	6	Q95DS5	Q95DS5 magnolia sa
142	2	18.2	9	8	Q9H9H8	Q9H9H8 alvotiana F	215	2	18.2	9	8	Q95DS0	Q95DS0 magnolia tr
143	2	18.2	8	8	Q8W3J7	Q8W3J7 lewis hirta	216	2	18.2	9	8	Q9TNF0	Q9TNF0 magnolia tr
144	2	18.2	8	8	Q94PX5	Q94PX5 felis silve	217	2	18.2	9	8	Q8HEM3	Q8HEM3 howittia tr
145	2	18.2	8	8	Q94490	Q94490 locusta mig	218	2	18.2	9	8	Q95DS1	Q95DS1 manglietia
146	2	18.2	8	8	Q944X7	Q944X7 felis silve	219	2	18.2	9	8	Q9TNE9	Q9TNE9 magnolia co
147	2	18.2	8	8	Q94PX6	Q94PX6 felis libyc	220	2	18.2	9	8	Q9TNF4	Q9TNF4 magnolia sc
148	2	18.2	8	9	Q37854	Q37854 bacterioph	221	2	18.2	9	8	Q9THL7	Q9THL7 magnolia si
149	2	18.2	8	9	Q8SBJ0	Q8SBJ0 bacterioph	222	2	18.2	9	8	Q9TNE0	Q9TNE0 michelia co
150	2	18.2	8	9	Q8H9K4	Q8H9K4 bacterioph	223	2	18.2	9	8	Q9TND8	Q9TND8 liriodendro
151	2	18.2	8	9	Q8H9K1	Q8H9K1 bacterioph	224	2	18.2	9	8	Q95GN1	Q95GN1 pelargonium
152	2	18.2	8	9	Q8H9J9	Q8H9J9 bacterioph	225	2	18.2	9	8	Q9TNE4	Q9TNE4 magnolia sa
153	2	18.2	8	9	Q8H9J7	Q8H9J7 bacterioph	226	2	18.2	9	8	Q95DS6	Q95DS6 magnolia w
154	2	18.2	8	9	Q8H9J5	Q8H9J5 bacterioph	227	2	18.2	9	8	Q9TNF6	Q9TNF6 magnolia gr
155	2	18.2	8	9	Q8H9J3	Q8H9J3 bacterioph	228	2	18.2	9	8	Q9THL5	Q9THL5 magnolia li
156	2	18.2	8	9	Q8H9J1	Q8H9J1 bacterioph	229	2	18.2	9	8	Q9TNF1	Q9TNF1 magnolia he
157	2	18.2	8	9	Q8H9I9	Q8H9I9 bacterioph	230	2	18.2	9	8	Q95DT3	Q95DT3 magnolia il
158	2	18.2	8	9	Q8H9I8	Q8H9I8 bacterioph	231	2	18.2	9	8	Q9THM0	Q9THM0 magnolia fr
159	2	18.2	8	9	Q8H9I6	Q8H9I6 bacterioph	232	2	18.2	9	8	Q95DS2	Q95DS2 magnolia ov
160	2	18.2	8	9	Q8H9I4	Q8H9I4 bacterioph	233	2	18.2	9	8	Q9T3P4	Q9T3P4 magnolia ma
161	2	18.2	8	9	Q8H9I3	Q8H9I3 bacterioph	234	2	18.2	9	8	Q9TND7	Q9TND7 liriodendro
162	2	18.2	8	9	Q8H9I2	Q8H9I2 bacterioph	235	2	18.2	9	8	Q9THL8	Q9THL8 magnolia of

235	2	18.2	9	8	Q9TNE2	Q9TNE2 magnolia ac	309	2	18.2	10	4	Q8N6B1	Q8N6B1 homo sapien
236	2	18.2	9	8	Q9TNE5	Q9TNE5 magnolia gu	310	2	18.2	10	5	Q26093	Q26093 pisaster oc
237	2	18.2	9	8	Q9TNE5	Q9TNE5 magnolia ko	311	2	18.2	10	5	P82221	P82221 bombyx mori
238	2	18.2	9	8	Q9TNE5	Q9TNE5 magnolia ji	312	2	18.2	10	5	P82223	P82223 bombyx mori
239	2	18.2	9	8	Q9TNE1	Q9TNE1 magnolia st	313	2	18.2	10	5	P82224	P82224 bombyx mori
240	2	18.2	9	8	Q9TNE1	Q9TNE1 magnolia st	314	2	18.2	10	6	Q8M178	Q8M178 bos mutus g
241	2	18.2	9	8	Q9TNE9	Q9TNE9 michelia si	315	2	18.2	10	6	Q9TJ48	Q9TJ48 bos taurus g
242	2	18.2	9	8	Q9TNE6	Q9TNE6 magnolia si	316	2	18.2	10	8	Q9XMB4	Q9XMB4 aegilops ta
243	2	18.2	9	8	Q9TNE5A	Q9TNE5A magnolia co	317	2	18.2	10	8	Q9TJ24	Q9TJ24 rattus sp.
244	2	18.2	9	8	Q9TNE5	Q9TNE5 magnolia st	318	2	18.2	10	8	Q95DT0	Q95DT0 magnolia po
245	2	18.2	9	8	Q9TNE6	Q9TNE6 magnolia de	319	2	18.2	10	8	Q37103	Q37103 saccharomyc
246	2	18.2	9	8	Q9TNE5	Q9TNE5 magnolia si	320	2	18.2	10	8	Q95DS8	Q95DS8 magnolia de
247	2	18.2	9	8	Q9TNE5	Q9TNE5 magnolia si	321	2	18.2	10	8	Q95DS9	Q95DS9 magnolia sp
248	2	18.2	9	8	Q9TNE6	Q9TNE6 magnolia de	322	2	18.2	10	8	Q95DS3	Q95DS3 magnolia me
249	2	18.2	9	8	Q9TNE2	Q9TNE2 magnolia ta	323	2	18.2	10	8	Q95DT2	Q95DT2 magnolia pa
250	2	18.2	9	8	Q9TNE3	Q9TNE3 magnolia vi	324	2	18.2	10	8	Q95DT1	Q95DT1 magnolia yo
251	2	18.2	9	8	Q9TNE7	Q9TNE7 magnolia ni	325	2	18.2	10	8	Q95DK7	Q95DK7 magnolia sc
252	2	18.2	9	8	Q8WGE7	Q8WGE7 procambarus	326	2	18.2	10	8	P82136	P82136 spinacia ol
253	2	18.2	9	8	Q95DR9	Q95DR9 manihetia	327	2	18.2	10	8	G8LLJ0	G8LLJ0 oryza sativ
254	2	18.2	9	8	Q95DR8	Q95DR8 michelia ma	328	2	18.2	10	10	P81899	P81899 prunus dulc
255	2	18.2	9	8	Q9XJN0	Q9XJN0 bacterioph	329	2	18.2	10	10	P81899	P81899 prunus dulc
256	2	18.2	9	10	Q8LPT5	Q8LPT5 zea mays (m	330	2	18.2	10	11	Q63389	Q63389 rattus norv
257	2	18.2	9	10	Q8LPT5	Q8LPT5 zea mays (m	331	2	18.2	10	11	Q63389	Q63389 rattus norv
258	2	18.2	9	11	Q8R514	Q8R514 rattus norv	332	2	18.2	10	11	Q9QV21	Q9QV21 rattus sp.
259	2	18.2	9	11	Q99MC3	Q99MC3 mus muscul	333	2	18.2	10	11	Q8CJE0	Q8CJE0 rattus norv
260	2	18.2	9	11	Q9QW70	Q9QW70 mus muscul	334	2	18.2	10	12	Q69347	Q69347 herpes simp
261	2	18.2	9	11	Q62530	Q62530 mus muscul	335	2	18.2	10	12	Q84266	Q84266 human papil
262	2	18.2	9	12	Q82622	Q82622 avian infec	336	2	18.2	10	12	Q86580	Q86580 simian para
263	2	18.2	9	12	Q88953	Q88953 vaccineinia vi	337	2	18.2	10	13	Q9TJX9	Q9TJX9 eptaretus
264	2	18.2	9	12	Q8QV23	Q8QV23 vaccineinia vi	338	2	18.2	10	13	Q9PRU1	Q9PRU1 cynops pyr
265	2	18.2	9	12	Q67605	Q67605 squash leaf	339	2	18.2	10	15	Q64980	Q64980 avian myelo
266	2	18.2	9	12	Q71069	Q71069 canine dist	340	2	18.2	10	15	Q8UT83	Q8UT83 human immun
267	2	18.2	9	12	Q92765	Q92766 canine dist	341	2	18.2	10	15	Q87617	Q87617 chimpazee
268	2	18.2	9	12	Q67606	Q67606 squash leaf	342	2	18.2	11	2	Q9R790	Q9R790 borrella ga
269	2	18.2	9	13	Q8J118	Q8J118 danio aequi	343	2	18.2	11	2	Q47451	Q47451 escherichia
270	2	18.2	9	13	Q8CJ14	Q8CJ14 danio frank	344	2	18.2	11	2	Q9A127	Q9A127 carsonella
271	2	18.2	9	13	Q8CJ10	Q8CJ10 tottrapis ch	345	2	18.2	11	2	Q8RKN1	Q8RKN1 escherichia
272	2	18.2	9	13	Q8CJ16	Q8CJ16 danio albo	346	2	18.2	11	2	Q514F7	Q514F7 bacillus ce
273	2	18.2	9	15	Q85599	Q85599 moloney mur	347	2	18.2	11	2	P77404	P77404 escherichia
274	2	18.2	9	15	Q70140	Q70140 human immun	348	2	18.2	11	2	Q9RQ60	Q9RQ60 bucherna ap
275	2	18.2	10	1	Q50843	Q50843 methanococc	349	2	18.2	11	2	P71228	P71228 escherichia
276	2	18.2	10	1	Q47651	Q47651 escherichia	350	2	18.2	11	2	Q93MI7	Q93MI7 escherichia
277	2	18.2	10	2	Q9R791	Q9R791 borrella bu	351	2	18.2	11	2	Q9RF22	Q9RF22 mycoplasma
278	2	18.2	10	2	Q9XBN9	Q9XBN9 bacillus ce	352	2	18.2	11	2	P95518	P95518 pasteurella
279	2	18.2	10	2	Q9X533	Q9X533 escherichia	353	2	18.2	11	2	Q47345	Q47345 escherichia
280	2	18.2	10	2	Q9X5N4	Q9X5N4 clostridium	354	2	18.2	11	2	Q9A128	Q9A128 carsonella
281	2	18.2	10	2	Q9X534	Q9X534 tecleria a	355	2	18.2	11	2	Q44090	Q44090 acholeplasm
282	2	18.2	10	2	Q9VNR5	Q9VNR5 helicobacte	356	2	18.2	11	2	Q44237	Q44237 anabaena sp
283	2	18.2	10	2	Q941X4	Q941X4 vibrio chol	357	2	18.2	11	2	Q9R446	Q9R446 neisseria g
284	2	18.2	10	2	Q47475	Q47475 escherichia	358	2	18.2	11	2	Q8GMU3	Q8GMU3 acetobact
285	2	18.2	10	2	Q85801	Q85801 helicobacte	359	2	18.2	11	2	Q8GL24	Q8GL24 borrella bu
286	2	18.2	10	2	Q63194	Q63194 spiroplasma	360	2	18.2	11	2	Q8GL19	Q8GL19 borrella bu
287	2	18.2	10	2	Q63194	Q63194 spiroplasma	361	2	18.2	11	4	Q60761	Q60761 homo sapien
288	2	18.2	10	2	Q915W6	Q915W6 fiberibacte	362	2	18.2	11	4	Q75811	Q75811 homo sapien
289	2	18.2	10	2	Q9JNC9	Q9JNC9 streptococ	363	2	18.2	11	4	Q9H4H5	Q9H4H5 homo sapien
290	2	18.2	10	2	Q9AEL9	Q9AEL9 streptococ	364	2	18.2	11	4	Q15997	Q15997 homo sapien
291	2	18.2	10	2	Q9R7J9	Q9R7J9 helicobacte	365	2	18.2	11	4	Q9UCP5	Q9UCP5 homo sapien
292	2	18.2	10	2	P83067	P83067 bacillus ce	366	2	18.2	11	4	Q9URM2	Q9URM2 homo sapien
293	2	18.2	10	2	P83066	P83066 bacillus ce	367	2	18.2	11	4	Q9H3V7	Q9H3V7 homo sapien
294	2	18.2	10	2	P83160	P83160 anabaena sp	368	2	18.2	11	4	Q8N103	Q8N103 homo sapien
295	2	18.2	10	2	P83154	P83154 anabaena sp	369	2	18.2	11	5	Q26092	Q26092 pisaster oc
296	2	18.2	10	2	Q838W5	Q838W5 borrella bu	370	2	18.2	11	5	Q9NL65	Q9NL65 ascaris suu
297	2	18.2	10	3	Q9UVW2	Q9UVW2 schizophyll	371	2	18.2	11	5	Q9TJX6	Q9TJX6 manduca sex
298	2	18.2	10	3	Q8J0C2	Q8J0C2 encephalito	372	2	18.2	11	5	Q8MPO3	Q8MPO3 caenorhabdi
299	2	18.2	10	4	Q9UNF2	Q9UNF2 homo sapien	373	2	18.2	11	6	Q9TRR7	Q9TRR7 cryotolagus
300	2	18.2	10	4	Q14096	Q14096 homo sapien	374	2	18.2	11	6	Q9TTQ0	Q9TTQ0 gorilla gor
301	2	18.2	10	4	Q9H121	Q9H121 homo sapien	375	2	18.2	11	7	Q77872	Q77872 oreochromis
302	2	18.2	10	4	Q9UMK9	Q9UMK9 homo sapien	376	2	18.2	11	7	Q77880	Q77880 oreochromis
303	2	18.2	10	4	Q9UC30	Q9UC30 homo sapien	377	2	18.2	11	7	Q77908	Q77908 oreochromis
304	2	18.2	10	4	Q90DE8	Q90DE8 homo sapien	378	2	18.2	11	7	Q77873	Q77873 oreochromis
305	2	18.2	10	4	Q96Q19	Q96Q19 homo sapien	379	2	18.2	11	7	Q77871	Q77871 oreochromis
306	2	18.2	10	4	Q9UJ48	Q9UJ48 homo sapien	380	2	18.2	11	7	Q77907	Q77907 oreochromis
307	2	18.2	10	4	Q9NP06	Q9NP06 homo sapien	381	2	18.2	11	7	Q77897	Q77897 oreochromis
308	2	18.2	10	4	Q9NP07	Q9NP07 homo sapien							

382	2	18.2	11	8	Q8ME62	Q8me62 porphyra ca	455	2	18.2	12	7	077877	077877 oreochromis
383	2	18.2	11	8	Q8ME17	Q8me17 sida hooker	456	2	18.2	12	7	077882	077882 oreochromis
384	2	18.2	11	8	Q8G5Y0	Q8g5y0 pseudotrache	457	2	18.2	12	8	Q8SER7	Q8se87 grateloupia
385	2	18.2	11	8	Q8MEM2	Q8mem2 lagunaria p	458	2	18.2	12	8	Q8MEP4	Q8me84 hibiscus ni
386	2	18.2	11	8	Q8MES5	Q8mes5 abelmoschus	459	2	18.2	12	8	Q8MES0	Q8me80 anoda crist
387	2	18.2	11	8	Q8MEP0	Q8nep0 hibiscus pe	460	2	18.2	12	8	Q8MEQ6	Q8me86 hibiscus en
388	2	18.2	11	8	Q8MER8	Q8mer8 dombeya til	461	2	18.2	12	8	Q8MEM5	Q8me85 hibiscus va
389	2	18.2	11	8	Q82704	Q82704 nicotiana t	462	2	18.2	12	8	Q8MEN4	Q8me84 hibiscus sc
390	2	18.2	11	8	Q8MES1	Q8mes1 aliyadyne pi	463	2	18.2	12	8	Q8MER4	Q8me84 gossypium s
391	2	18.2	11	8	Q8MEP3	Q8nep3 hibiscus no	464	2	18.2	12	8	Q8MEQ1	Q8me81 hibiscus in
392	2	18.2	11	8	Q8MEQ7	Q8me87 hibiscus dr	465	2	18.2	12	8	Q8MES6	Q8me86 abelmoschus
393	2	18.2	11	8	Q8ME15	Q8me15 pavonia has	466	2	18.2	12	8	Q8MEQ8	Q8me88 hibiscus do
394	2	18.2	11	8	Q8MER0	Q8mer0 hibiscus co	467	2	18.2	12	8	Q8MES2	Q8me82 alyogyne hu
395	2	18.2	11	8	Q8MES3	Q8mes3 alyogyne cr	468	2	18.2	12	8	Q8MEP7	Q8me87 hibiscus me
396	2	18.2	11	8	Q8MEP5	Q8nep5 hibiscus mi	469	2	18.2	12	8	Q8MEN5	Q8me85 hibiscus sa
397	2	18.2	11	8	Q8MER1	Q8mer1 hibiscus ca	470	2	18.2	12	8	Q8MER9	Q8me89 decaschisti
398	2	18.2	11	8	Q8SKP8	Q8skp8 ctenophorus	471	2	18.2	12	8	Q8MEM6	Q8me86 hibiscus tr
399	2	18.2	11	8	Q8MER7	Q8mer7 tiortia viti	472	2	18.2	12	8	Q8MEP1	Q8me81 hibiscus pe
400	2	18.2	11	8	Q8HQX5	Q8hqx5 rhabdhamn	473	2	18.2	12	8	Q8MEQ4	Q8me84 hibiscus fr
401	2	18.2	11	9	Q37925	Q37925 bacterioph	474	2	18.2	12	8	Q8MEQ0	Q8me80 hibiscus lu
402	2	18.2	11	10	Q06626	Q06626 solanum tub	475	2	18.2	12	8	Q8MEM0	Q8me80 malvaviscus
403	2	18.2	11	10	Q65901	Q65901 leavenworth	476	2	18.2	12	8	Q8MEP2	Q8me82 hibiscus pe
404	2	18.2	11	10	Q8RV30	Q8rv30 zea mays (m	477	2	18.2	12	8	Q8MEQ2	Q8me82 hibiscus he
405	2	18.2	11	10	Q8RUE7	Q8rue7 zea mays (m	478	2	19.2	12	8	Q8MER3	Q8me83 hibiscus br
406	2	18.2	11	10	P82436	P82436 nicotiana t	479	2	18.2	12	8	Q8MEL6	Q8me16 thespesia t
407	2	18.2	11	10	P82336	P82336 pisum sativ	480	2	18.2	12	8	Q8MER2	Q8me82 hibiscus bu
408	2	18.2	11	11	Q9AXM6	Q9axm6 mus musculu	481	2	18.2	12	8	Q8MEP6	Q8me86 hibiscus me
409	2	18.2	11	11	Q99881	Q99881 mus musculu	482	2	18.2	12	8	Q8MEP7	Q8me87 hibiscus ti
410	2	18.2	11	11	Q93166	Q93166 rattus norv	483	2	18.2	12	8	Q8MEP8	Q8me88 brassica na
411	2	18.2	11	11	Q8R207	Q8r207 mesocricetu	484	2	18.2	12	8	Q8MEM9	Q8me89 hibiscus ma
412	2	18.2	11	11	Q9QXN6	Q9qxu6 mus musculu	485	2	18.2	12	8	Q8MEQ9	Q8me89 hibiscus su
413	2	18.2	11	12	P89263	P89263 xestia c-ni	486	2	18.2	12	8	Q8MEN8	Q8me88 arabidopsis
414	2	18.2	11	12	Q99701	Q99701 east africa	487	2	18.2	12	8	Q8MEP6	Q8me86 hibiscus ra
415	2	18.2	11	12	Q69264	Q69264 equine herp	488	2	18.2	12	8	Q8SEB8	Q8se88 grateloupia
416	2	18.2	11	12	Q86565	Q86565 var cellia-2	489	2	18.2	12	8	Q8LU67	Q8lu67 macrostelia
417	2	18.2	11	13	Q8AXM4	Q8axm4 oreochromis	490	2	18.2	12	8	Q8MEP9	Q8me89 hibiscus ma
418	2	18.2	11	13	Q8AXM6	Q8axm6 oreochromis	491	2	18.2	12	8	Q8MEQ9	Q8me89 hibiscus di
419	2	18.2	11	15	Q85620	Q85620 moloney mur	492	2	18.2	12	8	Q8SEB9	Q8se89 grateloupia
420	2	18.2	12	2	Q50959	Q50959 neissoria q	493	2	18.2	12	8	Q03816	Q03816 metasequoia
421	2	18.2	12	2	Q50342	Q50342 mycoplasma	494	2	18.2	12	8	Q6S142	Q6s142 aeonium sim
422	2	18.2	12	2	Q93208	Q93208 acinetobact	495	2	18.2	12	8	Q8MEM8	Q8me88 hibiscus sy
423	2	18.2	12	2	Q9K5F7	Q9k5f7 helicobacte	496	2	18.2	12	8	Q8MEN0	Q8me80 hibiscus st
424	2	18.2	12	2	Q9K5F5	Q9k5f5 helicobacte	497	2	18.2	12	8	Q8MEN6	Q8me86 hibiscus sa
425	2	18.2	12	2	Q53579	Q53579 rhodobacter	498	2	18.2	12	8	Q03815	Q03815 abies alba
426	2	18.2	12	2	Q50303	Q50303 bacillus st	499	2	18.2	12	8	Q8MEQ3	Q8me83 hibiscus fu
427	2	18.2	12	2	P97144	P97144 rhizobium i	500	2	18.2	12	8	Q8MEN1	Q8me81 hibiscus st
428	2	18.2	12	2	Q9K8R4	Q9k8r4 helicobacte							
429	2	18.2	12	2	Q9K8R4	Q9k8r4 helicobacte							
430	2	18.2	12	2	Q52112	Q52112 acinetobact							
431	2	18.2	12	2	Q858V1	Q85v1 acinetobact							
432	2	18.2	12	2	Q858V1	Q85v1 acinetobact							
433	2	18.2	12	2	Q858V1	Q85v1 acinetobact							
434	2	18.2	12	3	Q81146	Q81146 asibya goss							
435	2	18.2	12	4	Q9UMR0	Q9umr0 homo sapien							
436	2	18.2	12	4	Q9BQQ1	Q9bqq1 homo sapien							
437	2	18.2	12	4	Q9UC17	Q9uc17 homo sapien							
438	2	18.2	12	4	Q16452	Q16452 homo sapien							
439	2	18.2	12	4	Q9UMQ9	Q9umq9 homo sapien							
440	2	18.2	12	4	Q16405	Q16405 homo sapien							
441	2	18.2	12	4	Q96PK0	Q96pk0 homo sapien							
442	2	18.2	12	4	Q9UMZ8	Q9umz8 homo sapien							
443	2	18.2	12	5	Q8MY01	Q8my01 drosophila							
444	2	18.2	12	5	Q8T0Y4	Q8t0y6 apis mellif							
445	2	18.2	12	6	Q91QW3	Q91qw3 bos taurus							
446	2	18.2	12	6	Q9XS31	Q9xs31 sus scrofa							
447	2	18.2	12	6	Q8WNV9	Q8wnv9 ovis aries							
448	2	18.2	12	6	Q9TRT8	Q9trt8 bos taurus							
449	2	18.2	12	6	Q9MZS4	Q9mzs4 canis famil							
450	2	18.2	12	6	P83127	P83127 bos indicus							
451	2	18.2	12	7	Q77878	Q77878 oreochromis							
452	2	18.2	12	7	Q77879	Q77879 oreochromis							
453	2	18.2	12	7	Q77881	Q77881 oreochromis							
454	2	18.2	12	7	Q77909	Q77909 oreochromis							

ALIGNMENTS

RESULT 1

019957
 ID 019957 PRELIMINARY: PRT: 8 AA.
 AC 019957;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Ribosomal protein L16 (Fragment).
 GN RPL16.
 OS Gossypium hirsutum (Upland cotton).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
 OX NCBI_taxid:1635;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
 RI *the tortoise and the hare: choosing between noncoding plastome and
 RI nuclear adh sequences for phylogeny reconstruction in a recently
 RI diverged plant group.*;
 RL Am. J. Bot. 85:1301-1315(1998).

```

DK EMBL: AF031452; AAC63546.1;
KW Chloroplast. 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA: 971 MW: 718587340454.427 CRC64:

Query Match 36.4% Score 4; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PKRN 8
    ||||
Db 1 PKRN 4

RESULT 2
Q9BX14
ID Q9BX14 PRELIMINARY: PRI: 9 AA.
AC Q9BX14 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE BA254M13.1 (Novel protein) (Fragment).
GN DJ094515.3
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
CX NCBI_TaxID:9606;
RN 11
RP SEQUENCE FROM N.A.
RA Milne S.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AL353599; CAC34530.1;
FT NON_TER 9
SQ SEQUENCE 9 AA: 1009 MW: 6918018901342563 CRC64:

Query Match 36.4% Score 4; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASKK 4
    ||||
Db 2 ASKK 5

RESULT 3
Q9Q0W9
ID Q9Q0W9 PRELIMINARY: PRI: 10 AA.
AC Q9Q0W9 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID:10632;
RN 11
RP SEQUENCE FROM N.A.
RA MEDLINE-20087544; PubMed:10618230;
RA Hofilli-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
    populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119350; AAF24106.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 406A97771A32763 CRC64:

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKPK 6
    ||||
Db 2 KKPK 5

RESULT 4
Q8JV70
ID Q8JV70 PRELIMINARY: PRI: 10 AA.
AC Q8JV70 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID:10632;
RN 11
RP SEQUENCE FROM N.A.
RA MEDLINE-21465052; PubMed:11581397;
RA Hofilli-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell P.,
    Girones R.;
RT "Potential transmission of human polyomaviruses through the
    gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL: AF304387; AAM97804.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 406A97771A32763 CRC64:

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKPK 6
    ||||
Db 2 KKPK 5

RESULT 5
Q9Q0W1
ID Q9Q0W1 PRELIMINARY: PRI: 10 AA.
AC Q9Q0W1 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID:10632;
RN 11
RP SEQUENCE FROM N.A.
RA MEDLINE-20087544; PubMed:10618230;
RA Hofilli-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
    populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119354; AAF24114.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 406A97771A32763 CRC64:

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KKPK 6
    ||||
Db 2 KKPK 5

RESULT 6
Q8JV68
ID Q8JV68 PRELIMINARY: PRI: 10 AA.
AC Q8JV68

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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-USA 6;
RA MEDLINE=21465052; PubMed=11581397;
RA Bojilli-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.*";
RL J. Virol. 75:10290-10299(2001);
DR EMBL; AF304388; AAM97806.1; -;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

RESULT 7
Q9Q0W7 PRELIMINARY; PRT; 10 AA.
ID Q9Q0W7
AC Q9Q0W7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CSFE;
RA MEDLINE=2087544; PubMed=10618230;
RA Bojilli-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.*";
RL Appl. Environ. Microbiol. 66:238-245(2000);
DR EMBL; AF119355; AAF24116.1; -;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

RESULT 8
Q8JV84 PRELIMINARY; PRT; 10 AA.
ID Q8JV84
AC Q8JV84
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CSF K;
RA MEDLINE=21465052; PubMed=11581397;
RA Bojilli-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.*";
RL J. Virol. 75:10290-10299(2001);

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RP SEQUENCE FROM N.A.
RC STRAIN-G1;
RX MEDLINE=21465052; PubMed=11581397;
RA Bojilli-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.*";
RL J. Virol. 75:10290-10299(2001);
DR EMBL; AF303943; AAM97790.1; -;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1180 MW: 4CD6A97771A32763 CRC64;

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

RESULT 9
Q9Q0W7 PRELIMINARY; PRT; 10 AA.
ID Q9Q0W7
AC Q9Q0W7
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NANCY2;
RA MEDLINE=2087544; PubMed=10618230;
RA Bojilli-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.*";
RL Appl. Environ. Microbiol. 66:238-245(2000);
DR EMBL; AF119351; AAF24108.1; -;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

RESULT 10
Q8JV66 PRELIMINARY; PRT; 10 AA.
ID Q8JV66
AC Q8JV66
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CSF K;
RA MEDLINE=21465052; PubMed=11581397;
RA Bojilli-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.*";
RL J. Virol. 75:10290-10299(2001);

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DR EMBL: AF194389; AAM97808.1; -
 FT NON_TER 1
 SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64:

Query Match 36.4% Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKPK 6
 IIII
 DB 2 KKPK 5

RESULT 11

Q9QGV7 PRELIMINARY: PRT; 10 AA.
 AC Q9QGV7
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DI 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 CX NCBI_TaxID:10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN:SFJ.
 RX MEDLINE:20087544; PubMed:19818239;
 RA Hofill-Mas S., Pina S., Girones R.;
 RT "documenting the epidemiologic patterns of polyomaviruses in human
 populations by studying their presence in urban sewage";
 RL Appl. Environ. Microbiol. 66:238-245(2000).
 DR EMBL: AF19456; AAF24118.1;
 FT NON_TER 1
 SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64:

Query Match 36.4% Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKPK 6
 IIII
 DB 2 KKPK 5

RESULT 12

Q8JV82 PRELIMINARY: PRT; 10 AA.
 AC Q8JV82
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DI 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 CX NCBI_TaxID:10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN:EL.
 RX MEDLINE:21465052; PubMed:11581397;
 RA Hofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 gastrointestinal tract after exposure to virions of viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL: AF303944; AAM97792.1;
 FT NON_TER 1
 SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64:

Query Match 36.4% Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
 IIII
 DB 2 KKPK 5

RESULT 13

Q8JV76 PRELIMINARY: PRT; 10 AA.
 AC Q8JV76
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DI 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 CX NCBI_TaxID:10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN:USA2;
 RX MEDLINE:21465052; PubMed:11581397;
 RA Hofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 gastrointestinal tract after exposure to virions of viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL: AF303947; AAM97798.1;
 FT NON_TER 1
 SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match 36.4% Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 KKPK 6
 IIII
 DB 2 KKPK 5

RESULT 14

Q8JV74 PRELIMINARY: PRT; 10 AA.
 AC Q8JV74
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DI 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DE Large T antigen (Fragment).
 OS Polyomavirus JC.
 OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
 CX NCBI_TaxID:10632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN:USA3;
 RX MEDLINE:21465052; PubMed:11581397;
 RA Hofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
 Girones R.;
 RT "Potential transmission of human polyomaviruses through the
 gastrointestinal tract after exposure to virions of viral DNA.";
 RL J. Virol. 75:10290-10299(2001).
 DR EMBL: AF303948; AAM97800.1;
 FT NON_TER 1
 SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match 36.4% Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
 IIII
 DB 2 KKPK 5

RESULT 15

Q9QGX7

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IG Q90X7 PRELIMINARY: PRI: 10 AA
AC Q90X7
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Large T antigen (Fragment)
OS Polyomavirus JC
OC Viruses: dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus
OX NCBI_TaxID:10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BCN2;
RX Botill-Mas S., Pina S., Girones R.;
*Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.*;
RI Appl. Environ. Microbiol. 66:238-245(2000);
RL EMBL: AF119146; AAF24398.1;
DR EMBL: AF119146; AAF24398.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1180 MW: 4036447771A32763 CRC64;

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

RESULT 16
ID Q8JV78 PRELIMINARY: PRI: 10 AA
AC Q8JV78
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
DE Large T antigen (Fragment)
OS Polyomavirus JC
OC Viruses: dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus
OX NCBI_TaxID:10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-USA1;
RX Botill-Mas S., Formiga-Cruz M., Clemente-Benades P., Palacios F.,
Girones R.;
*Potential transmission of human polyomaviruses through the
gastrointestinal tract after exposure to excretions of viral DNA.*;
RI Appl. Environ. Microbiol. 75:10290-10299(2001);
RL EMBL: AF104946; AAM97796.1;
DR EMBL: AF104946; AAM97796.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1183 MW: 4036447771A32763 CRC64;

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

RESULT 17
ID Q90W5 PRELIMINARY: PRI: 10 AA
AC Q90W5
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Large T antigen (Fragment)
OS Polyomavirus JC
OC Viruses: dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus
OX NCBI_TaxID:10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BCN16;
RX Botill-Mas S., Pina S., Girones R.;
*Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.*;
RI Appl. Environ. Microbiol. 66:238-245(2000);
RL EMBL: AF119146; AAF24398.1;
DR EMBL: AF119146; AAF24398.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4036447771A32763 CRC64;

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

RESULT 18
ID Q90X3 PRELIMINARY: PRI: 10 AA
AC Q90X3
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Large T antigen (Fragment)
OS Polyomavirus JC
OC Viruses: dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus
OX NCBI_TaxID:10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BCN8;
RX Botill-Mas S., Pina S., Girones R.;
*Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.*;
RI Appl. Environ. Microbiol. 66:238-245(2000);
RL EMBL: AF119146; AAF24102.1;
DR EMBL: AF119146; AAF24102.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4036447771A32763 CRC64;

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

RESULT 19
ID Q90X5 PRELIMINARY: PRI: 10 AA
AC Q90X5
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Large T antigen (Fragment)
OS Polyomavirus JC
OC Viruses: dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus
OX NCBI_TaxID:10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BCN16;
RX Botill-Mas S., Pina S., Girones R.;
*Documenting the epidemiologic patterns of polyomaviruses in human
populations by studying their presence in urban sewage.*;
RI Appl. Environ. Microbiol. 66:238-245(2000);
RL EMBL: AF119146; AAF24102.1;
DR EMBL: AF119146; AAF24102.1;
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4036447771A32763 CRC64;

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 2 KKPK 5

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DR EMBL: AF119347; AAF24100.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match: 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
   III
Db 2 KKPK 5

RESULT 20
Q900W3 ID Q900W3 PRELIMINARY; PRT; 10 AA.
AC Q900W3:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PRETORIAL;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
   populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119345; AAF24112.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match: 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
   III
Db 2 KKPK 5

RESULT 21
Q8JV80 ID Q8JV80 PRELIMINARY; PRT; 10 AA.
AC Q8JV80:
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=F2;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente Casares F., Catafelli F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
   gastrointestinal tract after exposure to viruses of viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL: AF303945; AAM97794.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match: 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3 KKPK 6
   III
Db 2 KKPK 5

RESULT 22
Q900X1 ID Q900X1 PRELIMINARY; PRT; 10 AA.
AC Q900X1:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCN15;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
   populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119349; AAF24104.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match: 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
   III
Db 2 KKPK 5

RESULT 23
Q900X9 ID Q900X9 PRELIMINARY; PRT; 10 AA.
AC Q900X9:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BCNU;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
   populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119345; AAF24096.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1167 MW: 4CD6A97771A32763 CRC64;

Query Match: 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
   III
Db 2 KKPK 5

RESULT 24
Q8JV72 ID Q8JV72 PRELIMINARY; PRT; 10 AA.
AC Q8JV72:

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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA 4;
RX MEDLINE=21465052; PubMed=11581397;
RA Botill-Mas S., Formiga-Cruz M., Clemente-Diazas P., Calatayud F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions of viral DNA.";
RL J. Virol. 75:10290-10299(2001);
DR EMBL; AF0404386; AAM97802.1;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CDA6A9777AA2763 CR664;

Query Match 36.4%; Score 4; DB 12; Length 10;
Best local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKPK 6
Db 2 KKPK 5

RESULT 25
Q93SR0 PRELIMINARY; PRT; 8 AA.
AC Q93SR0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Beta-lactamase repressor Bial (Fragment).
GN BIAL;
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=6;
RA Sidhu M.S., Heir E., Sorum H., Holck A.L.;
RT "Genetic linkage between quaternary ammonium compound and beta-lactam
RT resistance in Staphylococcus isolated from food.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY028779; AAK38454.1;
KW Plasmid.
FT NON_TER 1
SQ SEQUENCE 8 AA; 930 MW; 4E4425802A64424 CR664;

Query Match 27.3%; Score 3; DB 2; Length 8;
Best local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SKK 4
Db 6 SKK 8

RESULT 26
Q56759 PRELIMINARY; PRT; 8 AA.
AC Q56759;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Halocid dehalogenase (Fragment).
GN DHLB;
OS Xanthobacter autotrophicus.

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OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhymicrobiaceae; Xanthobacter.
OX NCBI_TaxID=280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GJ10, and CV. K50;
RX MEDLINE=95171113; PubMed=7868610;
RA Van der Ploeg J., Willemson M., van Hall G., Jaansen D.B.;
RT "Adaptation of Xanthobacter autotrophicus GJ10 to bromoacetate due to
RT activation and mobilization of the haloacetate dehalogenase gene by
RT insertion element IS1247.";
RL J. Bacteriol. 177:1348-1356(1995).
DR EMBL; X84038; CAA58857.1;
FT NON_TER 8
SQ SEQUENCE 8 AA; 922 MW; F3A9D2D2CDD33056 CR664;

Query Match 27.4%; Score 3; DB 2; Length 8;
Best local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 IKA 11
Db 2 IKA 4

RESULT 27
Q921E9 PRELIMINARY; PRT; 8 AA.
AC Q921E9;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Carbamoyl-phosphate synthase subunit B (Fragment).
GN CARB;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1527;
RX MEDLINE=95291461; PubMed=7773412;
RA Lawson F.S., Billowes F.M., Dillon J.A.;
RT "Organization of carbamoyl-phosphate synthase genes in Neisseria
RT gonorrhoeae includes a large, variable intergenic sequence which is
RT also present in other Neisseria species.";
RL Microbiology 141:0-0(0);
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1527;
RA Brinkman F.S.L., Francis F.M., Dillon J.R.;
RT "Complexity of the variable sequence between the carbamoyl-phosphate
RT synthase genes of Neisseria species.";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF029361; AAC78449.1;
FT NON_TER 8
SQ SEQUENCE 8 AA; 988 MW; FA372AB1B4032766 CR664;

Query Match 27.3%; Score 3; DB 2; Length 8;
Best local Similarity 100.0%; Pred. No. 8.3e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
Db 2 PKR 4

RESULT 28
O19961 PRELIMINARY; PRT; 8 AA.
AC O19961;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein L16 (Fragment).
GN RPL16.
OS Gossypium darwini (Darwin's cotton).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=34276;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL: AF031456; AAC63550.1; -.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 958 MW; 71B5B73411B40327 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
DB 1 PKR 3

RESULT 29
O19958
ID O19958 PRELIMINARY: PRT: 8 AA.
DT 01 JAN-1998 (TrEMBLrel. 05, Created)
DT 01 JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01 DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein L16 (Fragment).
GN RPL16.
OS Gossypium barbadense (Sea-island cotton) (Egyptian cotton).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=3634;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL: AF031453; AAC63547.1; -.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 958 MW; 71B5B73411B40327 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
DB 1 PKR 3

RESULT 30
O19960
ID O19960 PRELIMINARY: PRT: 8 AA.
DT 01 JAN-1998 (TrEMBLrel. 05, Created)
DT 01 JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01 DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein L16 (Fragment).
GN RPL16.
OS Gossypium mustelinum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=34275;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL: AF031455; AAC63549.1; -.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 958 MW; 71B5B73411B40327 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
DB 1 PKR 3

RESULT 32
O19956
ID O19956 PRELIMINARY: PRT: 8 AA.
DT 01 JAN-1998 (TrEMBLrel. 05, Created)
DT 01 JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01 DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribosomal protein L16 (Fragment).
GN RPL16.
OS Gossypium tomentosum.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
OX NCBI_TaxID=34277;
RN [1]
RP SEQUENCE FROM N.A.
RA Small R.L., Ryburn J.A., Cronn R.C., Seelanan T., Wendel J.F.;
RT "The tortoise and the hare: choosing between noncoding plastome and
RT nuclear Adh sequences for phylogeny reconstruction in a recently
RT diverged plant group.";
RL Am. J. Bot. 85:1301-1315(1998).
DR EMBL: AF031454; AAC63548.1; -.
KW Chloroplast.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 958 MW; 71B5B73411B40327 CRC64;

Query Match 27.3%; Score 3; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
DB 1 PKR 3

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01 01-JAN-1998 (TrEMBLrel. 05, Created)
02 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
03 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
04 Ribosomal protein L16 (Fragment)
05 RPL16
06 Gossypium arboreum (Tree cotton)
07 Chloroplast
08 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
09 Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae
10 eucosids II; Malvales; Malvaceae; Malvoideae; Gossypium
11 NCBI_taxid=29723;
12 [[ ]]
13 SEQUENCE FROM N.A.
14 Small R.L., Hyburn J.A., Cronin R.G., Seelanan R., Wendell J.F.
15 "The tortoise and the hare: choosing between noncoding plastome and
16 nuclear Adh sequences for phylogeny reconstruction in a recently
17 diverged plant group."
18 Am. J. Bot. 85:1301-1315(1998).
19 DR EMBL: AF031451; AAC63545.1;
20 KW Chloroplast.
21 FT NON_TER 1 1
22 FT NON_TER 8 8
23 SQ SEQUENCE 8 AA: 958 MW: 71858734.11845323 CRC64:
24
25 Query Match: 27.3%; Score 3; DB 6; Length 8;
26 Best local Similarity 100.0%; Pred. No. 8.3e-05;
27 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
28
29 QY 5 KPK 7
30 DB 1 KPK 3
31
32 RESULT 33
33 Q16605
34 ID Q16605 PRELIMINARY; PRT; 9 AA.
35 AC Q16605;
36 DT 01-NOV-1996 (TrEMBLrel. 05, Created)
37 DT 01-NOV-1996 (TrEMBLrel. 05, Last sequence update)
38 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
39 GN Glutathione S-transferase 2 (Fragment)
40 OS Homo sapiens (Human)
41 EC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
42 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
43 NCBI_taxid=9606;
44 KW [[ ]]
45 SEQUENCE FROM N.A.
46 MEDLINE 8830756; PubMed:8830756;
47 FA Chow N.W., Whang-Peng J., Kao-Shan C., Chen C.M., Fan H.C., Lin C.P.,
48 "Human glutathione S-transferases: the human gene family encodes
49 products of different but evolutionally and structurally related
50 genes."
51 J. Biol. Chem. 263:12797-12803(1988)
52 DR EMBL: M21867; AAA52617.1;
53 DR EMBL: M21866; AAA35938.1;
54 FT NON_TER 9 9
55 SQ SEQUENCE 9 AA: 1116 MW: 11885274.2636341041
56
57 Query Match: 27.3%; Score 3; DB 6; Length 9;
58 Best local Similarity 100.0%; Pred. No. 8.3e-05;
59 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
60
61 QY 4 KPK 6
62 DB 1 KPK 3
63
64 RESULT 34
65 Q90QW0
66 ID Q90QW0 PRELIMINARY; PRT; 9 AA.
67 AC Q90QW0;
68 DT 01-MAY-2000 (TrEMBLrel. 19, Created)
69 DT 01-MAY-2000 (TrEMBLrel. 19, Last sequence update)

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01 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
02 Prolactin precursor (Fragment)
03 Homo sapiens (Human)
04 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
05 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
06 NCBI_taxid=9606;
07 KW [[ ]]
08 SEQUENCE FROM N.A.
09 MEDLINE 84182507; PubMed:84182507;
10 RA Truong A.T., Puez G., Belayew A., Renard A., Pictet R., Sell G.I.,
11 Martial J.A.
12 "Isolation and characterization of the human prolactin gene."
13 EMBO J. 3:429-437(1984).
14 KW [[ ]]
15 SEQUENCE FROM N.A.
16 MEDLINE 9307683; PubMed:9307683;
17 RA Peers B., Naidu A.M., Monnet P., Voz M.L., Belayew A., Martial J.A.
18 "Binding of a 100-kDa ubiquitous factor to the human prolactin
19 promoter is required for its basal and hormone-regulated activity."
20 Eur. J. Biochem. 210:53-58(1992).
21 DR EMBL: X00366; CAA25108.1;
22 KW Signal.
23 FT SIGNAL 1 8 POTENTIAL
24 FT NON_TER 9 9
25 SQ SEQUENCE 9 AA: 1060 MW: 0A1A5775B8733054 CRC64:
26
27 Query Match: 27.3%; Score 3; DB 4; Length 9;
28 Best local Similarity 100.0%; Pred. No. 8.3e-05;
29 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
30
31 QY 8 NIK 10
32 DB 2 NIK 4
33
34 RESULT 35
35 Q912L0
36 ID Q912L0 PRELIMINARY; PRT; 9 AA.
37 AC Q912L0;
38 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
39 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
40 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
41 DE EUC 11-11GHI harvesting chlorophyll protein II (fragment).
42 OS Spinacia oleracea (Spinach)
43 EC Chloroplast
44 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
45 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
46 Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia
47 NCBI_taxid=4562;
48 KW [[ ]]
49 SEQUENCE
50 MEDLINE 9137386; PubMed:9137386;
51 FA Michels H., Griffin P.R., Shabanowitz J., Hunt D.F., Bennett J.
52 " tandem mass spectrometry identifies sites of three post-translational
53 modifications of spinach light harvesting chlorophyll protein II.
54 PT Proteolytic cleavage, acetylation, and phosphorylation."
55 J. Biol. Chem. 266:17584-17591(1991).
56 FT NON_TER 1 1
57 FT NON_TER 9 9
58 SQ SEQUENCE 9 AA: 999 MW: 54U927633875C1A3 CRC64:
59
60 Query Match: 27.3%; Score 3; DB 8; Length 9;
61 Best local Similarity 100.0%; Pred. No. 8.3e-05;
62 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
63
64 QY 4 KPK 6
65 DB 6 KPK 8
66
67 RESULT 36
68 Q912L0 PRELIMINARY; PRT; 9 AA.
69 ID Q912L0

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AC Q9T2L1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01 JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE LHC II-LIGHT-harvesting chlorophyll protein II (Fragment)
OS Spinacia oleracea (Spinach)
OG Chloroplast
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia
CX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE
RX MEDLINE=9137386; PubMed=1894441;
RA Michel H., Griffin P.R., Shabawatziz Z., Hunt D.F., Branton D.
RT "Random mass spectrometry identifies sites of three post-translational
RT modifications of spinach light-harvesting chlorophyll protein II.
RT Proteolytic cleavage, acetylation, and phosphorylation";
RL J. Biol. Chem. 266:17584-17591(1991).
FT NON_TER 1 9
FT NON_TER 9 1
SQ SEQUENCE 9 AA; 985 MW; 549276538750bps (8-b4);

Query Match 27.3%; Score 3; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKR 6
DB 6 PKR 8

RESULT 37
071067 ID 071067 PRELIMINARY: PRT; 9 AA.
AC 071067
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DI 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DI 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
CX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN Fitch #174/91;
RA Lieberman H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses";
RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF026215; AAC09165.1;
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 1088 MW; 10900327605B1444 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
DB 5 PKR 8

RESULT 38
071068 ID 071068 PRELIMINARY: PRT; 9 AA.
AC 071068
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DI 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

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DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OS Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbilliviruses.
CX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Marten #1;
RA Lieberman H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses";
RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF026215; AAC09166.1;
FT NON_TER 9
FT NON_TER 9
SQ SEQUENCE 9 AA; 1088 MW; 10900327605B1444 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
DB 6 PKR 8

RESULT 39
09JN49 ID 09JN49 PRELIMINARY: PRT; 10 AA.
AC 09JN49
DI 01-OCT-2000 (TrEMBLrel. 15, Created)
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DI 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Plasmid pEl94 ermc leader region (Fragment).
OS Staphylococcus aureus.
CX Plasmid pEl94
CX Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041917; PubMed=3904662;
RA Narayanan C.S., Dubnau D.;
RT "Evidence for the translational attenuation model: ribosome-binding
RT studies and structural analysis with an in vitro run-off transcript
RT of ermc";
RL Nucleic Acids Res. 13:7307-7326(1985).
DR EMBL; X03097; CAA26884.1;
KW Plasmid.
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1228 MW; 586C88E33054433B CRC64;

Query Match 27.3%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NIK 10
DB 5 NIK 7

RESULT 40
081ZA2 ID 081ZA2 PRELIMINARY: PRT; 10 AA.
AC 081ZA2
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DI 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DI 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Cardiac troponin T (Fragment).
GN TNNT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE:Blood;
 RA Bahl A., Kubo I., Steffensen J., Steffensen M., McKenna W.J.,
 RA Koepsen J.;
 RT "Homo sapiens Troponin T (TNNT2) isoforms 4 and 2 and exons 7";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases;
 DR EMBL: AY160215; AAN71650.1;
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA: 1099 MW: 442440.62566134.6 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKR 6

DB 7 PKR 9

RESULT 41

Q8HUB4 PRELIMINARY; PRT; 1 AA.
 AC Q8HUB4;
 DT 01-MAR-2003 (TRENBLrel. 23, Created)
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Ribosomal protein L16 (Fragment).
 GN RPL16.
 OS Anopheles gambiae.
 CC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 CC Bryopsida; Bryidae; Bryales; Bryaceae; Anomaliaceae.
 OX NCBI_TaxID:67232;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AJ607;
 RA Pedersen N., Cox C., Hedenas L.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases;
 DR EMBL: AF548765; AAN62980.1;
 KW Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 30 10
 SQ SEQUENCE 10 AA: 1326 MW: 641424.6972104 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7

DB 1 PKR 3

RESULT 42

Q8LPT7 PRELIMINARY; PRT; 1 AA.
 AC Q8LPT7;
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TRENBLrel. 22, Last annotation update)
 DE Beta-expansin-like protein (Fragment).
 OS Zea mays (Maize).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Fractosphyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC PACAD clade; Panicoideae; Andropogoneae; Zea
 OX NCBI_TaxID:4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-cv. H98;
 RA Ching A.S., Caldwell K.S., Jung M., Datta M., Smith G.S., Lindey S.;

RA Morgante M., Rafalski J.A.;
 RT "SNP frequency, haplotype structure and linkage disequilibrium in
 RT elite maize inbred lines";
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases;
 DR EMBL: AY094308; AAM21834.1;
 FT NON_TER 1 1
 SQ SEQUENCE 10 AA: 1048 MW: 5C55B7D2CB1AAAA3 CRC64;

Query Match 27.3%; Score 3; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASK 3

DB 1 ASK 3

RESULT 43

O73594 PRELIMINARY; PRT; 10 AA.
 AC O73594;
 DT 01-AUG-1998 (TRENBLrel. 07, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
 DE Zax-2 (Fragment).
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Choriata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 CC Gallus.
 OX NCBI_TaxID:96031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-White leghorn; TISSUE:Embryo;
 RA MEDLINE:96141813; PubMed:9473273;
 RA Peale F.V. Jr., Mason K., Hunter A.W., Bothwell M.;
 RT "Multiplex display polymerase chain reaction amplifies and resolves
 RT related sequences sharing a single moderately conserved domain";
 RL Anal. Biochem. 256:158-168(1998).
 DR EMBL: U34617; AAC36455.1;
 FT NON_TER 1 1
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA: 1068 MW: 9A7598276728705A CRC64;

Query Match 27.3%; Score 3; DB 13; Length 10;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7

DB 7 PKR 9

RESULT 44

O9S618 PRELIMINARY; PRT; 11 AA.
 AC O9S618;
 DT 01-MAY-2000 (TRENBLrel. 13, Created)
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
 DE Cytochrome b6/f complex subunit IV (Fragment).
 GN PETD.
 OS Prochlorococcus sp.
 CC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;
 CC Prochlorococcus.
 OX NCBI_TaxID:1220;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Urbach E., Chisholm S.W.;
 RT "Genetic diversity in Prochlorococcus populations flow cytometrically
 RT sorted from the Sargasso Sea and Gulf Stream";
 RL Limnol. Oceanogr. 43:1615-1630(1998).
 DR EMBL: AF070332; AAD20740.1;
 FT NON_TER 11 11

SQ SEQUENCE 11 AA: 1297 MW: 5CC38013B7633337 CRC64;
 Query Match: 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KKP 5
 DB 5 KKP 7
 RESULT 45
 Q25916 PRELIMINARY; PRT; 11 AA.
 AC Q25916;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical 1.3 kDa protein.
 GN ZK1236.8.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RX MEDLINE=99069613; PubMed=9851516;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 investigating biology. The C. elegans Sequencing Consortium."
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Favella A.;
 RT "Ibe sequence of C. elegans cosmid ZK1236."
 RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Waterston R.;
 RT "Direct Submission."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; L13209; AAL11108.1;
 DR WormPep; ZK1236.8; CE29629.
 KW Hypothetical protein.
 SQ SEQUENCE 11 AA: 1304 MW: DFAF510A25A76422 CRC44;
 Query Match: 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SKK 4
 DB 7 SKK 9
 RESULT 46
 Q25916 PRELIMINARY; PRT; 11 AA.
 AC Q25916;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Malaria antigen (7H8/2) (Fragment).
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=91164876; PubMed=1706114;
 RX Limpaloon T., Taylor D., Jones G., Geyson H.M., Saul A.;

RT *Characterization of a Plasmodium falciparum epitope recognized by a
 RT monoclonal antibody with broad isolate and species specificity.*;
 RL Southeast Asian J. Trop. Med. Public Health 21:388-396(1990).
 DR EMBL; M31305; AAA29645.1;
 FT NON_TER 1
 SQ SEQUENCE 11 AA: 1415 MW: DR03D3BC42C33699 CRC64;
 Query Match: 27.3%; Score 3; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RNI 9
 DB 9 RNI 11
 RESULT 47
 Q9TQSO PRELIMINARY; PRT; 11 AA.
 AC Q9TQSO;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE C-KIT (Fragment).
 GN KIT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Olsen H.G., Vage D.I., Lien S., Klungland H.;
 RT "A polymorphism in the bovine c-kit gene."
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ243424; CAB60775.1;
 DR EMBL; AJ243066; CAB60774.1;
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA: 1126 MW: DD785FF8A2D2D772 CRC64;
 Query Match: 27.3%; Score 3; DB 6; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 IKA 11
 DB 1 IKA 3
 RESULT 48
 Q38415 PRELIMINARY; PRT; 11 AA.
 AC Q38415;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Anti protein (Fragment).
 OS Bacteriophage P7.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
 OC P1-like viruses.
 OX NCBI_TaxID=10682;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90335968; PubMed=1696181;
 RA Citron M., Schuster H.;
 RT "The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.";
 RL Cell 62:591-598(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92319637; PubMed=1620606;
 RA Citron M., Schuster H.;
 RT "The c4 repressor of bacteriophage P1 is a processed 77 base antisense

RT RNA:";
 AC Nucleic Acids Res. 20:3065-3090(1992).
 LR EMBL: M35139; AAA32437.1; ..
 FT NON_TER 11
 SQ SEQUENCE 11 AA: 1315 MW: 38A50C6D11B20737 CR664;
 Query Match 27.38; Score 4; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 KKP 5
 DB 2 KKP 4

RESULT 49
 Q04131
 ID Q04131 PRELIMINARY; PRI: 11 AA;
 AC Q04131;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE Wound induced protein (Fragment).
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Asteridae; lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=pi8-rod; TISSUE=Pericarp;
 RX MEDLINE=9155536; PubMed-1715787;
 RA Parsons B.L., Mattoo A.K.;
 RT "Wound regulated accumulation of specific transcripts in tomato fruit:
 RT Interactions with fruit development, ethylene and light.";
 RL Plant Mol. Biol. 17:453-464(1991).
 DR EMBL: X59864; CAA42539.1; ..
 FT NON_TER 1
 SQ SEQUENCE 11 AA: 1278 MW: 92CB25782H734425 CR664;

Query Match 27.38; Score 4; DB 10; Length 11;
 Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SKK 4
 DB 4 SKK 6

RESULT 50
 Q86866
 ID Q86866 PRELIMINARY; PRI: 11 AA;
 AC Q86866;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE S-RNA product protein (Fragment).
 OS S-RNA PRODUCT.
 OC Lymphocytic choriomeningitis virus.
 OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
 OX NCBI_TaxID=11623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=9519090; PubMed-7534851;
 RA Moskephidis D., Zinkernagel R.M.;
 RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
 RT choriomeningitis virus.";
 RL J. Virol. 69:2187-2193(1995).
 DR EMBL: S75748; AAB33668.1; ..
 FT NON_TER 1
 SQ SEQUENCE 11 AA: 1200 MW: 54245C80C9C45B57 CR664;
 Query Match 27.38; Score 3; DB 12; Length 11;

Best Local Similarity 100.0%; Pred. No. 8.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 IKA 11
 DB 1 IKA 3

Search completed: September 30, 2003, 10:16:23
 Job time : 59.6667 secs

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CM protein - protein search, using sw mode.

R.n on: September 30, 2003, 10:27:05 : Search time 11:54:33 Seconds
(without documents)
19,443 Million coll updates/sec

Title: US-09-787-443-1
Perfect score: 11
Sequence: 1 ASKPKRNKA 11

Scoring table: GUSO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 423,0658 residues

Word size : 0

Total number of hits satisfying chosen parameters: 78459

Minimum LB seq length: 8
Maximum LB seq length: 15

Post-Processing: listing first 500 summaries

Database : Issued Patents,AA:*

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- 2: /cgn2_6/ptodata/1/1aa/8_00MB.pat*
- 3: /cgn2_6/ptodata/1/1aa/FA_00MB.pat*
- 4: /cgn2_6/ptodata/1/1aa/8_00MB.pat*
- 5: /cgn2_6/ptodata/1/1aa/10_00MB.pat*
- 6: /cgn2_6/ptodata/1/1aa/backlist.pat*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY:

Result No.	Score	Query	Match	Length	DB ID	Description
1	4	46.4	8	1	US-08-266-814-20	Sequence 12, Appl
2	4	46.4	8	2	US-09-664-614-20	Sequence 12, Appl
3	4	46.4	8	5	US-07-281-617-91	Sequence 45, Appl
4	4	46.4	9	1	US-08-156-626-11	Sequence 14, Appl
5	4	46.4	9	3	US-08-156-626-11	Sequence 14, Appl
6	4	46.4	9	3	US-08-156-626-11	Sequence 14, Appl
7	4	46.4	9	3	US-08-156-626-11	Sequence 14, Appl
8	4	46.4	9	3	US-08-156-626-11	Sequence 14, Appl
9	4	46.4	10	1	US-08-401-612-63	Sequence 57, Appl
10	4	46.4	10	1	US-08-242-630-1	Sequence 6, Appl
11	4	46.4	10	2	US-08-406-630-12	Sequence 19, Appl
12	4	46.4	10	2	US-07-885-639-27	Sequence 27, Appl
13	4	46.4	10	2	US-08-556-639-27	Sequence 19, Appl
14	4	46.4	11	1	US-08-416-636-8	Sequence 7, Appl
15	4	46.4	13	5	US-08-556-639-27	Sequence 7, Appl
16	4	46.4	15	2	US-08-614-632-6	Sequence 5, Appl
17	4	46.4	15	2	US-08-614-632-6	Sequence 5, Appl
18	4	46.4	15	2	US-08-614-632-6	Sequence 5, Appl
19	4	46.4	15	2	US-08-614-632-6	Sequence 5, Appl
20	4	46.4	15	2	US-08-614-632-6	Sequence 5, Appl
21	4	46.4	15	3	US-09-641-637-18	Sequence 17, Appl
22	4	46.4	15	3	US-09-641-637-18	Sequence 17, Appl
23	4	46.4	15	3	US-08-614-632-6	Sequence 18, Appl
24	4	46.4	15	3	US-08-614-632-6	Sequence 18, Appl
25	4	46.4	15	4	US-09-641-637-18	Sequence 17, Appl
26	4	46.4	15	4	US-09-641-637-18	Sequence 17, Appl
27	4	46.4	15	4	US-09-641-637-18	Sequence 17, Appl

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29	3	27.3	8	1	US-07-920-597-1	Sequence 1, Appl
30	3	27.3	8	1	US-07-920-597-2	Sequence 2, Appl
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32	3	27.3	8	1	US-08-261-525A-3	Sequence 3, Appl
33	3	27.3	8	1	US-08-240-514-39	Sequence 39, Appl
34	3	27.3	8	1	US-08-249-367-5	Sequence 5, Appl
35	3	27.3	8	1	US-08-467-264-19	Sequence 19, Appl
36	3	27.3	8	1	US-08-416-035-9	Sequence 3, Appl
37	3	27.3	8	1	US-08-416-035-9	Sequence 9, Appl
38	3	27.3	8	1	US-08-024-253-13	Sequence 13, Appl
39	3	27.3	8	1	US-08-209-261B-10	Sequence 10, Appl
40	3	27.3	8	2	US-08-612-302A-39	Sequence 39, Appl
41	3	27.3	8	2	US-08-373-190-48	Sequence 48, Appl
42	3	27.3	8	2	US-08-968-676-82	Sequence 82, Appl
43	3	27.3	8	2	US-09-016-366A-47	Sequence 47, Appl
44	3	27.3	8	2	US-08-438-190A-48	Sequence 48, Appl
45	3	27.3	8	2	US-08-318-856A-3	Sequence 3, Appl
46	3	27.3	8	2	US-08-318-856A-29	Sequence 29, Appl
47	3	27.3	8	2	US-08-318-856A-68	Sequence 68, Appl
48	3	27.3	8	2	US-08-318-856A-69	Sequence 69, Appl
49	3	27.3	8	2	US-08-819-013-11	Sequence 11, Appl
50	3	27.3	8	2	US-08-482-627-2	Sequence 2, Appl
51	3	27.3	8	3	US-08-350-215-48	Sequence 48, Appl
52	3	27.3	8	3	US-08-159-339A-1052	Sequence 1052, Ap
53	3	27.3	8	3	US-08-159-339A-1122	Sequence 1122, Ap
54	3	27.3	8	3	US-09-287-145A-48	Sequence 48, Appl
55	3	27.3	8	3	US-08-444-818-631	Sequence 631, Appl
56	3	27.3	8	3	US-09-092-636-11	Sequence 11, Appl
57	3	27.3	8	3	US-09-060-410-26	Sequence 26, Appl
58	3	27.3	8	3	US-09-190-964-12	Sequence 12, Appl
59	3	27.3	8	3	US-08-563-524A-27	Sequence 27, Appl
60	3	27.3	8	3	US-09-100-930A-19	Sequence 19, Appl
61	3	27.3	8	3	US-09-366-103-5	Sequence 5, Appl
62	3	27.3	8	3	US-08-392-459-48	Sequence 48, Appl
63	3	27.3	8	3	US-09-276-141-6	Sequence 6, Appl
64	3	27.3	8	4	US-09-230-548-9	Sequence 9, Appl
65	3	27.3	8	4	US-09-230-548-12	Sequence 12, Appl
66	3	27.3	8	4	US-09-556-111-48	Sequence 48, Appl
67	3	27.3	8	4	US-08-197-484-17	Sequence 17, Appl
68	3	27.3	8	4	US-09-484-848-8	Sequence 8, Appl
69	3	27.3	8	4	US-09-670-075A-1	Sequence 1, Appl
70	3	27.3	8	4	US-09-007-288E-62	Sequence 62, Appl
71	3	27.3	8	4	US-08-635-886C-350	Sequence 150, App
72	3	27.3	8	4	US-09-367-777-72	Sequence 72, Appl
73	3	27.3	8	4	US-09-367-777-90	Sequence 90, Appl
74	3	27.3	8	4	US-09-367-777-91	Sequence 91, Appl
75	3	27.3	8	4	US-09-367-777-92	Sequence 92, Appl
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78	3	27.3	8	4	US-09-367-791A-33	Sequence 33, Appl
79	3	27.3	8	4	US-09-367-791A-35	Sequence 35, Appl
80	3	27.3	8	4	US-09-367-791A-66	Sequence 66, Appl
81	3	27.3	8	4	US-09-367-791A-67	Sequence 67, Appl
82	3	27.3	8	4	US-09-367-791A-88	Sequence 88, Appl
83	3	27.3	8	4	US-08-817-832B-9	Sequence 9, Appl
84	3	27.3	8	4	US-08-817-832B-14	Sequence 14, Appl
85	3	27.3	8	4	US-09-723-458-26	Sequence 26, Appl
86	3	27.3	8	5	US-09-08525-48	Sequence 48, Appl
87	3	27.3	8	5	US-09-08525-48	Sequence 17, Appl
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192	3	27.3	9	1	US-08-454-207A-28	Sequence 28, Appl	175	3	27.3	9	3	US-08-159-339A-346	Sequence 346, App
193	3	27.3	9	1	US-08-454-207A-29	Sequence 29, Appl	176	3	27.3	9	3	US-08-159-339A-491	Sequence 491, App
194	3	27.3	9	1	US-08-454-207A-30	Sequence 30, Appl	177	3	27.3	9	3	US-08-159-339A-492	Sequence 492, App
195	3	27.3	9	1	US-08-454-207A-31	Sequence 31, Appl	178	3	27.3	9	3	US-08-159-339A-1019	Sequence 1019, App
196	3	27.3	9	1	US-08-454-207A-32	Sequence 32, Appl	179	3	27.3	9	3	US-08-159-339A-1061	Sequence 1061, App
197	3	27.3	9	1	US-08-454-207A-33	Sequence 33, Appl	180	3	27.3	9	3	US-08-159-339A-1089	Sequence 1089, App
198	3	27.3	9	1	US-08-454-207A-34	Sequence 34, Appl	181	3	27.3	9	3	US-08-159-339A-1090	Sequence 1090, App
199	3	27.3	9	1	US-08-454-207A-35	Sequence 35, Appl	182	3	27.3	9	3	US-09-231-797-85	Sequence 85, Appl
200	3	27.3	9	1	US-08-454-207A-36	Sequence 36, Appl	183	3	27.3	9	3	US-03-952-967-14	Sequence 14, Appl
201	3	27.3	9	1	US-08-454-207A-37	Sequence 37, Appl	184	3	27.3	9	3	US-04-952-967-16	Sequence 16, Appl
202	3	27.3	9	1	US-08-454-207A-38	Sequence 38, Appl	185	3	27.3	9	3	US-04-089-397A-20	Sequence 20, Appl
203	3	27.3	9	1	US-08-454-207A-39	Sequence 39, Appl	186	3	27.3	9	3	US-06-756-849-117	Sequence 117, App
204	3	27.3	9	1	US-06-454-207A-40	Sequence 40, Appl	187	3	27.3	9	3	US-06-756-849-119	Sequence 119, App
205	3	27.3	9	1	US-08-454-207A-41	Sequence 41, Appl	188	3	27.3	9	3	US-06-934-224-85	Sequence 85, Appl
206	3	27.3	9	1	US-08-454-207A-42	Sequence 42, Appl	189	3	27.3	9	3	US-08-643-819-25	Sequence 25, Appl
207	3	27.3	9	1	US-08-454-207A-43	Sequence 43, Appl	190	3	27.3	9	3	US-08-933-843-85	Sequence 85, Appl
208	3	27.3	9	1	US-08-454-207A-44	Sequence 44, Appl	191	3	27.3	9	3	US-08-934-223-85	Sequence 85, Appl
209	3	27.3	9	1	US-08-454-207A-45	Sequence 45, Appl	192	3	27.3	9	3	US-08-723-425A-183	Sequence 183, App
210	3	27.3	9	1	US-08-454-207A-46	Sequence 46, Appl	193	3	27.3	9	3	US-08-723-425A-184	Sequence 184, App
211	3	27.3	9	1	US-08-454-207A-47	Sequence 47, Appl	194	3	27.3	9	3	US-08-723-425A-185	Sequence 185, App
212	3	27.3	9	1	US-08-454-207A-48	Sequence 48, Appl	195	3	27.3	9	3	US-08-723-425A-186	Sequence 186, App
213	3	27.3	9	1	US-08-454-207A-49	Sequence 49, Appl	196	3	27.3	9	3	US-08-723-425A-187	Sequence 187, App
214	3	27.3	9	1	US-08-454-207A-50	Sequence 50, Appl	197	3	27.3	9	3	US-08-723-425A-188	Sequence 188, App
215	3	27.3	9	1	US-08-454-207A-51	Sequence 51, Appl	198	3	27.3	9	3	US-08-723-425A-189	Sequence 189, App
216	3	27.3	9	1	US-08-454-207A-52	Sequence 52, Appl	199	3	27.3	9	3	US-08-723-425A-190	Sequence 190, App
217	3	27.3	9	1	US-08-454-207A-53	Sequence 53, Appl	200	3	27.3	9	3	US-08-723-425A-191	Sequence 191, App
218	3	27.3	9	1	US-08-454-207A-54	Sequence 54, Appl	201	3	27.3	9	3	US-08-723-425A-192	Sequence 192, App
219	3	27.3	9	1	US-08-454-207A-55	Sequence 55, Appl	202	3	27.3	9	3	US-08-723-425A-193	Sequence 193, App
220	3	27.3	9	1	US-08-454-207A-56	Sequence 56, Appl	203	3	27.3	9	3	US-08-723-425A-194	Sequence 194, App
221	3	27.3	9	1	US-08-454-207A-57	Sequence 57, Appl	204	3	27.3	9	3	US-08-723-425A-195	Sequence 195, App
222	3	27.3	9	1	US-08-454-207A-58	Sequence 58, Appl	205	3	27.3	9	3	US-08-723-425A-427	Sequence 427, App
223	3	27.3	9	1	US-08-454-207A-59	Sequence 59, Appl	206	3	27.3	9	3	US-08-723-425A-428	Sequence 428, App
224	3	27.3	9	1	US-08-454-207A-60	Sequence 60, Appl	207	3	27.3	9	3	US-08-723-425A-429	Sequence 429, App
225	3	27.3	9	1	US-08-454-207A-61	Sequence 61, Appl	208	3	27.3	9	3	US-08-723-425A-430	Sequence 430, App
226	3	27.3	9	1	US-08-454-207A-62	Sequence 62, Appl	209	3	27.3	9	3	US-08-723-425A-431	Sequence 431, App
227	3	27.3	9	1	US-08-454-207A-63	Sequence 63, Appl	210	3	27.3	9	3	US-08-723-425A-432	Sequence 432, App
228	3	27.3	9	1	US-08-454-207A-64	Sequence 64, Appl	211	3	27.3	9	3	US-08-723-425A-433	Sequence 433, App
229	3	27.3	9	1	US-08-454-207A-65	Sequence 65, Appl	212	3	27.3	9	3	US-09-068-753B-1	Sequence 1, Appl1
230	3	27.3	9	1	US-08-454-207A-66	Sequence 66, Appl	213	3	27.3	9	3	US-09-258-754-145	Sequence 145, App
231	3	27.3	9	1	US-08-454-207A-67	Sequence 67, Appl	214	3	27.3	9	3	US-08-604-365-13	Sequence 13, Appl1
232	3	27.3	9	1	US-08-454-207A-68	Sequence 68, Appl	215	3	27.3	9	3	US-09-306-044-1	Sequence 1, Appl1
233	3	27.3	9	1	US-08-454-207A-69	Sequence 69, Appl	216	3	27.3	9	3	US-08-482-918-69	Sequence 69, Appl
234	3	27.3	9	1	US-08-454-207A-70	Sequence 70, Appl	217	3	27.3	9	3	US-09-224-681-69	Sequence 69, Appl
235	3	27.3	9	1	US-08-454-207A-71	Sequence 71, Appl	218	3	27.3	9	3	US-08-336-728A-69	Sequence 69, Appl
236	3	27.3	9	1	US-08-454-207A-72	Sequence 72, Appl	219	3	27.3	9	3	US-09-112-206-183	Sequence 183, App
237	3	27.3	9	1	US-08-454-207A-73	Sequence 73, Appl	220	3	27.3	9	3	US-09-112-206-184	Sequence 184, App
238	3	27.3	9	1	US-08-454-207A-74	Sequence 74, Appl	221	3	27.3	9	3	US-09-112-206-185	Sequence 185, App
239	3	27.3	9	1	US-08-454-207A-75	Sequence 75, Appl	222	3	27.3	9	3	US-09-112-206-186	Sequence 186, App
240	3	27.3	9	1	US-08-454-207A-76	Sequence 76, Appl	223	3	27.3	9	3	US-09-112-206-187	Sequence 187, App
241	3	27.3	9	1	US-08-454-207A-77	Sequence 77, Appl	224	3	27.3	9	3	US-09-112-206-188	Sequence 188, App
242	3	27.3	9	1	US-08-454-207A-78	Sequence 78, Appl	225	3	27.3	9	3	US-09-112-206-189	Sequence 189, App
243	3	27.3	9	1	US-08-454-207A-79	Sequence 79, Appl	226	3	27.3	9	3	US-09-112-206-190	Sequence 190, App
244	3	27.3	9	1	US-08-454-207A-80	Sequence 80, Appl	227	3	27.3	9	3	US-09-112-206-191	Sequence 191, App
245	3	27.3	9	1	US-08-454-207A-81	Sequence 81, Appl	228	3	27.3	9	3	US-09-112-206-192	Sequence 192, App
246	3	27.3	9	1	US-08-454-207A-82	Sequence 82, Appl	229	3	27.3	9	3	US-09-112-206-193	Sequence 193, App
247	3	27.3	9	1	US-08-454-207A-83	Sequence 83, Appl	230	3	27.3	9	3	US-09-112-206-194	Sequence 194, App
248	3	27.3	9	1	US-08-454-207A-84	Sequence 84, Appl	231	3	27.3	9	3	US-09-112-206-195	Sequence 195, App
249	3	27.3	9	1	US-08-454-207A-85	Sequence 85, Appl	232	3	27.3	9	3	US-09-112-206-427	Sequence 427, App
250	3	27.3	9	1	US-08-454-207A-86	Sequence 86, Appl	233	3	27.3	9	3	US-09-112-206-428	Sequence 428, App
251	3	27.3	9	1	US-08-454-207A-87	Sequence 87, Appl	234	3	27.3	9	3	US-09-112-206-429	Sequence 429, App
252	3	27.3	9	1	US-08-454-207A-88	Sequence 88, Appl	235	3	27.3	9	3	US-09-112-206-430	Sequence 430, App
253	3	27.3	9	1	US-08-454-207A-89	Sequence 89, Appl	236	3	27.3	9	3	US-09-112-206-431	Sequence 431, App
254	3	27.3	9	1	US-08-454-207A-90	Sequence 90, Appl	237	3	27.3	9	3	US-09-112-206-432	Sequence 432, App
255	3	27.3	9	1	US-08-454-207A-91	Sequence 91, Appl	238	3	27.3	9	3	US-09-112-206-433	Sequence 433, App
256	3	27.3	9	1	US-08-454-207A-92	Sequence 92, Appl	239	3	27.3	9	3	US-09-042-107-145	Sequence 145, App
257	3	27.3	9	1	US-08-454-207A-93	Sequence 93, Appl	240	3	27.3	9	3	US-09-413-492-85	Sequence 85, Appl
258	3	27.3	9	1	US-08-454-207A-94	Sequence 94, Appl	241	3	27.3	9	3	US-08-910-820-18	Sequence 18, Appl
259	3	27.3	9	1	US-08-454-207A-95	Sequence 95, Appl	242	3	27.3	9	3	US-09-133-062D-8	Sequence 8, Appl1
260	3	27.3	9	1	US-08-454-207A-96	Sequence 96, Appl	243	3	27.3	9	3	US-09-133-062D-9	Sequence 9, Appl1
261	3	27.3	9	1	US-08-454-207A-97	Sequence 97, Appl	244	3	27.3	9	3	US-09-510-738A-134	Sequence 134, App
262	3	27.3	9	1	US-08-454-207A-98	Sequence 98, Appl	245	3	27.3	9	3	US-09-171-945-30	Sequence 30, Appl
263	3	27.3	9	1	US-08-454-207A-99	Sequence 99, Appl	246	3	27.3	9	3	US-09-502-600-97	Sequence 97, Appl

247	3	27.3	9	3	US-59-502-600-95	Sequence 94, Appl	320	3	27.3	10	4	US-09-396-347F-82	Sequence 82, Appl
248	3	27.3	9	3	US-09-502-600-106	Sequence 106, App	321	3	27.3	10	4	US-09-520-698-8	Sequence 8, Appl
249	3	27.3	9	3	US-09-502-600-157	Sequence 157, App	322	3	27.3	10	4	US-09-344-040C-101	Sequence 101, App
250	3	27.3	9	3	US-09-502-600-129	Sequence 129, App	323	3	27.3	10	4	US-09-206-576-10	Sequence 10, Appl
251	3	27.3	9	3	US-09-502-600-130	Sequence 130, App	324	3	27.3	10	4	US-09-151-450-15	Sequence 15, Appl
252	3	27.3	9	4	US-09-424-480H-1	Sequence 1, Appl	325	3	27.3	10	4	US-08-983-157B-13	Sequence 13, Appl
253	3	27.3	9	4	US-09-448-986-5	Sequence 25, Appl	326	3	27.3	10	4	US-08-983-157B-17	Sequence 17, Appl
254	3	27.3	9	4	US-09-351-296-40	Sequence 40, Appl	327	3	27.3	10	4	US-08-983-157B-18	Sequence 18, Appl
255	3	27.3	9	4	US-08-766-596A-50	Sequence 50, Appl	328	3	27.3	10	4	US-08-978-277A-5	Sequence 5, Appl
256	3	27.3	9	4	US-09-259-478A-5	Sequence 5, Appl	329	3	27.3	10	5	PCT-US92-00731-2	Sequence 2, Appl
257	3	27.3	9	4	US-09-461-425-62	Sequence 504, App	330	3	27.3	10	5	PCT-US92-00731-6	Sequence 6, Appl
258	3	27.3	9	4	US-09-129-1927-51	Sequence 51, Appl	331	3	27.3	10	5	PCT-US92-00731-7	Sequence 7, Appl
259	3	27.3	9	4	US-09-101-372B-77	Sequence 77, Appl	332	3	27.3	10	5	PCT-US93-07261-8	Sequence 8, Appl
260	3	27.3	9	4	US-09-861-766-134	Sequence 134, App	333	3	27.3	10	5	PCT-US94-04496-78	Sequence 78, Appl
261	3	27.3	9	4	US-08-774-189-24	Sequence 24, Appl	334	3	27.3	10	5	PCT-US95-07539-10	Sequence 10, Appl
262	3	27.3	9	4	US-09-311-784A-266	Sequence 266, App	335	3	27.3	10	6	5190919-19	Patent No. 5190919
263	3	27.3	9	4	US-09-387-715-10	Sequence 10, Appl	336	3	27.3	10	6	5223424-8	Patent No. 5223424
264	3	27.3	9	4	US-09-844-768-18	Sequence 18, Appl	337	3	27.3	11	1	US-07-666-719-18	Sequence 18, Appl
265	3	27.3	9	5	PCT-US94-09143-25	Sequence 20, Appl	338	3	27.3	11	1	US-07-842-089E-16	Sequence 16, Appl
266	3	27.3	9	6	5365712-5	Patent No. 5365712	339	3	27.3	11	1	US-07-842-089E-17	Sequence 17, Appl
267	3	27.3	10	1	US-07-666-315A-5	Sequence 5, Appl	340	3	27.3	11	1	US-07-603-675-8	Sequence 8, Appl
268	3	27.3	10	1	US-08-139-254-4	Sequence 4, Appl	341	3	27.3	11	1	US-08-264-485-16	Sequence 16, Appl
269	3	27.3	10	1	US-08-405-200-21	Sequence 21, Appl	342	3	27.3	11	1	US-08-264-485-17	Sequence 17, Appl
270	3	27.3	10	1	US-08-454-207A-2	Sequence 2, Appl	343	3	27.3	11	1	US-08-111-939-7	Sequence 7, Appl
271	3	27.3	10	1	US-08-454-207A-5	Sequence 5, Appl	344	3	27.3	11	1	US-08-116-733-1	Sequence 1, Appl
272	3	27.3	10	1	US-08-039-137-21	Sequence 21, Appl	345	3	27.3	11	1	US-08-116-733-31	Sequence 31, Appl
273	3	27.3	10	1	US-07-869-543-14	Sequence 14, Appl	346	3	27.3	11	1	US-08-116-733-32	Sequence 32, Appl
274	3	27.3	10	1	US-08-218-226-52	Sequence 52, Appl	347	3	27.3	11	1	US-08-116-733-36	Sequence 36, Appl
275	3	27.3	10	1	US-08-218-226-54	Sequence 54, Appl	348	3	27.3	11	1	US-08-116-733-37	Sequence 37, Appl
276	3	27.3	10	1	US-08-258-852-13	Sequence 13, Appl	349	3	27.3	11	1	US-08-116-733-38	Sequence 38, Appl
277	3	27.3	10	2	US-08-654-642-52	Sequence 52, Appl	350	3	27.3	11	1	US-08-116-733-39	Sequence 39, Appl
278	3	27.3	10	2	US-08-654-642-53	Sequence 53, Appl	351	3	27.3	11	1	US-08-116-733-40	Sequence 40, Appl
279	3	27.3	10	2	US-08-621-803-218	Sequence 218, App	352	3	27.3	11	1	US-08-116-733-41	Sequence 41, Appl
280	3	27.3	10	2	US-08-621-259A-210	Sequence 210, App	353	3	27.3	11	1	US-08-462-413-2	Sequence 2, Appl
281	3	27.3	10	2	US-08-643-148-5	Sequence 5, Appl	354	3	27.3	11	1	US-08-432-694-16	Sequence 16, Appl
282	3	27.3	10	2	US-08-643-148-14	Sequence 14, Appl	355	3	27.3	11	1	US-08-336-343A-23	Sequence 23, Appl
283	3	27.3	10	2	US-08-556-597-123	Sequence 123, App	356	3	27.3	11	1	US-08-314-202-1	Sequence 1, Appl
284	3	27.3	10	2	US-08-556-597-153	Sequence 153, App	357	3	27.3	11	1	US-08-366-953A-27	Sequence 27, Appl
285	3	27.3	10	2	US-08-535-116-15	Sequence 15, Appl	358	3	27.3	11	1	US-08-218-026-58	Sequence 58, Appl
286	3	27.3	10	3	US-08-159-339A-456	Sequence 456, App	359	3	27.3	11	1	US-08-408-604A-103	Sequence 103, App
287	3	27.3	10	3	US-08-159-339A-501	Sequence 501, App	360	3	27.3	11	2	US-08-653-632-58	Sequence 58, Appl
288	3	27.3	10	3	US-08-159-339A-1041	Sequence 1041, Ap	361	3	27.3	11	2	US-08-669-721-21	Sequence 21, Appl
289	3	27.3	10	3	US-08-159-339A-1095	Sequence 1095, Ap	362	3	27.3	11	2	US-08-856-663-8	Sequence 8, Appl
290	3	27.3	10	3	US-08-545-8630-78	Sequence 78, Appl	363	3	27.3	11	2	US-08-737-085A-12	Sequence 12, Appl
291	3	27.3	10	3	US-09-172-7548-10	Sequence 10, Appl	364	3	27.3	11	2	US-08-466-975A-3	Sequence 3, Appl
292	3	27.3	10	3	US-08-952-015-4	Sequence 4, Appl	365	3	27.3	11	2	US-08-391-671A-3	Sequence 3, Appl
293	3	27.3	10	3	US-09-133-663-19	Sequence 19, Appl	366	3	27.3	11	2	US-08-934-222-114	Sequence 114, App
294	3	27.3	10	3	US-08-846-076A-194	Sequence 194, App	367	3	27.3	11	2	US-08-933-402-114	Sequence 114, App
295	3	27.3	10	3	US-08-134-365-14	Sequence 14, Appl	368	3	27.3	11	2	US-09-207-621-114	Sequence 114, App
296	3	27.3	10	3	US-08-134-365-24	Sequence 24, Appl	369	3	27.3	11	2	US-08-350-260A-525	Sequence 525, App
297	3	27.3	10	3	US-08-134-365-24	Sequence 24, Appl	370	3	27.3	11	2	US-08-564-063-26	Sequence 26, Appl
298	3	27.3	10	3	US-09-134-365-24	Sequence 24, Appl	371	3	27.3	11	2	US-08-532-818-114	Sequence 114, App
299	3	27.3	10	3	US-09-134-365-24	Sequence 24, Appl	372	3	27.3	11	2	US-08-182-067-4	Sequence 4, Appl
300	3	27.3	10	3	US-09-134-365-24	Sequence 24, Appl	373	3	27.3	11	2	US-08-465-313-4	Sequence 4, Appl
301	3	27.3	10	3	US-09-134-365-24	Sequence 24, Appl	374	3	27.3	11	2	US-08-467-902A-3	Sequence 3, Appl
302	3	27.3	10	3	US-09-134-365-24	Sequence 24, Appl	375	3	27.3	11	3	US-08-974-899-13	Sequence 13, Appl
303	3	27.3	10	3	US-09-134-365-24	Sequence 24, Appl	376	3	27.3	11	3	US-09-246-258-12	Sequence 12, Appl
304	3	27.3	10	3	US-09-134-365-24	Sequence 24, Appl	377	3	27.3	11	3	US-09-231-797-114	Sequence 114, App
305	3	27.3	10	3	US-09-134-365-24	Sequence 24, Appl	378	3	27.3	11	3	US-08-934-224-114	Sequence 114, App
306	3	27.3	10	3	US-09-134-365-24	Sequence 24, Appl	379	3	27.3	11	3	US-08-933-843-114	Sequence 114, App
307	3	27.3	10	3	US-09-217-852-218	Sequence 218, App	380	3	27.3	11	3	US-08-446-668-1	Sequence 1, Appl
308	3	27.3	10	3	US-09-056-105-45	Sequence 45, Appl	381	3	27.3	11	3	US-08-934-223-114	Sequence 114, App
309	3	27.3	10	3	US-08-682-767-24	Sequence 24, Appl	382	3	27.3	11	3	US-09-189-627A-22	Sequence 22, Appl
310	3	27.3	10	4	US-09-230-548-7	Sequence 7, Appl	383	3	27.3	11	3	US-08-392-542-4	Sequence 4, Appl
311	3	27.3	10	4	US-09-230-548-7	Sequence 7, Appl	384	3	27.3	11	3	US-08-602-999A-285	Sequence 285, App
312	3	27.3	10	4	US-09-057-652-5	Sequence 5, Appl	385	3	27.3	11	3	US-08-652-877-64	Sequence 64, Appl
313	3	27.3	10	4	US-09-516-914-41	Sequence 41, Appl	386	3	27.3	11	3	US-09-189-344-21	Sequence 21, Appl
314	3	27.3	10	4	US-09-516-914-42	Sequence 42, Appl	387	3	27.3	11	3	US-08-647-405B-6	Sequence 6, Appl
315	3	27.3	10	4	US-09-044-718-54	Sequence 54, Appl	388	3	27.3	11	3	US-09-177-249-39	Sequence 39, Appl
316	3	27.3	10	4	US-09-413-485-1	Sequence 1, Appl	389	3	27.3	11	3	US-08-476-515A-64	Sequence 64, Appl
317	3	27.3	10	4	US-09-67-940A-4	Sequence 4, Appl	390	3	27.3	11	3	US-08-894-327-4	Sequence 4, Appl
318	3	27.3	10	4	US-09-206-342-22	Sequence 22, Appl	391	3	27.3	11	3	US-09-532-106-12	Sequence 12, Appl
319	3	27.3	10	4	US-09-914-259-74	Sequence 79, Appl	392	3	27.3	11	3	US-09-410-025-7	Sequence 7, Appl

393	3	27.3	11	3	US-09-413-492-114	Sequence 114, App	466	3	27.3	13	1	US-08-313-681A-23	Sequence 23, Appl
394	3	27.3	11	3	US-09-275-265-1	Sequence 3, Appl1	467	3	27.3	13	1	US-08-520-599-4	Sequence 4, Appl1
395	3	27.3	11	4	US-09-025-595-7	Sequence 7, Appl1	468	3	27.3	13	1	US-08-469-582-15	Sequence 15, Appl
396	3	27.3	11	4	US-09-710-861-22	Sequence 22, App	469	3	27.3	13	1	US-08-346-455B-46	Sequence 46, Appl
397	3	27.3	11	4	US-09-685-027-4	Sequence 4, Appl1	470	3	27.3	13	1	US-08-787-547-42	Sequence 42, Appl
398	3	27.3	11	4	US-09-149-476-69E	Sequence 69E, App	471	3	27.3	13	2	US-08-482-143-143	Sequence 143, App
399	3	27.3	11	4	US-09-500-124-285	Sequence 285, App	472	3	27.3	13	2	US-08-480-190-52	Sequence 52, Appl
400	3	27.3	11	4	US-09-347-926-7	Sequence 7, Appl1	473	3	27.3	13	2	US-08-480-190-52	Sequence 230, App
401	3	27.3	11	4	US-09-129-112-17	Sequence 17, Appl	474	3	27.3	13	2	US-08-467-603-97	Sequence 97, Appl
402	3	27.3	11	4	US-09-834-562-12	Sequence 12, App	475	3	27.3	13	2	US-08-677-298-15	Sequence 15, Appl
403	3	27.3	11	4	US-09-849-743-16	Sequence 16, App	476	3	27.3	13	2	US-08-488-379-52	Sequence 52, Appl
404	3	27.3	11	4	US-09-839-743-17	Sequence 17, App	477	3	27.3	13	2	US-08-488-379-52	Sequence 230, App
405	3	27.3	11	4	US-09-839-743-18	Sequence 18, App	478	3	27.3	13	2	US-08-146-028-39	Sequence 39, Appl
406	3	27.3	11	4	US-09-839-743-19	Sequence 19, App	479	3	27.3	13	2	US-08-466-793-97	Sequence 97, Appl
407	3	27.3	11	4	US-08-671-548-74	Sequence 74, App	480	3	27.3	13	2	US-08-430-521-9	Sequence 9, Appl1
408	3	27.3	11	4	US-09-104-337A-525	Sequence 525, App	481	3	27.3	13	2	US-08-491-861A-97	Sequence 97, Appl
409	3	27.3	11	4	US-09-266-764-17	Sequence 17, App	482	3	27.3	13	2	US-08-480-445A-9	Sequence 9, Appl1
410	3	27.3	11	4	US-09-380-895-7	Sequence 7, Appl1	483	3	27.3	13	2	US-08-478-572-143	Sequence 143, App
411	3	27.3	11	4	US-09-380-895-8	Sequence 8, Appl1	484	3	27.3	13	2	US-08-480-446-9	Sequence 9, Appl1
412	3	27.3	11	4	US-09-380-895-9	Sequence 9, Appl1	485	3	27.3	13	2	US-08-752-852A-175	Sequence 175, App
413	3	27.3	11	4	US-09-941-611-1	Sequence 1, Appl1	486	3	27.3	13	3	US-09-015-003-8	Sequence 8, Appl1
414	3	27.3	11	5	PCT-US86-08473-17	Sequence 17, App	487	3	27.3	13	3	US-09-041-889-37	Sequence 37, Appl
415	3	27.3	12	1	US-07-778-239B-9	Sequence 9, Appl1	488	3	27.3	13	3	US-08-977-221-46	Sequence 23, Appl
416	3	27.3	12	1	US-07-742-114A-3	Sequence 3, Appl1	489	3	27.3	13	3	US-09-322-911-23	Sequence 23, Appl
417	3	27.3	12	1	US-07-963-421-9	Sequence 9, Appl1	490	3	27.3	13	3	US-09-188-579-11	Sequence 11, Appl
418	3	27.3	12	1	US-07-995-657-7	Sequence 7, Appl1	491	3	27.3	13	3	US-08-723-425A-39	Sequence 39, Appl
419	3	27.3	12	1	US-08-290-641-9	Sequence 9, App	492	3	27.3	13	3	US-08-392-542-5	Sequence 5, Appl1
420	3	27.3	12	1	US-08-260-582-56	Sequence 56, App	493	3	27.3	13	3	US-08-392-542-7	Sequence 7, Appl1
421	3	27.3	12	1	US-08-423-399B-14	Sequence 13, App	494	3	27.3	13	3	US-08-915-314-26	Sequence 26, Appl
422	3	27.3	12	1	US-08-423-399B-24	Sequence 24, App	495	3	27.3	13	3	US-08-836-075A-171	Sequence 171, App
423	3	27.3	12	1	US-08-548-340-9	Sequence 9, Appl1	496	3	27.3	13	3	US-09-112-206-39	Sequence 39, Appl
424	3	27.3	12	1	US-08-548-340-135	Sequence 135, App	497	3	27.3	13	3	US-09-248-588-22	Sequence 22, Appl
425	3	27.3	12	1	US-08-474-587-7	Sequence 7, Appl1	498	3	27.3	13	3	US-09-315-444-11	Sequence 11, Appl
426	3	27.3	12	1	US-08-170-114A-3	Sequence 3, Appl1	499	3	27.3	13	3	US-08-894-327-5	Sequence 5, Appl1
427	3	27.3	12	2	US-08-411-492-148	Sequence 148, App	500	3	27.3	13	5	PCT-US95-04121-50	Sequence 50, Appl
428	3	27.3	12	2	US-08-482-651-52	Sequence 52, App							
429	3	27.3	12	2	US-08-908-525-2	Sequence 2, Appl1							
430	3	27.3	12	2	US-08-726-301A-136	Sequence 136, App							
431	3	27.3	12	2	US-08-850-150-17	Sequence 17, App							
432	3	27.3	12	2	US-08-846-234-37	Sequence 37, App							
433	3	27.3	12	2	US-08-752-852A-216	Sequence 218, App							
434	3	27.3	12	3	US-09-338-134-17	Sequence 17, App							
435	3	27.3	12	3	US-08-089-397A-8	Sequence 8, Appl1							
436	3	27.3	12	3	US-09-150-409A-13	Sequence 13, App							
437	3	27.3	12	3	US-08-915-314-70	Sequence 70, App							
438	3	27.3	12	3	US-08-610-052-55	Sequence 55, App							
439	3	27.3	12	3	US-08-477-928A-2	Sequence 23, App							
440	3	27.3	12	3	US-08-446-994-16	Sequence 16, App							
441	3	27.3	12	3	US-08-495-174-5	Sequence 57, App							
442	3	27.3	12	3	US-09-433-897-54	Sequence 54, App							
443	3	27.3	12	4	US-09-334-000-1	Sequence 1, Appl1							
444	3	27.3	12	4	US-09-471-134-1	Sequence 13, App							
445	3	27.3	12	4	US-09-317-513-19	Sequence 55, App							
446	3	27.3	12	4	US-09-513-786A-102	Sequence 102, App							
447	3	27.3	12	4	US-09-436-073A-16	Sequence 10, App							
448	3	27.3	12	4	US-09-500-253B-25	Sequence 25, App							
449	3	27.3	12	4	US-09-016-619-74	Sequence 74, App							
450	3	27.3	12	4	US-09-226-256-45	Sequence 645, App							
451	3	27.3	12	4	US-09-667-486-70	Sequence 70, App							
452	3	27.3	12	4	US-08-728-742A-43	Sequence 41, App							
453	3	27.3	12	4	US-08-728-742A-68	Sequence 68, App							
454	3	27.3	12	5	PCT-US94-05403-14	Sequence 14, App							
455	3	27.3	12	5	PCT-US95-03471-56	Sequence 56, App							
456	3	27.3	12	5	PCT-US96-09809-9	Sequence 9, Appl1							
457	3	27.3	12	5	PCT-US96-09809-135	Sequence 135, App							
458	3	27.3	12	6	PCT-US96-09809-135	Patent No. 5175099							
459	3	27.3	13	1	US-07-883-949B-1	Sequence 1, Appl1							
460	3	27.3	13	1	US-07-883-949B-4	Sequence 4, Appl1							
461	3	27.3	13	1	US-08-233-203A-4	Sequence 4, Appl1							
462	3	27.3	13	1	US-07-977-234C-1	Sequence 3, Appl1							
463	3	27.3	13	1	US-07-977-234C-4	Sequence 4, Appl1							
464	3	27.3	13	1	US-07-632-027-5	Sequence 5, Appl1							
465	3	27.3	13	1	US-08-316-733-10	Sequence 30, App							

ALIGNMENTS

RESULT 1

US-08-266-514-12
Sequence 12, Application: US/08266514
Patent No. 5594105
GENERAL INFORMATION:
APPLICANT: COMOGGIO, PAOLO
APPLICANT: PONZETTO, CAROLA
TITLE OF INVENTION: PEPTIDE INHIBITORS OF MITOGENESIS AND
TITLE OF INVENTION: MOIENOGENESIS
NUMBER OF SEQUENCE: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: GBLUN, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.O.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,514
FILING DATE: 27-JUN-1994
CLASSIFICATION: 510
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9313528
FILING DATE: 30-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9407673.4
FILING DATE: 18-APR-1994

ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5594105man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 769-423-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UK
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note- "The Tyr residue at position 1 may be phosphorylated."
US-08 266-514-12

Query Match: 36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : ASKK 4
Db : 3 ASKK 6

RESULT 2
US-08-654-604-12
Sequence 12, Application US/08654604
Patent No. 5912183
GENERAL INFORMATION:
APPLICANT: COMOGLIO, PAOLO
APPLICANT: PONZETTO, CAROLA
TITLE OF INVENTION: PEPTIDE INHIBITORS OF MITOGENESIS AND
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/654,604
FILING DATE: 29-MAY-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/266,514
FILING DATE: 27-JUN-1994
APPLICATION NUMBER: GB 931352A
FILING DATE: 30-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9407673.4
FILING DATE: 18-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5912183man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 769-423-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note- "The Tyr residue at position 1 may be phosphorylated."
US-08-654-604-12

Query Match: 36.4%; Score 4; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : ASKK 4
Db : 3 ASKK 6

RESULT 3
PCT-US93-12679-25
Sequence 25, Application PC/US9312679
GENERAL INFORMATION:
APPLICANT: Rath, Matthias
TITLE OF INVENTION: SYNTHETIC OLIGOPEPTIDES ANALOGOUS TO
TITLE OF INVENTION: PROTEIN SIGNAL SEQUENCES -METHODS OF IDENTIFICATION AND
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHELDON & MAK
STREET: 401 Florence Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12679
FILING DATE: 30-DEC-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Cranfill, Raymond B
REGISTRATION NUMBER: 32,845
REFERENCE/DOCKET NUMBER: RATH-10016PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5333
TELEFAX: 415-322-5499
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US93-12679-25

Query Match: 36.4%; Score 4; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY : 3 KKK 6
Db : 2 KKK 5

RESULT 4
US-08-156-552A-14

```

: Sequence 14, Application US/08156552A
: Patent No. 5726155
: GENERAL INFORMATION:
: APPLICANT: Bokoch, Gary M
: TITLE OF INVENTION: REGULATION OF OXIDATIVE POST-TRANSLATIONAL
: MODIFICATION OF LIPID-DERIVED PEPTIDES AND ANALOGS
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: The Scripps Research Institute, Office of
: ADDRESSEE: Patent Counsel
: STREET: 10666 No. 5726155th Torrey Pines Road, Los
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/156,552A
: FILING DATE: 15-NOV-1993
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/102,944
: FILING DATE: 02-AUG-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Logan, April C.
: REGISTRATION NUMBER: 33,950
: REFERENCE/DOCKET NUMBER: SCRF 281.1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-554-2937
: TELEFAX: 619-554-6312
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-156-552A-14

Query Match: 36.4%; Score 4; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 3 KKPK 6

RESULT 5
US-09-335-249A-14
: Sequence 14, Application US/09035249A
: Patent No. 6184203
: GENERAL INFORMATION:
: APPLICANT: Bokoch, Gary M
: TITLE OF INVENTION: REGULATION OF OXIDATIVE POST-TRANSLATIONAL
: MODIFICATION OF LIPID-DERIVED PEPTIDES AND ANALOGS
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: The Scripps Research Institute, Office of
: ADDRESSEE: Patent Counsel
: STREET: 10666 No. 6184203th Torrey Pines Road, Los
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible

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: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/035,249A
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/156,552
: FILING DATE: 15-NOV-1993
: APPLICATION NUMBER: US 08/102,944
: FILING DATE: 02-AUG-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Logan, April C.
: REGISTRATION NUMBER: 33,950
: REFERENCE/DOCKET NUMBER: SCRF 281.1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-554-2937
: TELEFAX: 619-554-6312
: INFORMATION FOR SEQ ID NO: 14:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-09-035-249A-14

Query Match: 36.4%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPK 6
DB 3 KKPK 6

RESULT 6
US-09-518-046-86
: Sequence 86, Application US/09518046
: Patent No. 6294663
: GENERAL INFORMATION:
: APPLICANT: O'Brien, Timothy J.
: TITLE OF INVENTION: Transmembrane Sorine Protease Overexpressed
: TITLE OF INVENTION: An Ovarian Carcinoma and Uses Thereof
: FILE REFERENCE: D619201P
: CURRENT APPLICATION NUMBER: US/09/518,046
: CURRENT FILING DATE: 2003-04-02
: EARLIER APPLICATION NUMBER: 09/251,416
: EARLIER FILING DATE: 1999-03-03
: NUMBER OF SEQ ID NOS: 153
: SEQ ID NO 86
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: LOCATION: 296...304
: OTHER INFORMATION: TAGS: 12 peptide
: US-09-518-046-86

Query Match: 36.4%; Score 4; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKPK 7
DB 3 KKPK 6

RESULT 7
US-09-518-046-109
: Sequence 109, Application US/09518046
: Patent No. 6294663
: GENERAL INFORMATION:

```


1 APPLICANT: O'Brien, Timothy J.
 2 APPLICANT: Underwood, Lowell J.
 3 TITLE OF INVENTION: Transmembrane Sorting Protease Overexpressed
 4 TITLE OF INVENTION: In Ovarian Carcinoma and Uses Thereof
 5 FILE REFERENCE: D6192CIP
 6 CURRENT APPLICATION NUMBER: US/09/518,045
 7 CURRENT FILING DATE: 2000-03-02
 8 EARLIER APPLICATION NUMBER: 09/261,416
 9 EARLIER FILING DATE: 1999-03-03
 10 NUMBER OF SEQ ID NOS: 153
 11 SEQ ID NO 109
 12 LENGTH: 9
 13 TYPE: EST
 14 ORGANISM: Homo sapiens
 15 FEATURE:
 16 LOCATION: 298...306
 17 OTHER INFORMATION: TAGG-12 peptide
 18 US 09-518 045-109

Query Match: 36.4%, Score 4, DB 1, Length 9;
 Best Local Similarity 100.0%, Pred No. 2 Seqs 5;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KPRR 7
 ID 1 1 1
 1 KPRR 4

RESULT 8
 US-09-518-045-112
 1 Sequence 112, Application US/095,8945
 2 Patent No. 6294663
 3 GENERAL INFORMATION:
 4 APPLICANT: O'Brien, Timothy J.
 5 APPLICANT: Underwood, Lowell J.
 6 TITLE OF INVENTION: Transmembrane Sorting Protease Overexpressed
 7 TITLE OF INVENTION: In Ovarian Carcinoma and Uses Thereof
 8 FILE REFERENCE: D6192CIP
 9 CURRENT APPLICATION NUMBER: US/09/518,045
 10 CURRENT FILING DATE: 2000-03-02
 11 EARLIER APPLICATION NUMBER: 09/261,416
 12 EARLIER FILING DATE: 1999-03-03
 13 NUMBER OF SEQ ID NOS: 153
 14 SEQ ID NO 112
 15 LENGTH: 9
 16 TYPE: EST
 17 ORGANISM: Homo sapiens
 18 FEATURE:
 19 LOCATION: 294...302
 20 OTHER INFORMATION: TAGG-12 peptide
 21 US 09-518-045-112

Query Match: 36.4%, Score 4, DB 1, Length 9;
 Best Local Similarity 100.0%, Pred No. 2 Seqs 5;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KPRR 7
 ID 1 1 1
 5 KPRR 8

RESULT 9
 US 09-401 512-57
 1 Sequence 57, Application US/08401512
 2 Patent No. 559673
 3 GENERAL INFORMATION:
 4 APPLICANT: Keating, Mark T.
 5 APPLICANT: Curran, Mark E.
 6 APPLICANT: Wang, Qing
 7 TITLE OF INVENTION: Long QF Synchro-Genes
 8 NUMBER OF SEQUENCES: 81
 9 CORRESPONDENCE ADDRESS:
 10 ADDRESSEE: Venable, Baetjer, Howard & Givens, LLP

1 STREET: 1201 New York Avenue, Suite 1000
 2 CITY: Washington
 3 STATE: DC
 4 COUNTRY: USA
 5 ZIP: 20005-3917
 6 COMPUTER RELEASABLE FORM:
 7 MEDIUM TYPE: Floppy disk
 8 COMPUTER: IBM PC compatible
 9 OPERATING SYSTEM: PC-DOS/MS-DOS
 10 SOFTWARE: Patent In Release #1.0, Version #1.25
 11 CURRENT APPLICATION DATA:
 12 APPLICATION NUMBER: US/08/401,512
 13 FILING DATE: 09-MAY-1994
 14 CLASSIFICATION: 435
 15 ATTORNEY/AGENT INFORMATION:
 16 NAME: Sako, Stephen A.
 17 REGISTRATION NUMBER: 38,509
 18 REFERENCE/DOCKET NUMBER: 19780-113879
 19 TELECOMMUNICATION INFORMATION:
 20 TELEPHONE: 202-962-4848
 21 TELEFAX: 202-962-9100
 22 INFORMATION FOR SEQ ID NO: 57:
 23 SEQUENCE CHARACTERISTICS:
 24 LENGTH: 10 amino acids
 25 TYPE: amino acid
 26 TOPOLOGY: linear
 27 MOLECULE TYPE: peptide
 28 HYPOTHETICAL: NO
 29 US-08-401-512-57

Query Match: 36.4%, Score 4, DB 1, Length 10;
 Best Local Similarity 100.0%, Pred No. 1 Seq+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 SKKP 5
 ID 1 1 1
 2 SKKP 5

RESULT 10
 US 08-242-678D 6
 1 Sequence 6, Application US/08242678D
 2 Patent No. 5760000
 3 GENERAL INFORMATION:
 4 APPLICANT: HABIBI, Rafid R.
 5 TITLE OF INVENTION: INHIBITION OF LIVER CANCER BY THE USE OF
 6 TITLE OF INVENTION: GNRH AND GNRH ANALOGS
 7 NUMBER OF SEQUENCES: 12
 8 CORRESPONDENCE ADDRESS:
 9 ADDRESSEE: BURNS, DVANE, SWECKER & MATHIS
 10 STREET: P.O. Box 1404
 11 CITY: Alexandria
 12 STATE: Virginia
 13 COUNTRY: United States
 14 ZIP: 22303 1404
 15 COMPUTER RELEASABLE FORM:
 16 MEDIUM TYPE: Floppy disk
 17 COMPUTER: IBM PC compatible
 18 OPERATING SYSTEM: PC-DOS/MS-DOS
 19 SOFTWARE: Patent In Release #1.0, Version #1.30
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/08/242,678D
 22 FILING DATE: 13-MAY-1994
 23 CLASSIFICATION: 514
 24 ATTORNEY/AGENT INFORMATION:
 25 NAME: Dadio, Susan M.
 26 REGISTRATION NUMBER: 40,373
 27 REFERENCE/DOCKET NUMBER: 028722-103
 28 TELECOMMUNICATION INFORMATION:
 29 TELEPHONE: (703) 836-6620
 30 TELEFAX: (703) 836-2021
 31 INFORMATION FOR SEQ ID NO: 6:
 32 SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label AA1-4
OTHER INFORMATION: /note "AA1 is A-ETYL, BETA 2 NACHTHEYL D ALA, AA2 is
OTHER INFORMATION: D-P CHLORO ETHL, AA3 is BETA 3-PYR-ETHL-D-ALA"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /label AA5 6
OTHER INFORMATION: /note "AA5 5 are each N EPSTEIN-NICOTINYL-LYS, AA6 is also
OTHER INFORMATION: D-LYS"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 8
OTHER INFORMATION: /label AA8
OTHER INFORMATION: /note "AA8 is N EPSTEIN IS PROPYL-LYS"
FEATURE:
NAME/KEY: Modified site
LOCATION: 10
OTHER INFORMATION: /label AA10
OTHER INFORMATION: /note "AA10 is D-ALA"
US-08-406-330-19
Query Match 36.4% Score 4 DB 1 Length 10
Best Local Similarity 100.0% Pred. No. 1.5e+02
Matches 4: Conservative 0 Mismatches 0 Gaps 0
QY 1 ASKX 4
DB 3 ASKX 6
RESULT 11
US-08-406-330-19
: Sequence 19, Application US/08406330
: Patent No. 5817748
: GENERAL INFORMATION:
: APPLICANT: Miller, Jonathan L.
: TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES
: TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN IIb/IIIa
: NUMBER OF SEQUENCES: 81
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nixon, Harquadio, David A.
: STREET: Clinton Square 100, Box 1
: CITY: Rochester
: STATE: New York
: COUNTRY: USA
: ZIP: 14604
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/406-330
: FILING DATE:
: CLASSIFICATION: 530
: ATTORNEY/AGENT INFORMATION:
: NAME: Timlan, Susan J.
: REGISTRATION NUMBER: 34,103
: REFERENCE/DOCKET NUMBER: 20884/100
: TELEPHONE: (716) 263-1536
: TELEFAX: (716) 263-1600
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-406-330-19

LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-406-330-19
Query Match 36.4% Score 4 DB 2 Length 10
Best Local Similarity 100.0% Pred. No. 1.5e+02
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0
QY 2 SKKP 5
DB 2 SKKP 5
RESULT 12
US-07-885-089B-27
: Sequence 27, Application US/07885089B
: Patent No. 5830955
: GENERAL INFORMATION:
: APPLICANT: Shoyab, Mohammed
: APPLICANT: McDonald, Vicki L.
: APPLICANT: Bradley, James G.
: APPLICANT: Plowman, Gregory D.
: TITLE OF INVENTION: AMPHIREGULINS: A FAMILY OF
: TITLE OF INVENTION: HEPARIN-BINDING EPITHELIAL CELL GROWTH FACTORS
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds LLP
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/885,089B
: FILING DATE: 18-MAY-1992
: CLASSIFICATION: 540
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A.
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 5624-174
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 790-9090
: TELEFAX: 212 790-9041
: TELEX: 6614, PENNIE
: INFORMATION FOR SEQ ID NO: 27:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-885-089B-27
Query Match 36.4% Score 4 DB 2 Length 10
Best Local Similarity 100.0% Pred. No. 1.5e+02
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0
QY 4 KPKR 7
DB 3 KPKR 4
RESULT 13
US-08-556-597-19
: Sequence 19, Application US/08556597

Patent No. 5877155
 GENERAL INFORMATION:
 APPLICANT: Miller, Jonathan L.
 APPLICANT: Ly-e, Vicki A.
 TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
 NUMBER OF SEQUENCES: 173
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon, Hartgrave, Levans & Boyle LLP
 STREET: Clinton Square, P.O. Box 1051
 CITY: Rochester
 STATE: New York
 COUNTRY: USA
 ZIP: 14603
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.10
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/556,597
 FILING DATE: 17-MAR-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/406,310
 FILING DATE: 17-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Timian, Susan J.
 REGISTRATION NUMBER: 34,103
 REFERENCE/DOCKET NUMBER: 20884/103
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (716) 263-1635
 TELEFAX: (716) 263-1600
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US 08:556-597-19

Query Match 36.4%; Score 4; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 QY 2 SKKP 5
 Db 1 1
 2 SKKP 5

RESULT 14
 US-08-416-035-8
 Sequence 8, Application US/08416035
 Patent No. 5739278
 GENERAL INFORMATION:
 APPLICANT: Baum, Genter
 APPLICANT: Cool, Deborah E.
 TITLE OF INVENTION: Methods and Compositions for Proteins
 TITLE OF INVENTION: Tyrosine Phosphatases
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed and Berry
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/416,035
 FILING DATE: 30-MAR-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/059,949
 FILING DATE: 10-MAY-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Sharky, Richard G.
 REGISTRATION NUMBER: 32,629
 REFERENCE/DOCKET NUMBER: 940010.531
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 622-6031
 TELEX: 3721836
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-416-035-8

Query Match 36.4%; Score 4; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;
 QY 1 ASKK 4
 Db 7 ASKK 10
 1111

RESULT 15
 PCT-US93-05325-7
 Sequence 7, Application PCT/US9305325
 GENERAL INFORMATION:
 APPLICANT: SKI, INTERNATIONAL
 TITLE OF INVENTION: PEPTIDES CORRESPONDING TO ACTIVE DOMAINS
 TITLE OF INVENTION: OF PLATELET-DERIVED GROWTH FACTOR (PDGF)
 NUMBER OF SEQUENCES: 39
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SKI, INTERNATIONAL ATTN: INTELLECTUAL PROPERTY
 ADDRESSEE: COUNSEL
 STREET: 333 Ravenswood Avenue
 CITY: Menlo Park
 STATE: California
 COUNTRY: USA
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/05325
 FILING DATE: 19930603
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/894,497
 FILING DATE: 05-JUN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: CLARK, JANET P.
 REGISTRATION NUMBER: 34,799
 REFERENCE/DOCKET NUMBER: PCT-2679
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 859-2446
 TELEFAX: (415) 859-3880
 TELEX: 334486
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: AMINO ACID

```
1  TOPOLOGY: linear
2  MOLECULE TYPE: peptide
3  PRT US99-05425-7
4
5  Query Match 36.4% Score 4: DB 5: Length 12:
6  Best Local Similarity 100.0% Pred. No. 2e-02:
7  Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
8
9  QY 3 KKKK 5
10 Db 9 KKKK 12
11
12 RESULT 16
13 US-08-314-172A-5
14 : Sequence 5, Application US/08314172A
15 : Patent No. 5650154
16 : GENERAL INFORMATION:
17 : APPLICANT: Meeseusen, Etica
18 : APPLICANT: Bowles, Vernon
19 : APPLICANT: Brandon, Malcolm
20 : APPLICANT: Walker, John
21 : TITLE OF INVENTION: VACCINE COMPOSITION
22 : NUMBER OF SEQUENCES: 13
23 : CORRESPONDENCE ADDRESS:
24 : ADDRESSEE: Merchand & Gould
25 : STREET: 4130 No. 5650154west Center, 90 S. 7th Street
26 : CITY: Minneapolis
27 : STATE: Minnesota
28 : COUNTRY: USA
29 : ZIP: 55402
30 : COMPUTER READABLE FORM:
31 : MEDIUM TYPE: Diskette
32 : COMPUTER: IBM Compatible
33 : OPERATING SYSTEM: DOS
34 : SOFTWARE: FastSeq Version 1.5
35 : CURRENT APPLICATION DATA:
36 : APPLICATION NUMBER: US/08/314.172A
37 : FILING DATE: 28-SEP-1994
38 : CLASSIFICATION: 435
39 : PRIOR APPLICATION DATA:
40 : APPLICATION NUMBER: 08/072.652
41 : FILING DATE: 01-JUN-1993
42 : ATTORNEY/AGENT INFORMATION:
43 : NAME: Mark T. Skoog
44 : REGISTRATION NUMBER: 40,178
45 : REFERENCE/DOCKET NUMBER: 4159-580501
46 : TELECOMMUNICATION INFORMATION:
47 : TELEPHONE:
48 : TELEFAX:
49 :
50 : INFORMATION FOR SEQ ID NO: 6:
51 : SEQUENCE CHARACTERISTICS:
52 : LENGTH: 15 amino acids
53 : TYPE: amino acid
54 : STRANDEDNESS: single
55 : TOPOLOGY: linear
56 : MOLECULE TYPE: peptide
57 : HYPOTHETICAL: NO
58 : ANTI-SENSE: NO
59 : FRAGMENT TYPE: internal
60 : ORIGINAL SOURCE:
61 :
62 : US-08-314-172A-5
63
64  Query Match 36.4% Score 4: DB 1: Length 15:
65  Best Local Similarity 100.0% Pred. No. 2e-02:
66  Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
67
68  QY 2 SKKK 5
69 Db 9 SKKK 12
70
71 RESULT 17
72 US-08-637-418-9
73 : Sequence 9, Application US/08637418
74 : Patent No. 5891848
75 : GENERAL INFORMATION:
76 : APPLICANT: OOMURA, Yutaka
77 : TITLE OF INVENTION: PEPTIDE FRAGMENTS
78 : NUMBER OF SEQUENCES: 20
79 : CORRESPONDENCE ADDRESS:
80 : ADDRESSEE: Fisher, Christen & Sabol
81 : STREET: 1019 19th St., N.W., Suite 300
82 : CITY: Washington
83 : STATE: D.C.
84 : COUNTRY: U.S.A.
85 : ZIP: 20036
86 : COMPUTER READABLE FORM:
87 :
88 : MEDIUM TYPE: Floppy disk
89 : COMPUTER: IBM PC compatible
90 : OPERATING SYSTEM: PC-DOS/MS-DOS
91 : SOFTWARE: PatentIn Release #1.0, Version #1.30
92 : CURRENT APPLICATION DATA:
93 : APPLICATION NUMBER: US/08/637.418
94 : FILING DATE: 25-APR-1996
95 : CLASSIFICATION: 514
96 : PRIOR APPLICATION DATA:
97 : APPLICATION NUMBER: JP 125,947/1995
98 : FILING DATE: 25-APR-1995
99 : ATTORNEY/AGENT INFORMATION:
100 : NAME: Hollander, Barry I.
101 : REGISTRATION NUMBER: 28,566
102 : REFERENCE/DOCKET NUMBER: NZK-116
103 : TELECOMMUNICATION INFORMATION:
104 : TELEPHONE: (202) 659-2000
105 : TELEFAX: (202) 659-2015
106 : INFORMATION FOR SEQ ID NO: 9:
107 : SEQUENCE CHARACTERISTICS:
108 : LENGTH: 15 amino acids
109 : TYPE: amino acid
110 : STRANDEDNESS:
111 : TOPOLOGY: linear
112 : MOLECULE TYPE: peptide
113 : HYPOTHETICAL: NO
114 : ANTI-SENSE: NO
115 : FRAGMENT TYPE: N-terminal
116 : ORIGINAL SOURCE:
117 : ORGANISM: Homo sapiens
118 :
119 : US-08-637-418-9
120
121  Query Match 36.4% Score 4: DB 2: Length 15:
122  Best Local Similarity 100.0% Pred. No. 2e-02:
123  Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
124
125  QY 3 KKKK 5
126 Db 9 KKKK 12
127
128 RESULT 18
129 US-08-637-418-10
130 : Sequence 10, Application US/08637418
131 : Patent No. 5891848
132 : GENERAL INFORMATION:
133 : APPLICANT: OOMURA, Yutaka
134 : TITLE OF INVENTION: PEPTIDE FRAGMENTS
135 : NUMBER OF SEQUENCES: 20
136 : CORRESPONDENCE ADDRESS:
137 : ADDRESSEE: Fisher, Christen & Sabol
138 : STREET: 1019 19th St., N.W., Suite 300
139 : CITY: Washington
140 : STATE: D.C.
141 : COUNTRY: U.S.A.
142 : ZIP: 20036
143 : COMPUTER READABLE FORM:
144 :
```

```

: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/637,418
: FILING DATE: 25-APR-1996
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 125,947/1995
: FILING DATE: 25-APR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Hollander, Barry I.
: REGISTRATION NUMBER: 28,566
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 659-2000
: TELEFAX: (202) 659-2015
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: ORIGINAL SOURCE:
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 15
: OTHER INFORMATION: /product "Xaa is the amino form of
: (OTHER INFORMATION: Tyrosine."
: US-08-637 418-10

Query Match 36.4%; Score 4; IP 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPX 6
DB 9 KKPX 12

RESULT 19
US-08-637 418-19
: Sequence 19, Application US/09/637,418
: Patent No. 5891848
: GENERAL INFORMATION:
: APPLICANT: OOMURA, Yutaka
: TITLE OF INVENTION: PEPTIDE FRAGMENTS
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fisher, Christen & Sabol
: STREET: 1019 19th St., N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/637,418
: FILING DATE: 25-APR-1996
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 125,947/1995
: FILING DATE: 25-APR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Hollander, Barry I.
: REGISTRATION NUMBER: 28,566
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 659-2000
: TELEFAX: (202) 659-2015
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEtical: NO
: ANTI-SENSE: NO

```

```

: ATTORNEY/AGENT INFORMATION:
: NAME: Hollander, Barry I.
: REGISTRATION NUMBER: 28,566
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 659-2000
: TELEFAX: (202) 659-2015
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEtical: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: ORIGINAL SOURCE:
: ORGANISM: Bos taurus
: US-08-637-418-19

Query Match 36.4%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKPX 6
DB 9 KKPX 12

RESULT 20
US-08-637-418-20
: Sequence 20, Application US/08637418
: Patent No. 5891848
: GENERAL INFORMATION:
: APPLICANT: OOMURA, Yutaka
: TITLE OF INVENTION: PEPTIDE FRAGMENTS
: NUMBER OF SEQUENCES: 20
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fisher, Christen & Sabol
: STREET: 1019 19th St., N.W., Suite 300
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/637,418
: FILING DATE: 25-APR-1996
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 125,947/1995
: FILING DATE: 25-APR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Hollander, Barry I.
: REGISTRATION NUMBER: 28,566
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 659-2000
: TELEFAX: (202) 659-2015
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEtical: NO
: ANTI-SENSE: NO

```

```

1  FRAGMENT TYPE: N-terminal
2  ORIGINAL SOURCE: Bos taurus
3  ORGANISM: Bos taurus
4  FEATURE:
5  NAME/KEY: Modified-site
6  LOCATION: 15
7  OTHER INFORMATION: /product: "Xaa is the amino term of
8  OTHER INFORMATION: Tyrosine."
9  US 08-637-416 20
10
11  Query Match 36.4% Score 4; DB 3; Length 15;
12  Best Local Similarity 100.0%; Pred. No. 2e-02;
13  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
14
15  QY 4 KKK 6
16  111
17  9 KKK 12
18
19  RESULT 21
20  US 09-041-889-17
21  Sequence 17, Application US/09041889
22  Patent No. 603864
23  GENERAL INFORMATION:
24  APPLICANT: Braun, Jonathan
25  TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
26  TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
27  TITLE OF INVENTION: Microbial UC PANCA antigens
28  NUMBER OF SEQUENCES: 41
29  CORRESPONDENCE ADDRESS:
30  ADDRESSEE: Campbell & Flores LLP
31  STREET: 4870 La Jolla Village Drive, Suite 700
32  CITY: San Diego
33  STATE: California
34  COUNTRY: USA
35  ZIP: 92122
36  COMPUTER READABLE FORM:
37  MEDIUM TYPE: Floppy disk
38  COMPUTER: IBM PC compatible
39  OPERATING SYSTEM: PC-DOS/MS DOS
40  SOFTWARE: Patent In Release #1.0, Version #1.25
41  CURRENT APPLICATION DATA:
42  APPLICATION NUMBER: US/09/041,889
43  FILING DATE:
44  CLASSIFICATION:
45  PRIOR APPLICATION DATA:
46  APPLICATION NUMBER: US 08/847,058
47  FILING DATE: 11 APR-1997
48  ATTORNEY/AGENT INFORMATION:
49  NAME: Campbell, Cathryn A.
50  REGISTRATION NUMBER: 41,815
51  REFERENCE/DOCKET NUMBER: P-PM 3006
52  TELECOMMUNICATION INFORMATION:
53  TELEPHONE: (619) 535-9001
54  TELEFAX: (619) 535-8949
55  INFORMATION FOR SEQ ID NO: 17:
56  SEQUENCE CHARACTERISTICS:
57  LENGTH: 15 amino acids
58  TYPE: amino acid
59  TOPOLOGY: linear
60  US 09-041-889-18
61
62  Query Match 36.4% Score 4; DB 3; Length 15;
63  Best Local Similarity 100.0%; Pred. No. 2e-02;
64  Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
65
66  QY 3 KKK 6
67  111
68  2 KKK 6
69
70  RESULT 22
71  US 08-637-058-17
72  Sequence 17, Application US/08817058
73  Patent No. 6074815
74  GENERAL INFORMATION:
75  APPLICANT: Braun, Jonathan
76  APPLICANT: Targan, Stephen K.
77  APPLICANT: Esena, Mark
78  TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
79  TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
80  NUMBER OF SEQUENCES: 26
81  TITLE OF INVENTION: HISTOC H
82  CORRESPONDENCE ADDRESS:
83  ADDRESSEE: Campbell & Flores LLP
84  STREET: 4870 La Jolla Village Drive, Suite 700
85  CITY: San Diego
86  STATE: California
87  COUNTRY: USA
88  ZIP: 92122
89  COMPUTER READABLE FORM:
90  MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,058
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 24-0
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-837-058 17

Query Match 36.4% Score 4: DB 3: Length 15
Best local Similarity 100.0% Pred. No. 2e+02
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 KKPK 6
DB 12 KKPK 15

US-08-837-058 18
Sequence 18, Application US/08837058
Patent No. 6074835
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Targan, Stephen R.
APPLICANT: Eggena, Mark
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes thereof, Using
TITLE OF INVENTION: Histone H1
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,058
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 24-0
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-837-058 18

Query Match 36.4% Score 4: DB 3: Length 15

Best local Similarity 100.0% Pred. No. 2e+02
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 3 KKPK 6
DB 2 KKPK 5
US-09-537-357 2
Sequence 2, Application US/09537357
Patent No. 6271018
GENERAL INFORMATION:
APPLICANT: Alao, Brian
APPLICANT: Nathalie Tillet
TITLE OF INVENTION: MUSKELON (CUCUMIS MELO) HYDROPEROXIDE
FILE REFERENCE: 06027-0002
CURRENT APPLICATION NUMBER: US/09/537,357
CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 15
TYPE: PKT
ORGANISM: Cucumis melo
US-09-537-357 2

Query Match 36.4% Score 4: DB 3: Length 15
Best local Similarity 100.0% Pred. No. 2e+02
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 6 KRNI 9
DB 10 KRNI 13

US-09-417-264-17

Sequence 17, Application US/09417264
Patent No. 6537768
GENERAL INFORMATION:
APPLICANT: Brauch, Jonathan
APPLICANT: Cohavy, Ofier
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
TITLE OF INVENTION: Microbial UC PANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/041,889
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

```

: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-09-417-264-17

Query Match: 36.4%, Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 20002;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKKK 6
ID 12 KKKK 15

RESULT 27
US-09-417-264-18
: Sequence 18, Application US/09417264
: Patent No. 6537768
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
: TITLE OF INVENTION: Microbial UC PAN-A Antigens
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores Ltd
: STREET: 4370 La Jolla Village Drive, Suite 750
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/417,264
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 09/041,889
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 41,815
: REFERENCE/DOCKET NUMBER: P 18
: INFORMATION FOR SEQ ID NO: 18:
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-09-417-264-18

Query Match: 36.4%, Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 20002;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKKK 6
ID 2 KKKK 5

RESULT 28
US-09-417-264-19
: Sequence 19, Application US/07737852

```

```

: Patent No. 5243027
: GENERAL INFORMATION:
: APPLICANT: Mimura, Tsutomu
: APPLICANT: Kohama, Yasuhiko
: APPLICANT: Nagata, Kazuhiko
: APPLICANT: Tsurutani, Ryoeichi
: TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME
: TITLE OF INVENTION: INHIBITOR
: NUMBER OF SEQUENCES: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Squirrup, Michi, Zinn, Macpeak & Seas
: STREET: 2109 Pennsylvania Avenue
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A
: ZIP: 20037-4202
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.24
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/737,852
: FILING DATE: 19910731
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 02-45975
: FILING DATE: 25-FEB-1990
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)293-7060
: TELEFAX: (202)293-7860
: TELEX: 6491103
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: AMINO ACIDS
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: ORIGINAL SOURCE:
: ORGANISM: Bacillus stearothermophilus
: STRAIN: NCA 150;
US-07-737-852-3

Query Match: 27.3%, Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASK 3
ID 4 ASK 6

RESULT 29
US-07-737-852-4
: Sequence 1, Application US/07920597
: Patent No. 5447915
: GENERAL INFORMATION:
: APPLICANT: Schreiber, Stuart
: APPLICANT: Hatakey, Steven
: TITLE OF INVENTION: terminally-blocked Antiviral Peptides
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Allaretti & Witcoff, Ltd.
: STREET: 16 South Wacker Drive, Suite 3000
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: Patent Release #1.0, Version #1.25

```



```

: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/920,597
: FILING DATE: 19920828
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO pct/us91/01142
: FILING DATE: 28-FEB-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5447915nad, Kevin E
: REGISTRATION NUMBER: 35,303
: REFERENCE/DOCKET NUMBER: 91,174-E
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-715-1000
: TELEFAX: 312-715-1234
: TELEX: 910-221-5317
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-07 920-597-1

Query Match 27.3% Score 3: DB 1: Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6
DB 1 1
2 KPK 4

RESULT 30
US-07-920-597-2
: Sequence 2, Application US/07920597
: Patent No. 5447915
: GENERAL INFORMATION:
: APPLICANT: Schreiber, Stuart
: TITLE OF INVENTION: Terminally-Blocked Antiviral Peptides
: NUMBER OF SEQUENCES: 12
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Allgretta & Wilcott, Ltd.
: STREET: 10 South Wacker Drive, Suite 3000
: CITY: Chicago
: STATE: IL
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC DOS/MS DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/920,597
: FILING DATE: 19920828
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO pct/us91/01142
: FILING DATE: 28-FEB-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: No. 5447915nad, Kevin E
: REGISTRATION NUMBER: 35,303
: REFERENCE/DOCKET NUMBER: 91,174 E
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-715-1000
: TELEFAX: 312-715-1234
: TELEX: 910-221-5317
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid

US-07-920-597-1

Query Match 27.3% Score 3: DB 1: Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6
DB 1 1
2 KPK 4

RESULT 31
US-08-432-617-2
: Sequence 2, Application US/08432617
: Patent No. 5495000
: GENERAL INFORMATION:
: APPLICANT: Krstiansky, John L.
: TITLE OF INVENTION: Anticoagulant Peptides
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marion Merrell Dow Inc.
: STREET: 2110 East Galbraith Rd.
: CITY: Cincinnati P. O. Box 156300
: STATE: Ohio
: COUNTRY: USA
: ZIP: 45215-6300
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/432,617
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/971,909
: FILING DATE: 18-DEC-1992
: APPLICATION NUMBER: US 07/557,288
: FILING DATE: 24-JUL-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/US91/04658
: FILING DATE: 28-JUN-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Boudreaux, William R
: REGISTRATION NUMBER: 35,796
: REFERENCE/DOCKET NUMBER: M01556 US-A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (513) 948-6566
: TELEFAX: (513) 948-7961
: TELEX: 214320
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-432-617-2

Query Match 27.3% Score 3: DB 1: Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
DB 1 1
1 PKR 3

RESULT 32
US-08-261-525A-3
```

Sequence 3, Application US/08261525A
Patent No. 5569598
GENERAL INFORMATION:
APPLICANT: PARK, Soon Jae
APPLICANT: LEE, Young Mee
APPLICANT: WON, Teug Yeon
APPLICANT: KWON, Soon Chang
APPLICANT: LEE, Seung Joo
APPLICANT: KIM, Jung Ho
TITLE OF INVENTION: NOVEL AMINOPEPTIDASE, PROTEASES FOR
TITLE OF INVENTION: THE PREPARATION OF AMINOPEPTIDASE AND
TITLE OF INVENTION: PROTEIN THEREFROM
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: PARK, Soon Jae
STREET: Lucky Apt. 6-101, Doryong-dong, Yuseong-gu
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 305-340
ADDRESSEE: LEE, Young Mee
STREET: Shinsung Apt. 3-306, 28 4, Nae-dong, Seo-gu
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 302-181
ADDRESSEE: WON, Teug Yeon
STREET: Gungjak Hanyang Apt. 4-1201, 85b,
STREET: Tanbang-dong, Seo-gu
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 302-223
ADDRESSEE: KWON, Soon Chang
STREET: Shinsung Apt. 3-107, 28 4, Nae-dong, Seo-gu
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 302-181
ADDRESSEE: LEE, Seung Joo
STREET: Lucky Apt. 8-107, 45b-4, Doryong-dong,
STREET: Yuseong-gu
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 305-340
ADDRESSEE: KIM, Jung Ho
STREET: Lucky Dormitory 502, 486-1, Doryong-dong,
STREET: Yuseong-gu
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 305-340
ADDRESSEE: KIM, Bum Joon
STREET: Lucky Dormitory 502, 486-1, Doryong-dong,
STREET: Yuseong-gu
CITY: Daejeon
STATE: Daejeon
COUNTRY: Republic of Korea
ZIP: 305-340
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44MB STORAGE
COMPUTER: IBM PC/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261525A
FILING DATE: 17-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 93-11107
FILING DATE: 17-JUN-1993

ATTORNEY/AGENT INFORMATION:
NAME: Shahan Islam
REGISTRATION NUMBER: 32,507
REFERENCE/DOCKET NUMBER: A-9883
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-1000
TELEFAX: (212) 953-7249
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Streptomyces thermotritificans
US-08-261-525A-3
Query Match 27.3% Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 2 SKK 4
Db 3 SKK 5
RESULT 33
US-08-240-514-39
Sequence 39, Application US/08240514
Patent No. 5670347
GENERAL INFORMATION:
APPLICANT: GOPAL, T. Venkat
TITLE OF INVENTION: PEPTIDE-MEDIATED GENE TRANSFER
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/240,514
FILING DATE: 11-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 73521/102/CLIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-240-514-39
Query Match 27.3% Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy 4 KPK 6
Db 3

1c 6 KKK 8

RESULT 14

US-08-249-387-5
Sequence 5, Application US/08249387
Patent No. 5681700
GENERAL INFORMATION:
APPLICANT: Reichlin, Morris
TITLE OF INVENTION: Assay for Pathogenicity of Anti-ENA
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,387
FILING DATE: 01-01-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 08P145
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 815-6558
TELEFAX: (404) 815-6555
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SYNTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal

US-08-249-387-5

Query Match 27.3% Score 61 DB 1: Length 9
Best Local Similarity 100.0% Pred No. 2 5e+05
Matches 3: Conservative 0: Mismatches 0: Indels 0: Caps 0:
QY 2 SKK 4
DB 2 SKK 4

US-08-249-387-5

GENERAL INFORMATION:
APPLICANT: Pabst, Ira
APPLICANT: FitzGerald, David
APPLICANT: Chaudhary, Vijay K.
TITLE OF INVENTION: Pseudomonas Exoenzyme A and A-related
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Towns
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California

RESULT 15

US-08-467-264-19
Sequence 19, Application US/08467264
Patent No. 5705156
GENERAL INFORMATION:
APPLICANT: Baum, Gunter
APPLICANT: Fogel, Deborah E.
TITLE OF INVENTION: Methods and Compositions for Protein
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6400 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,035
FILING DATE: 30-MAR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/59,949
FILING DATE: 10-MAY-1994
ATTORNEY/AGENT INFORMATION:

COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,264
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/522,182
FILING DATE: 11-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/130,122
FILING DATE: 01-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 48,498
REFERENCE/DOCKET NUMBER: 15280-125-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-467-264-19

Query Match 27.3% Score 3: DB 1: Length 8:
Best Local Similarity 100.0% Pred No. 2 5e+05:
Matches 3: Conservative 0: Mismatches 0: Indels 0: Caps 0:

QY 2 SKK 4

DB 3 SKK 5

RESULT 16

US-08-416-035-3
Sequence 3, Application US/08416035
Patent No. 5739278
GENERAL INFORMATION:
APPLICANT: Baum, Gunter
APPLICANT: Fogel, Deborah E.
TITLE OF INVENTION: Methods and Compositions for Protein
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry
STREET: 6400 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,035
FILING DATE: 30-MAR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/59,949
FILING DATE: 10-MAY-1994
ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 42,624
REFERENCE/DOCKET NUMBER: 940610.54;
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
TELEX: 3723836

INFORMATION FOR SEQ ID NO: 1;
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
FEATURE:
MOLECULE TYPE: peptide

NAME/KEY: modified site
LOCATION: 3

OTHER INFORMATION: /note: "Wherein ty is is
OTHER INFORMATION: phosphorylated."
US-08-416-035-3

Query Match 27.3%, Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 ASK 3
DB 6 ASK 8

RESULT 47
US-08-416-035-4
Sequence 9, Application US/0841606;
Patent No. 5739278

GENERAL INFORMATION:

APPLICANT: Boon, Genter

APPLICANT: Coon, Deborah E.

APPLICANT: Fischer, Edward B.

TITLE OF INVENTION: Methods and Compositions for Protein

TITLE OF INVENTION: Tyrosine Phosphatases

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed and Betty

STREET: 6400 Columbia Center, 7th Floor, Avenue

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/416-035

FILING DATE: 30-MAR-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/059,949

FILING DATE: 10-MAY-1993

ATTORNEY/AGENT INFORMATION:

NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 42,624

REFERENCE/DOCKET NUMBER: 940610.54;

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

TELEX: 3723836

INFORMATION FOR SEQ ID NO: 9;

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-416-035-9

Query Match 27.3%, Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 1 ASK 3
DB 6 ASK 8

RESULT 48

US-08-024-253-5

Sequence 13, Application US/08024253

Patent No. 5785968

GENERAL INFORMATION:

APPLICANT: KIMACHI, Kazuhiko

APPLICANT: MAEDA, Hitoshi

APPLICANT: NISHIYAMA, Kiyoto

APPLICANT: TOKIYOSHI, Sachio

APPLICANT: TOHYA, Yukinobu

APPLICANT: MIKAMI, Takeshi

TITLE OF INVENTION: ANTI-FELINE CALCIVIRUS RECOMBINANT

TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT ENCODING THE SAME

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: WEBER, GENTER, MUELLER & PLAYER

STREET: 233 20th Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20036-8218

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/024,253

FILING DATE: 1993-01

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 79189/1992

FILING DATE: 28 FEB-1992

ATTORNEY/AGENT INFORMATION:

NAME: GENTER, Herbert L.

REGISTRATION NUMBER: 24,392

REFERENCE/DOCKET NUMBER: P-500 23744

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-0409

TELEFAX: (202) 885-0605

TELEX: 440736 WBCOR

INFORMATION FOR SEQ ID NO: 13;

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-024-253-13

Query Match 27.3%, Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

QY 8 NIK 10
DB 1 NIK 3

RESULT 49

US-08-209-261B-1C

Sequence 10, Application US/08259261B

Patent No. 5759152

```

: GENERAL INFORMATION:
: APPLICANT: Black, Christopher
: APPLICANT: Tosi, Pierre-Francois
: APPLICANT: Atkin, Andrew
: APPLICANT: Lazarre, Jaime E.
: APPLICANT: Nicolau, Yves Claude
: TITLE OF INVENTION: Diagnostic Device and Method
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Jones & Askew
: STREET: 191 Peachtree Street, Ste. 4700
: CITY: Atlanta
: STATE: Georgia
: COUNTRY: USA
: ZIP: 30333-1769
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.10
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/209,261B
: FILING DATE: 16-MAR-1994
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Sults, Larry W.
: REGISTRATION NUMBER: 34,025
: REFERENCE/DOCKET NUMBER: 05213-0061
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (404) 818-3700
: TELEFAX: (404) 818-3799
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-209-261B-10

Query Match 27.3%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 NIK 10
ID 6 NIK 8

US-08-612-302A-19
: Sequence 39, Application US/08/213-0061
: Patent No. 581297 5780297
: GENERAL INFORMATION:
: APPLICANT: GOPAL, T. Venkat
: TITLE OF INVENTION: PEPTIDE-MEDIATED GENE TRANSFER
: NUMBER OF SEQUENCES: 56
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Ratner & Pres'ia
: STREET: One Westlakes, Betwyn
: CITY: Valley Forge
: STATE: Pennsylvania
: COUNTRY: USA
: ZIP: 19482
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS DOS 5.0
: SOFTWARE: PatentIn Release #1.0, Version #1.10
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/612,302A
: FILING DATE: 7 March 1996
: CLASSIFICATION: 424

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: ATTORNEY/AGENT INFORMATION:
: NAME: Amzel, Viviana
: REGISTRATION NUMBER: 30,930
: REFERENCE/DOCKET NUMBER: AMBA-020
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (610) 407-0700
: TELEFAX: (610) 407-0701
: TELEX: n.a.
: INFORMATION FOR SEQ ID NO: 39:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: n.a.
: TOPOLOGY: n.a.
: US-08-512-302A-39

Query Match 27.3%; Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6
DB 6 KPK 8

US-08-373-190-48
: Sequence 48, Application US/08373190
: Patent No. 5851829
: GENERAL INFORMATION:
: APPLICANT: MARASCO, WAYNE
: APPLICANT: HASELLINE, WILLIAM
: TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF PROTEINS
: NUMBER OF SEQUENCES: 79
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
: STREET: 140 WAIVER STREET
: CITY: BOSTON
: STATE: MA
: COUNTRY: US
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/373,190
: FILING DATE: 17-JAN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/06735
: FILING DATE: 16-JUL-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: RESNICK, DAVID S.
: REGISTRATION NUMBER: 34,235
: REFERENCE/DOCKET NUMBER: 41956-PCT-US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-523-3400
: TELEFAX: 617-523-6440
: TELEX: STRE UR 2002
: INFORMATION FOR SEQ ID NO: 48:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: N-terminal
: ORIGINAL SOURCE:
: US-08-373-190-48

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Query Match 27.3%; Score 3; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6
 DB 6 KPK 8

RESULT 42
 US-08-968-676-82
 : Sequence 82; Application US/08-968676
 : Patent No. 5919639
 : GENERAL INFORMATION:
 : APPLICANT: Humphreys, Robert E.
 : APPLICANT: Adams, Sharon
 : TITLE OF INVENTION: IMMUNOTHERAPY BY MODULATION OF ANTIGEN
 : NUMBER OF SEQUENCES: 165
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Kevin M. Farrell, P.C.
 : STREET: P.O. Box 999
 : CITY: York Harbor
 : STATE: ME
 : COUNTRY: USA
 : ZIP: 03911
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08-968-676
 : FILING DATE:
 : CLASSIFICATION: 424
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Farrell, Kevin M.
 : REGISTRATION NUMBER: 35,505
 : REFERENCE/DOCKET NUMBER: RH-9601
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (207) 363-0558
 : TELEFAX: (207) 363-0528
 : INFORMATION FOR SEQ ID NO: 82:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 8 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: peptide
 : US-08-968-676-82

Query Match 27.3%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KRN 8
 DB 4 KRN 6

RESULT 43
 US-09-016-365A-47
 : Sequence 47; Application US/0901636A
 : Patent No. 5955431
 : GENERAL INFORMATION:
 : APPLICANT: Stevens, Richard L.
 : APPLICANT: Huang, Chifu
 : TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
 : NUMBER OF SEQUENCES: 165
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Wolf, Greenfield & Sacks, P.C.

STREET: 600 Atlantic Avenue
 CITY: Boston
 STATE: MA
 COUNTRY: U.S.A.
 ZIP: 02210-2211
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/016.366A
 FILING DATE: January 30, 1998
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/037,090
 FILING DATE: 05-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Plumer, Elizabeth R.
 REGISTRATION NUMBER: 36,647
 REFERENCE/DOCKET NUMBER: B0801/7093
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 TELEX:
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-016-366A-47

Query Match 27.3%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKR 7
 DB 4 PKR 6

RESULT 44
 US-08-438-190A-48
 : Sequence 48; Application US/08438190A
 : Patent No. 5965371
 : GENERAL INFORMATION:
 : APPLICANT: MARASCO, WAYNE
 : APPLICANT: HASELTINE, WILLIAM
 : TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
 : PROTEINS
 : NUMBER OF SEQUENCES: 78
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
 : ADDRESSEE: CUSHMAN
 : STREET: 130 WATER STREET
 : CITY: BOSTON
 : STATE: MASSACHUSETTS
 : COUNTRY: US
 : ZIP: 02109
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/438.190A
 : FILING DATE:
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: EISENSTEIN, RONALD I.
 : REGISTRATION NUMBER: 30628

REFERENCE/DOCKET NUMBER: 41956
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 523-3400
TELEFAX: (617) 523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-438 190A-48

Query Match 27.3% Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6
DB 5 KPK 8

RESULT 45
US-08-318 856A-3
Sequence 3, Application US/08318856A
Patent No. 5972351
GENERAL INFORMATION:
APPLICANT: Adrian V.S. Hill, et al.
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1+
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,856A
FILING DATE: October 3, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 08 068 B
FILING DATE: April 3, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 17 704 7
FILING DATE: August 20, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: April 5, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 263-PP1K1577US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 721-8200
TELEFAX: (202) 721-8250
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Plasmodium falciparum
US-08-318-856A-3

Query Match 27.3% Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 KPK 6
DB 1 KPK 3
RESULT 46
US-08-318-856A-29
Sequence 29, Application US/08318856A
Patent No. 5972351
GENERAL INFORMATION:
APPLICANT: Adrian V.S. Hill, et al.
TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
TITLE OF INVENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STA
TITLE OF INVENTION: ANTIGENS (AS AMENDED)
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1+
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,856A
FILING DATE: October 3, 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 08 068 B
FILING DATE: April 3, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 17 704 7
FILING DATE: August 20, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: April 5, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 263-PP1K1577US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 721-8200
TELEFAX: (202) 721-8250
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-318-856A-29

Query Match 27.3% Score 3; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KPK 6
DB 1 KPK 3

RESULT 47
US-08-318-856A-68
Sequence 68, Application US/08318856A
Patent No. 5972351
GENERAL INFORMATION:

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1  APPLICANT: Adrian V.S. Hill, et al.
2  TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
3  TITLE OF INVENTION: RESTRICTED CTL EPTIDES DERIVED FROM PRE-ERYTHROCYTIC STAGE
4  TITLE OF INVENTION: ANTIGENS (AS AMENDED)
5  NUMBER OF SEQUENCES: 86
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Wenderoth, Lind & Ponsack, L.L.P.
8  STREET: 2033 K Street, N.W., Suite 800
9  CITY: Washington
10 STATE: D.C.
11 COUNTRY: U.S.A.
12 ZIP: 20006
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: WordPerfect 5.1+
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/418,856A
21 FILING DATE: October 3, 1994
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: GB 92 08 368.8
24 FILING DATE: April 3, 1992
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: GB 92 17 704.7
27 FILING DATE: August 20, 1992
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: WO PCT/GB93/00711
30 FILING DATE: April 5, 1993
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Lee Cheng
33 REGISTRATION NUMBER: 40,949
34 REFERENCE/DOCKET NUMBER: 463-PP1R15770S
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: (202) 721-8200
37 TELEFAX: (202) 721-8250
38 INFORMATION FOR SEQ ID NO: 69:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 8 amino acid residues
41 TYPE: amino acid
42 STRANDEDNESS: single
43 TOPOLOGY: linear
44 MOLECULE TYPE: peptide
45 US 08-418 856A-69
46
47 Query Match 27.4% Score 3: DB 2: Length 8;
48 Best Local Similarity 100.0% Pred No 2.5e+05;
49 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
50
51 QY 4 KPK 6
52 ILI
53 DB 1 KPR 3
54
55 RESULT 49
56 US-08-619 013-11
57 Sequence 11, Application US/08019013
58 Patent No. 5,945,221
59 GENERAL INFORMATION:
60 APPLICANT: Chan, Andrew C.
61 TITLE OF INVENTION: B-LINK PROTEINS
62 NUMBER OF SEQUENCES: 13
63 CORRESPONDENCE ADDRESS:
64 ADDRESSEE: Fehr, Wilhelm, Test, Albritton & Herbert
65 STREET: Four Embarcadero Center, Suite 3400
66 CITY: San Francisco
67 STATE: California
68 COUNTRY: United States
69 ZIP: 94111-4187
70
71 COMPUTER READABLE FORM:
72 MEDIUM TYPE: Floppy disk
73 COMPUTER: IBM PC compatible
74 OPERATING SYSTEM: PC-DOS/MS-DOS
75 SOFTWARE: PatentIn Release #1.0, Version #1.30
76 CURRENT APPLICATION DATA:
77 APPLICATION NUMBER: US/08/819,013
78 FILING DATE: 17-MAR-1997
79 CLASSIFICATION: 435
80 PRIOR APPLICATION DATA:
81 APPLICATION NUMBER: US 08/788,322
82 FILING DATE: 24-JAN-1997
83 ATTORNEY/AGENT INFORMATION:
84 NAME: Silva, Robin M.
85 REGISTRATION NUMBER: 38,304
86 REFERENCE/DOCKET NUMBER: A-64383-1/RFT/RMS
87 TELECOMMUNICATION INFORMATION:
88 TELEPHONE: (415) 781-1989

```

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1  APPLICANT: Adrian V.S. Hill, et al.
2  TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
3  TITLE OF INVENTION: RESTRICTED CTL EPTIDES DERIVED FROM PRE-ERYTHROCYTIC STAGE
4  TITLE OF INVENTION: ANTIGENS (AS AMENDED)
5  NUMBER OF SEQUENCES: 86
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Wenderoth, Lind & Ponsack, L.L.P.
8  STREET: 2033 K Street, N.W., Suite 800
9  CITY: Washington
10 STATE: D.C.
11 COUNTRY: U.S.A.
12 ZIP: 20006
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: WordPerfect 5.1+
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/418,856A
21 FILING DATE: October 3, 1994
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: GB 92 08 368.8
24 FILING DATE: April 3, 1992
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: GB 92 17 704.7
27 FILING DATE: August 20, 1992
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: WO PCT/GB93/00711
30 FILING DATE: April 5, 1993
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Lee Cheng
33 REGISTRATION NUMBER: 40,949
34 REFERENCE/DOCKET NUMBER: 463-PP1R15770S
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: (202) 721-8200
37 TELEFAX: (202) 721-8250
38 INFORMATION FOR SEQ ID NO: 69:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 8 amino acid residues
41 TYPE: amino acid
42 STRANDEDNESS: single
43 TOPOLOGY: linear
44 MOLECULE TYPE: peptide
45 US 08-418 856A-69
46
47 Query Match 27.4% Score 3: DB 2: Length 8;
48 Best Local Similarity 100.0% Pred No 2.5e+05;
49 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
50
51 QY 4 KPK 6
52 ILI
53 DB 1 KPR 3
54
55 RESULT 49
56 US-08-418 856A-69
57 Sequence 69, Application US/08/418856A
58 Patent No. 5972351
59 GENERAL INFORMATION:
60 APPLICANT: Adrian V.S. Hill, et al.
61 TITLE OF INVENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
62 TITLE OF INVENTION: RESTRICTED CTL EPTIDES DERIVED FROM PRE-ERYTHROCYTIC STAGE
63 NUMBER OF SEQUENCES: 86
64 CORRESPONDENCE ADDRESS:
65 ADDRESSEE: Wenderoth, Lind & Ponsack, L.L.P.
66 STREET: 2033 K Street, N.W., Suite 800
67 CITY: Washington
68 STATE: D.C.
69 COUNTRY: U.S.A.
70 ZIP: 20006
71
72 COMPUTER READABLE FORM:
73 MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb

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Search completed: September 30, 2003, 10:28:23
Job time : 20.9167 secs

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1 TELEFAX: (415) 398-3249
2 TELEX: 910 277299
3 INFORMATION FOR SEQ ID NO: 11:
4 SEQUENCE CHARACTERISTICS:
5 LENGTH: 8 amino acids
6 TYPE: amino acid
7 STRANDEDNESS: unknown
8 TOPOLOGY: unknown
9 MOLECULE TYPE: protein
10 US-08-819-013-11

Query Match: 27.38; Score 11.00; Length 8;
Best Local Similarity 100.00; Pref No. 2 3 4 5 6
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKP 5
DB 1 KKP 3

RESULT 50
US-08-482-627-2
1 Sequence 2, Application US/08482627
2 Patent No. 5998134
3 GENERAL INFORMATION:
4 APPLICANT: Lee, Wen-Hwa
5 APPLICANT: Lee, Eva Y-H, P
6 TITLE OF INVENTION: Retinoblastoma Gene - Cancer Suppressor
7 TITLE OF INVENTION: and Regulator
8 NUMBER OF SEQUENCES: 5
9 CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Campbell and Flores
11 STREET: 4370 La Jolla Village Drive, Suite 700
12 CITY: San Diego
13 STATE: California
14 COUNTRY: United States
15 ZIP: 92122
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: Floppy disk
18 COMPUTER: IBM PC compatible
19 OPERATING SYSTEM: PC-DOS/MS-DOS
20 SOFTWARE: Patent In Release #1.0, Version #1.0
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/482-627
23 FILING DATE: 07-JUN-1995
24 CLASSIFICATION: 435
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 07/951,947
27 FILING DATE: 28-SEP-1992
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Campbell, Cathryn A.
30 REGISTRATION NUMBER: 31,815
31 REFERENCE/DOCKET NUMBER: P-UC 1992
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (619) 535-9001
34 TELEFAX: (619) 535-8949
35 INFORMATION FOR SEQ ID NO: 2:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 8 amino acids
38 TYPE: amino acid
39 STRANDEDNESS:
40 TOPOLOGY: linear
41 US-08-482-627-2

Query Match: 27.38; Score 11.00; Length 8;
Best Local Similarity 100.00; Pref No. 2 3 4 5 6
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 IKA 11
DB 1 IKA 3
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:04 : Search time 11.3333 Seconds
(without alignments)
93.340 Million cell updates/sec

Title: US-09-787-443-2

Perfect score: 11

Sequence: 1 AKKEHQKDTQ 1:

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2054

Minimum DB seq length: 8
Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3	27.3	9	2 A42266	peptidylglycine mg
2	3	27.3	10	2 FQ0785	NADH2 dehydrogenas
3	3	27.3	11	2 PT3217	T-cell receptor be
4	3	27.3	11	2 PD0441	translacion elonua
5	3	27.3	12	2 F64573	hypothetical prote
6	3	27.3	13	2 T05533	hypothetical prote
7	3	27.3	13	2 S22995	hypothetical prote
8	3	27.3	13	2 S47356	T-cell antigen rec
9	3	27.3	13	2 S47357	T-cell antigen rec
10	3	27.3	13	2 S47376	T-cell antigen rec
11	3	27.3	13	2 S47377	T-cell antigen rec
12	3	27.3	13	2 S47378	T-cell antigen rec
13	3	27.3	13	2 S47382	T-cell antigen rec
14	3	27.3	13	2 S47385	T-cell antigen rec
15	3	27.3	13	2 S47392	T-cell antigen rec
16	3	27.3	13	2 AB6126	hypothetical prote
17	3	27.3	14	1 QMVAVV	mastoparan - Yello
18	3	27.3	14	1 QMVAHM	mastoparan M - hor
19	3	27.3	14	1 QMVAHX	mastoparan X - hor
20	3	27.3	14	1 QMVAH2	mastoparan C - hor
21	3	27.3	14	2 S29632	xylan 1,4-beta-xy
22	3	27.3	14	2 B34135	DNA binding protei
23	3	27.3	14	2 PC1215	homeotic protein E
24	3	27.3	14	2 S14336	mastoparan B - hor
25	3	27.3	14	2 PH0135	T-cell receptor be
26	3	27.3	14	2 PH1471	T-cell receptor be
27	3	27.3	14	2 PH0765	T-cell receptor be
28	3	27.3	14	2 PC7079	unidentified 27-2K
29	3	27.3	14	2 F81754	hypothetical prote

30	3	27.3	15	2 S02381	probable membrane
31	3	27.3	15	2 A60156	cellulase (EC 3.2.2
32	3	27.3	15	2 PS0450	23K protein 4307 -
33	3	27.3	15	2 PA0076	fructose-bisphosph
34	3	27.3	15	2 PA0061	protein QF200039 -
35	3	27.3	15	2 A49177	22K protein pl, mi
36	3	27.3	15	2 S77987	cytochrome-c oxida
37	3	27.3	15	2 PH1788	T cell receptor al
38	3	27.3	15	2 G49655	T-cell-receptor be
39	3	27.3	15	2 PH0764	T-cell receptor be
40	3	27.3	15	2 S29175	D-galactose-bindin
41	3	27.3	15	2 S29175	D-galactose-bindin
42	3	27.3	15	2 S37141	neuropeptide B - b
43	2	18.2	8	2 A21440	variant surface gl
44	2	18.2	8	2 P-0323	lq heavy chain CRD
45	2	18.2	8	2 A48934	apolipoprotein A-I
46	2	18.2	8	2 A54823	olfactory receptor
47	2	18.2	8	2 PT0653	T-cell receptor be
48	2	18.2	8	2 A48935	apolipoprotein A-I
49	2	18.2	8	2 B54823	olfactory receptor
50	2	18.2	8	2 A61597	cytochrome P450 AL
51	2	18.2	8	2 S15532	gene Tnslow prote
52	2	18.2	8	2 A47618	beta-galactosidase
53	2	18.2	8	2 I64832	Ca2+-transporting
54	2	18.2	8	2 PC1002	leucine-tRNA ligas
55	2	18.2	9	1 Y8PG	thymic factor - pi
56	2	18.2	9	2 A60957	thymocyte growth p
57	2	18.2	9	2 S35538	ribosomal protein
58	2	18.2	9	2 A44873	caldesmon - rabbit
59	2	18.2	9	2 S30494	cat gene leader pe
60	2	18.2	9	2 H24362	chloramphenicol O-
61	2	18.2	9	2 S02384	probable membrane
62	2	18.2	9	2 C36730	hufu protein - Kle
63	2	18.2	9	2 S19523	orf AB protein - S
64	2	18.2	9	2 D57444	neuropeptide Grb-A
65	2	18.2	9	2 A61620	locustamytotropin I
66	2	18.2	9	2 S77984	cytochrome-c oxida
67	2	18.2	9	2 S54379	gene NF2 protein -
68	2	18.2	9	2 PT0315	lq heavy chain CRD
69	2	18.2	9	2 PC2197	zymogen granule me
70	2	18.2	9	2 C60070	gastrin - domestic
71	2	18.2	9	2 S66635	alpha-2-macroglobu
72	2	18.2	9	2 S66636	alpha-2-macroglobu
73	2	18.2	9	2 C56978	collagen alpha 1(I
74	2	18.2	9	2 S78762	ribosomal protein
75	2	18.2	9	2 PC7076	spectrin alpha cha
76	2	18.2	9	2 PC7078	unidentified 48.7K
77	2	18.2	9	2 PH0943	T-cell receptor be
78	2	18.2	9	2 PH0937	T-cell receptor be
79	2	18.2	9	2 S78426	52.5K protein - sp
80	2	18.2	10	2 S28055	cytochrome B559 co
81	2	18.2	10	2 S39392	calpain (bc 3.4.22
82	2	18.2	10	2 S33844	alpha-2-macroglobu
83	2	18.2	10	2 A60410	beta-neoendorphin
84	2	18.2	10	2 B49581	stathokinin II - ye
85	2	18.2	10	2 A24867	scyllokinin I - s
86	2	18.2	10	2 D37397	hypothetical prote
87	2	18.2	10	2 JQ0943	hypothetical i.3K
88	2	18.2	10	2 S18396	probable glucose-6
89	2	18.2	10	2 S48182	bacterioferritin -
90	2	18.2	10	2 S70251	nitrogenase (EC 1.
91	2	18.2	10	2 I40032	trpE protein - Bac
92	2	18.2	10	2 F44644	neurotoxin-associa
93	2	18.2	10	2 A44646	neurotoxin-associa
94	2	18.2	10	2 I44644	neurotoxin-associa
95	2	18.2	10	2 JP0072	ribosomal protein
96	2	18.2	10	2 S62880	polygalacturonase
97	2	18.2	10	2 PH0165	triose-phosphate 1
98	2	18.2	10	2 H61308	hemocyanin subunit
99	2	18.2	10	2 A42089	transcription fact
100	2	18.2	10	2 B56899	serum heterodimer,
101	2	18.2	10	2 S43625	cytochrome-c oxida
102	2	18.2	10	2 PT0251	lq heavy chain CRD

103	2	18.2	10	2	PTC284	Ig heavy chain CRD	176	2	18.2	12	2	SL5815	translation elonga
104	2	18.2	10	2	S23370	T-cell receptor al	177	2	18.2	12	2	SL1298	hemagglutinin prec
105	2	18.2	10	2	F49034	T-cell receptor ga	178	2	18.2	12	2	A44874	proboospectia - fr
106	2	18.2	10	2	S71948	matrix metalloprot	179	2	18.2	12	2	S29859	gene p10 protein -
107	2	18.2	10	2	C54823	factory receptor	180	2	18.2	12	2	A58501	24K kidney and bla
108	2	18.2	10	2	PTC664	T-cell receptor be	181	2	18.2	12	2	B58503	outer membrane por
109	2	18.2	10	2	C54823	factory receptor	182	2	18.2	12	2	C49215	urease (EC 3.5.1.5
110	2	18.2	10	2	S65367	cytochrome c oxida	183	2	18.2	12	2	B44618	extracellular lipa
111	2	18.2	10	2	PH0894	T-cell receptor be	184	2	18.2	12	2	S56122	type 1 DNA methyl
112	2	18.2	10	2	PH0894	T-cell receptor be	185	2	18.2	12	2	S71034	potB protein - Sal
113	2	18.2	10	2	PH0894	T-cell receptor be	186	2	18.2	12	2	S69123	proton-translocat
114	2	18.2	10	2	PH0894	T-cell receptor be	187	2	18.2	12	2	A40763	sucrose-6-phosphat
115	2	18.2	10	2	PH0894	T-cell receptor be	188	2	18.2	12	2	D28551	hypothetical prote
116	2	18.2	10	2	PH0894	T-cell receptor be	189	2	18.2	12	2	T44420	hypothetical prote
117	2	18.2	10	2	PH0894	T-cell receptor be	190	2	18.2	12	2	H61497	seed protein ws-17
118	2	18.2	10	2	PH0894	T-cell receptor be	191	2	18.2	12	2	J00356	cycloleonorin -
119	2	18.2	10	2	PH0894	T-cell receptor be	192	2	18.2	12	2	C34135	DNA-binding protei
120	2	18.2	10	2	PH0894	T-cell receptor be	193	2	18.2	12	2	A33099	163K exoantigen -
121	2	18.2	10	2	PH0894	T-cell receptor be	194	2	18.2	12	2	A56878	light yellow cell
122	2	18.2	10	2	PH0894	T-cell receptor be	195	2	18.2	12	2	SL0624	lipovitellin - Afr
123	2	18.2	10	2	PH0894	T-cell receptor be	196	2	18.2	12	2	SL0626	lipovitellin - Afr
124	2	18.2	10	2	PH0894	T-cell receptor be	197	2	18.2	12	2	A34858	proteinase E - bla
125	2	18.2	10	2	PH0894	T-cell receptor be	198	2	18.2	12	2	S29830	dimethylalanine mo
126	2	18.2	10	2	PH0894	T-cell receptor be	199	2	18.2	12	2	S29830	acetylcholine rece
127	2	18.2	10	2	PH0894	T-cell receptor be	200	2	18.2	12	2	S47360	T-cell antigen rec
128	2	18.2	10	2	PH0894	T-cell receptor be	201	2	18.2	12	2	PH1174	T-cell receptor al
129	2	18.2	10	2	PH0894	T-cell receptor be	202	2	18.2	12	2	A49033	T-cell receptor de
130	2	18.2	10	2	PH0894	T-cell receptor be	203	2	18.2	12	2	B49033	T-cell receptor de
131	2	18.2	10	2	PH0894	T-cell receptor be	204	2	18.2	12	2	S74196	3-hydroxy-3-methyl
132	2	18.2	10	2	PH0894	T-cell receptor be	205	2	18.2	12	2	S74196	gene Bata protein
133	2	18.2	10	2	PH0894	T-cell receptor be	206	2	18.2	12	2	S68402	NAD(+)-glycohydrol
134	2	18.2	10	2	PH0894	T-cell receptor be	207	2	18.2	12	2	PH1611	Ig H chain V-D-J r
135	2	18.2	10	2	PH0894	T-cell receptor be	208	2	18.2	12	2	S68271	major urinary prot
136	2	18.2	10	2	PH0894	T-cell receptor be	209	2	18.2	12	2	PH0802	T-cell receptor al
137	2	18.2	10	2	PH0894	T-cell receptor be	210	2	18.2	12	2	PH0790	T-cell receptor al
138	2	18.2	10	2	PH0894	T-cell receptor be	211	2	18.2	12	2	PH0931	T-cell receptor be
139	2	18.2	10	2	PH0894	T-cell receptor be	212	2	18.2	12	2	PC4377	telomeric and tetr
140	2	18.2	10	2	PH0894	T-cell receptor be	213	2	18.2	12	2	S71380	lebetin 1 isoform
141	2	18.2	10	2	PH0894	T-cell receptor be	214	2	18.2	12	2	S22163	glutamine-tRNA lig
142	2	18.2	10	2	PH0894	T-cell receptor be	215	2	18.2	12	2	S22163	NAD ADP-ribosyltra
143	2	18.2	10	2	PH0894	T-cell receptor be	216	2	18.2	12	2	PH0776	NADH2 dehydrogenas
144	2	18.2	10	2	PH0894	T-cell receptor be	217	2	18.2	12	2	JX0315	aminotransferase c
145	2	18.2	10	2	PH0894	T-cell receptor be	218	2	18.2	12	2	PC2121	aminotransferase c
146	2	18.2	10	2	PH0894	T-cell receptor be	219	2	18.2	12	2	A44818	extracellular lipa
147	2	18.2	10	2	PH0894	T-cell receptor be	220	2	18.2	12	2	S78519	ribosomal protein
148	2	18.2	10	2	PH0894	T-cell receptor be	221	2	18.2	12	2	S39413	tubulin beta chain
149	2	18.2	10	2	PH0894	T-cell receptor be	222	2	18.2	12	2	A33208	calreticulin, hepa
150	2	18.2	10	2	PH0894	T-cell receptor be	223	2	18.2	12	2	A60336	outer membrane pro
151	2	18.2	10	2	PH0894	T-cell receptor be	224	2	18.2	12	2	E39778	lactose phosphotra
152	2	18.2	10	2	PH0894	T-cell receptor be	225	2	18.2	12	2	PN0122	OLL protein - vacc
153	2	18.2	10	2	PH0894	T-cell receptor be	226	2	18.2	12	2	JZVHP1	crabrolin - Europe
154	2	18.2	10	2	PH0894	T-cell receptor be	227	2	18.2	12	2	A59387	VCAM-1 5'UTR bindi
155	2	18.2	10	2	PH0894	T-cell receptor be	228	2	18.2	12	2	A60458	protocatechuate 3,
156	2	18.2	10	2	PH0894	T-cell receptor be	229	2	18.2	12	2	B36342	oxfX protein - Esc
157	2	18.2	10	2	PH0894	T-cell receptor be	230	2	18.2	12	2	S12388	argX protein - Sal
158	2	18.2	10	2	PH0894	T-cell receptor be	231	2	18.2	12	2	PC2371	probable endopepti
159	2	18.2	10	2	PH0894	T-cell receptor be	232	2	18.2	12	2	PC2369	unidentified 85K p
160	2	18.2	10	2	PH0894	T-cell receptor be	233	2	18.2	12	2	A61288	spore proteinase g
161	2	18.2	10	2	PH0894	T-cell receptor be	234	2	18.2	12	2	A32453	phloroglucinol red
162	2	18.2	10	2	PH0894	T-cell receptor be	235	2	18.2	12	2	S36887	ribosomal protein
163	2	18.2	10	2	PH0894	T-cell receptor be	236	2	18.2	12	2	PA0031	protein QA300045 -
164	2	18.2	10	2	PH0894	T-cell receptor be	237	2	18.2	12	2	PA0023	protein QA300052 -
165	2	18.2	10	2	PH0894	T-cell receptor be	238	2	18.2	12	2	S28425	20K protein - rape
166	2	18.2	10	2	PH0894	T-cell receptor be	239	2	18.2	12	2	S09716	2S albumin large c
167	2	18.2	10	2	PH0894	T-cell receptor be	240	2	18.2	12	2	S00316	photosystem I 13K
168	2	18.2	10	2	PH0894	T-cell receptor be	241	2	18.2	12	2	JQ2109	hypothetical 1.6K
169	2	18.2	10	2	PH0894	T-cell receptor be	242	2	18.2	12	2	B44957	protein L7 - commo
170	2	18.2	10	2	PH0894	T-cell receptor be	243	2	18.2	12	2	JQ2119	hypothetical 1.6K
171	2	18.2	10	2	PH0894	T-cell receptor be	244	2	18.2	12	2	JQ1350	hypothetical prote
172	2	18.2	10	2	PH0894	T-cell receptor be	245	2	18.2	12	2	S29488	GTP-binding protei
173	2	18.2	10	2	PH0894	T-cell receptor be	246	2	18.2	12	2	S184603	deoxynucleotidyltr
174	2	18.2	10	2	PH0894	T-cell receptor be	247	2	18.2	12	2	PT0305	Ig heavy chain CRD
175	2	18.2	10	2	PH0894	T-cell receptor be	248	2	18.2	12	2	B61458	Ig kappa chain V-I

249	2	18.2	13	2	A61458	Ig kappa chain V-1	322	2	18.2	14	2	A23996	beta-granin - rat
250	2	18.2	13	2	PL0157	Ig lambda chain V-1	323	2	18.2	14	2	A37789	heat shock cognate
251	2	18.2	13	2	G61458	Ig kappa chain V-1	324	2	18.2	14	2	PC4376	telomeric and tetr
252	2	18.2	13	2	G56046	T-cell-specific tr	325	2	18.2	14	2	S68095	calcium-binding pr
253	2	18.2	13	2	G56046	urinary tract ston	326	2	18.2	14	2	PC4382	dehydrin 4.5K poly
254	2	18.2	13	2	A39836	aggreccin - bovine	327	2	18.2	14	2	H83778	hypothetical prote
255	2	18.2	13	2	PH5595	Ig H chain V-D-J r	328	2	18.2	14	2	H83836	hypothetical prote
256	2	18.2	13	2	G37265	Ig heavy chain C r	329	2	18.2	14	2	S39931	S-allele-associate
257	2	18.2	13	2	PH0788	Ig heavy chain C r	330	2	18.2	14	2	S39930	S-allele-associate
258	2	18.2	13	2	PH0788	T-cell receptor al	331	2	18.2	14	2	F81280	probable proteolys
259	2	18.2	13	2	PH0348	unidentified CM32	332	2	18.2	14	2	F33160	H-transferrin tw
260	2	18.2	13	2	G61576	ribosomal protein	333	2	18.2	14	2	S21747	glutamate dehydrog
261	2	18.2	13	2	H85575	hypothetical prote	334	2	18.2	14	2	PA0044	NADH2 dehydrogenas
262	2	18.2	13	2	S01504	H-transferrin tw	335	2	18.2	14	2	S21241	oligo-1,6-glucosid
263	2	18.2	14	1	BSTC	hemoglobin fire-be	336	2	18.2	15	2	S21240	alpha-glucosidase
264	2	18.2	14	1	QWAPPP	polistes mastopara	337	2	18.2	15	2	S21202	glucan 1,4-alpha-g
265	2	18.2	14	2	PH2373	probable IMP dehyd	338	2	18.2	15	2	A47146	topoisomerase I -
266	2	18.2	14	2	C40944	hypothetical prote	339	2	18.2	15	2	A49155	vasotocin-associat
267	2	18.2	14	2	S39932	S-allele-associate	340	2	18.2	15	2	S26518	T-cell receptor al
268	2	18.2	14	2	JN0389	histamine releasin	341	2	18.2	15	2	S26531	T-cell receptor al
269	2	18.2	14	2	S14332	histone H4-1 prec	342	2	18.2	15	2	PN0118	hemoglobin beta ch
270	2	18.2	14	2	A44515	Irf EG leader pept	343	2	18.2	15	2	A38304	heterogeneous ribo
271	2	18.2	14	2	A32654	fibrinopeptide A -	344	2	18.2	15	2	S16888	ribosomal protein
272	2	18.2	14	2	GH0328	probrusin tetradec	345	2	18.2	15	2	A28497	neurotensin-relate
273	2	18.2	14	2	S54945	gene C protein - E	346	2	18.2	15	2	S58116	Dp116 - human
274	2	18.2	14	2	S53388	Km(r) protein - ES	347	2	18.2	15	2	S46512	troponin - rabbit
275	2	18.2	14	2	A41589	25K elastin bindin	348	2	18.2	15	2	S46512	placental calcium-
276	2	18.2	14	2	S63535	amylopectinase -	349	2	18.2	15	2	H33208	calreticulin, uter
277	2	18.2	14	2	T46634	acyl carrier prote	350	2	18.2	15	2	JP0101	fibrinogen alpha c
278	2	18.2	14	2	S58862	botulinum neurotox	351	2	18.2	15	2	S29501	fibrinopeptide A -
279	2	18.2	14	2	S58866	botulinum neurotox	352	2	18.2	15	2	S65717	prostaglandin D-sy
280	2	18.2	14	2	S36892	ribosomal protein	353	2	18.2	15	2	PH0681	photosystem I 19.0
281	2	18.2	14	2	S48685	extension protein	354	2	18.2	15	2	PH0692	photosystem I 18.5
282	2	18.2	14	2	S13864	methyl coenzyme M	355	2	18.2	15	2	PH0004	chlorophyll a/b-bi
283	2	18.2	14	2	S29783	hypothetical prote	356	2	18.2	15	2	PH0017	terminal protein -
284	2	18.2	14	2	PA0109	perin forl Arabi	357	2	18.2	15	2	S40665	livBN leader pepti
285	2	18.2	14	2	PH0345	perin forl Arabi	358	2	18.2	15	2	PH0610	leukocyte chemoatt
286	2	18.2	14	2	PH0326	calotropis Di - mu	359	2	18.2	15	2	PH0629	integration host f
287	2	18.2	14	2	PH0147	omega-gliadin 1 d	360	2	18.2	15	2	S21411	modulation protein
288	2	18.2	14	2	PH0151	omega-gliadin 2	361	2	18.2	15	2	S71920	proteinase ECP 32
289	2	18.2	14	2	S33901	chaperone, TGP-re	362	2	18.2	15	2	S15389	urease (EC 3.5.1.5
290	2	18.2	14	2	S33902	chaperone, TGP-re	363	2	18.2	15	2	S33781	acetylactate synth
291	2	18.2	14	2	S33803	chaperone, TGP-re	364	2	18.2	15	2	S41383	23K variable histo
292	2	18.2	14	2	S35267	acetyl CoA carboxy	365	2	18.2	15	2	C41383	32K variable histo
293	2	18.2	14	2	A35289	actin 5 - slime mo	366	2	18.2	15	2	A56863	photosystem I reac
294	2	18.2	14	2	PA0103	protein QE203026	367	2	18.2	15	2	A17340	ribonucleoside-dip
295	2	18.2	14	2	PA0104	protein QE203070	368	2	18.2	15	2	S36891	ribosomal protein
296	2	18.2	14	2	A61308	ribosyltransferase	369	2	18.2	15	2	S36890	ribosomal protein
297	2	18.2	14	2	G61308	ribosyltransferase	370	2	18.2	15	2	S36889	benzoyl-CoA liase
298	2	18.2	14	2	G61308	ribosyltransferase	371	2	18.2	15	2	A48372	benzoyl-CoA liase
299	2	18.2	14	2	S03150	ribosyltransferase	372	2	18.2	15	2	T09463	ribosomal protein
300	2	18.2	14	2	S03150	ribosyltransferase	373	2	18.2	15	2	A28965	ribulose-bisphosph
301	2	18.2	14	2	S4284	glutathione - duck	374	2	18.2	15	2	PA0040	malate dehydrogena
302	2	18.2	14	2	PH0252	Ig heavy chain Ck	375	2	18.2	15	2	PA0018	photosystem I 9K p
303	2	18.2	14	2	PH0252	Ig heavy chain Ck	376	2	18.2	15	2	PA0001	photosystem I iron
304	2	18.2	14	2	S20294	Ig heavy chain Ck	377	2	18.2	15	2	PA0029	protein QA100012 -
305	2	18.2	14	2	S20294	Ig heavy chain Ck	378	2	18.2	15	2	PA0020	protein QA100028 -
306	2	18.2	14	2	S37562	Ig heavy chain J s	379	2	18.2	15	2	PA0046	protein QA100044 -
307	2	18.2	14	2	A28018	T-cell receptor be	380	2	18.2	15	2	PA0034	protein QA300050 -
308	2	18.2	14	2	A28018	very late antigen-	381	2	18.2	15	2	PT0082	protein QA600023 -
309	2	18.2	14	2	B28018	very late antigen-	382	2	18.2	15	2	PA0009	seed storage prote
310	2	18.2	14	2	PH0340	glycogen phosphory	383	2	18.2	15	2	A56970	GLYMA1 - soybean
311	2	18.2	14	2	A47421	leukotriene B-4 12	384	2	18.2	15	2	PA0006	lectin A3 - Psopho
312	2	18.2	14	2	A47421	leukotriene B-4 12	385	2	18.2	15	2	PA0008	lectin B2 - Psopho
313	2	18.2	14	2	C44823	synaptosomal-assoc	386	2	18.2	15	2	PN0148	omega-gliadin 3 -
314	2	18.2	14	2	A61032	troponin T, cardia	387	2	18.2	15	2	PS0218	24K protein 4413 -
315	2	18.2	14	2	PH1617	Ig H chain V-D-J r	388	2	18.2	15	2	PC4268	alpha-globulin - r
316	2	18.2	14	2	PH1598	Ig H chain V-D-J r	389	2	18.2	15	2	PA0114	photosystem I, iro
317	2	18.2	14	2	PH0752	T-cell receptor al	390	2	18.2	15	2	PA0057	adenylate isopente
318	2	18.2	14	2	PH0800	T-cell receptor al	391	2	18.2	15	2	PA0087	cytochrome c2 - fu
319	2	18.2	14	2	PH0795	T-cell receptor al	392	2	18.2	15	2	PA0093	enninatin synthetas
320	2	18.2	14	2	PH2210	T-cell receptor al	393	2	18.2	15	2	PA0102	fructose-bisphosph
321	2	18.2	14	2	PH0762	T-cell receptor be	394	2	18.2	15	2	PA0105	heat shock protein

395	2	18.2	15	2	PA0553	protein QF20006 -
396	2	18.2	15	2	PA0552	protein QF200015 -
397	2	18.2	15	2	PA0554	protein QF200017 -
398	2	18.2	15	2	PA0559	protein QF200021 -
399	2	18.2	15	2	PA0586	protein QF200044 -
400	2	18.2	15	2	PA0586	serine proteinase
401	2	18.2	15	2	PA0586	serine proteinase
402	2	18.2	15	2	PA0586	serine proteinase
403	2	18.2	15	2	PA0586	serine proteinase
404	2	18.2	15	2	PA0586	serine proteinase
405	2	18.2	15	2	PA0586	serine proteinase
406	2	18.2	15	2	PA0586	serine proteinase
407	2	18.2	15	2	PA0586	serine proteinase
408	2	18.2	15	2	PA0586	serine proteinase
409	2	18.2	15	2	PA0586	serine proteinase
410	2	18.2	15	2	PA0586	serine proteinase
411	2	18.2	15	2	PA0586	serine proteinase
412	2	18.2	15	2	PA0586	serine proteinase
413	2	18.2	15	2	PA0586	serine proteinase
414	2	18.2	15	2	PA0586	serine proteinase
415	2	18.2	15	2	PA0586	serine proteinase
416	2	18.2	15	2	PA0586	serine proteinase
417	2	18.2	15	2	PA0586	serine proteinase
418	2	18.2	15	2	PA0586	serine proteinase
419	2	18.2	15	2	PA0586	serine proteinase
420	2	18.2	15	2	PA0586	serine proteinase
421	2	18.2	15	2	PA0586	serine proteinase
422	2	18.2	15	2	PA0586	serine proteinase
423	2	18.2	15	2	PA0586	serine proteinase
424	2	18.2	15	2	PA0586	serine proteinase
425	2	18.2	15	2	PA0586	serine proteinase
426	2	18.2	15	2	PA0586	serine proteinase
427	2	18.2	15	2	PA0586	serine proteinase
428	2	18.2	15	2	PA0586	serine proteinase
429	2	18.2	15	2	PA0586	serine proteinase
430	2	18.2	15	2	PA0586	serine proteinase
431	2	18.2	15	2	PA0586	serine proteinase
432	2	18.2	15	2	PA0586	serine proteinase
433	2	18.2	15	2	PA0586	serine proteinase
434	2	18.2	15	2	PA0586	serine proteinase
435	2	18.2	15	2	PA0586	serine proteinase
436	2	18.2	15	2	PA0586	serine proteinase
437	2	18.2	15	2	PA0586	serine proteinase
438	2	18.2	15	2	PA0586	serine proteinase
439	2	18.2	15	2	PA0586	serine proteinase
440	2	18.2	15	2	PA0586	serine proteinase
441	2	18.2	15	2	PA0586	serine proteinase
442	2	18.2	15	2	PA0586	serine proteinase
443	2	18.2	15	2	PA0586	serine proteinase
444	2	18.2	15	2	PA0586	serine proteinase
445	2	18.2	15	2	PA0586	serine proteinase
446	2	18.2	15	2	PA0586	serine proteinase
447	2	18.2	15	2	PA0586	serine proteinase
448	2	18.2	15	2	PA0586	serine proteinase
449	2	18.2	15	2	PA0586	serine proteinase
450	2	18.2	15	2	PA0586	serine proteinase
451	2	18.2	15	2	PA0586	serine proteinase
452	2	18.2	15	2	PA0586	serine proteinase
453	2	18.2	15	2	PA0586	serine proteinase
454	2	18.2	15	2	PA0586	serine proteinase
455	2	18.2	15	2	PA0586	serine proteinase
456	2	18.2	15	2	PA0586	serine proteinase
457	2	18.2	15	2	PA0586	serine proteinase
458	2	18.2	15	2	PA0586	serine proteinase
459	2	18.2	15	2	PA0586	serine proteinase
460	2	18.2	15	2	PA0586	serine proteinase
461	2	18.2	15	2	PA0586	serine proteinase
462	2	18.2	15	2	PA0586	serine proteinase
463	2	18.2	15	2	PA0586	serine proteinase
464	2	18.2	15	2	PA0586	serine proteinase
465	2	18.2	15	2	PA0586	serine proteinase
466	2	18.2	15	2	PA0586	serine proteinase
467	2	18.2	15	2	PA0586	serine proteinase
468	2	18.2	15	2	PA0586	serine proteinase
469	2	18.2	15	2	PA0586	serine proteinase
470	2	18.2	15	2	PA0586	serine proteinase
471	2	18.2	15	2	PA0586	serine proteinase
472	2	18.2	15	2	PA0586	serine proteinase
473	2	18.2	15	2	PA0586	serine proteinase
474	2	18.2	15	2	PA0586	serine proteinase
475	2	18.2	15	2	PA0586	serine proteinase
476	2	18.2	15	2	PA0586	serine proteinase
477	2	18.2	15	2	PA0586	serine proteinase
478	2	18.2	15	2	PA0586	serine proteinase
479	2	18.2	15	2	PA0586	serine proteinase
480	2	18.2	15	2	PA0586	serine proteinase
481	2	18.2	15	2	PA0586	serine proteinase
482	2	18.2	15	2	PA0586	serine proteinase
483	2	18.2	15	2	PA0586	serine proteinase
484	2	18.2	15	2	PA0586	serine proteinase
485	2	18.2	15	2	PA0586	serine proteinase
486	2	18.2	15	2	PA0586	serine proteinase
487	2	18.2	15	2	PA0586	serine proteinase
488	2	18.2	15	2	PA0586	serine proteinase
489	2	18.2	15	2	PA0586	serine proteinase
490	2	18.2	15	2	PA0586	serine proteinase
491	2	18.2	15	2	PA0586	serine proteinase
492	2	18.2	15	2	PA0586	serine proteinase
493	2	18.2	15	2	PA0586	serine proteinase
494	2	18.2	15	2	PA0586	serine proteinase
495	2	18.2	15	2	PA0586	serine proteinase
496	2	18.2	15	2	PA0586	serine proteinase
497	2	18.2	15	2	PA0586	serine proteinase
498	2	18.2	15	2	PA0586	serine proteinase
499	2	18.2	15	2	PA0586	serine proteinase
500	2	18.2	15	2	PA0586	serine proteinase

ALIGNMENTS

RESULT: 1
 A42266
 peptidylglycine monooxygenase (EC 1.14.17.3), rPAM-5 - rat (fragment)
 N: Alternate names: peptidylglycine alpha-amidating monooxygenase
 C: Species: Rattus norvegicus (Norway rat)
 G: Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-1995
 G: Accession: A42266
 R: Ripper, B.A.; Green, C.B.; Campbell, T.A.; Stoffers, D.A.; Keutmann, H.T.; Mains, J. Biol. Chem. 267: 4008-4015, 1992
 A: Title: Alternative splicing and endoproteolytic processing generate tissue-specific
 A: Reference number: A42266; PMID:92156145; PMID:1740449
 A: Address: A42266
 A: Status: preliminary
 A: Molecule type: mRNA
 A: Biosource: 19-ELP
 A: Experimental source: pituitary
 A: Notes: sequence extracted from NCBI backbone (NCBI:82733, NCBI:82750)
 C: Keywords: oxidoreductase
 G: Match: 27.8% Score 3; DB 2; Length 9;
 Best Local Similarity 100.0% Pred No 2.8e-05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 GY 8 KD: 10
 ID 6 KD: 8
 RESULT: 2
 P02785
 NAM2 deoxyfructose (3'-phosphoryl) 27K chain - fava bean mitochondrion (fragment)
 N: Alternate names: complex 1 27K chain; NADH-ubiquinone reductase 27K chain
 C: Species: mitochondrion; Fava faba (fava bean)
 G: Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 03-Jun-2002
 G: Accession: P02785

R:Lettere, S.; Bouley, M.
Plant Physiol. 102, 435-443, 1993
A:Title: Purification and preliminary characterization of mitochondrial fat complex 1 (NAOH)
A:Reference number: PQ0775; NCID:94151437; PMID:6108509
A:Accession: PQ0785
A:Molecule type: protein
A:Residues: 1-10 <1F>
C:Comment: Complex 1, mitochondrial NADH-ubiquinone reductase, is the first of the three ranging from 5K to 75K.

C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by
A:Genome: mitochondrion
C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 27.3% Score 3; DB 2; Length 101
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KER 5

LB 7 KER 9

RESULT 3
P0217
T-cell receptor beta chain V- β region (4-1 E-2) - mouse (transmembrane)
C:Species: Mus musculus (house mouse)
C:Date: 31 Dec-1991 #sequence_revision 31 Dec-1991 #text_change 30 May-1997
C:Accession: P0217
R:Nakano, N.; Kikufumi, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted
A:Reference number: P0209; NCID:9217621; PMID:1902501
A:Accession: P0217
A:Molecule type: mRNA
A:Residues: 1-11 <NA>
C:Keywords: T cell receptor

Query Match 27.3% Score 3; DB 2; Length 11
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTG 11

LB 9 DTG 11

RESULT 4
P0441
Translation elongation factor T₁ (aka p₁) from rat mitochondrion (transmembrane)
C:Species: Mus musculus (house mouse)
C:Date: 21 Aug-1995 #sequence_revision 21 Aug-1995 #text_change 21 Aug-1995
C:Accession: P00441
R:Kawakami, T.; Uchida, T.; Sakai, T.; Kame, M.; Hara, S.; Ito, S.; Iwata, A.
submitted to JIPID, August 1998
A:Description: Proteome analysis of mouse brain
A:Reference number: P00441
A:Accession: P00441
A:Molecule type: protein
A:Residues: 1-11 <NA>
A:Experimental source: striatum
C:Keywords: mitochondrion

Query Match 27.3% Score 3; DB 2; Length 11
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3

LB 4 AKK 6

RESULT 5

P64573
Hypothetical protein HP0429 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
A:Accession: E64573
R:Tomb, J.F.; White, O.; Kellavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McSon, J.D.; Kelley, J.M.; Colton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathes, Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Frase
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64526; MUID:97394467; PMID:9252185
A:Accession: E64573

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-12 <10>
A:Cross-references: GH:AF000559; GH:AF000511; NID:92313536; PIDN:AAU07512.1; PID:92

Query Match 27.3% Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4

LB 6 KKE 8

RESULT 6
T08533
Hypothetical protein X - Enterobacter aerogenes plasmid R751
C:Species: Enterobacter aerogenes
C:Date: 11 Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T08533
R:Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.
Plasmid 36, 95-111, 1996
A:Title: Conservation of the genetic switch between replication and transfer genes
A:Reference number: Z16434; MUID:97118926; PMID:8954881
A:Accession: T08533
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-13 <10>
A:Cross-references: EMBL:U67194; NID:q1572520; PIDN:AAC64477.1; PID:q1572582
C:Genetics:
A:Genome: plasmid R751

Query Match 27.3% Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 4

LB 6 AKK 8

RESULT 7
S22995
Hypothetical protein X (traJ 5' region) - Escherichia coli plasmid R751
C:Species: Escherichia coli
C:Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 08-Oct-1999
C:Accession: S22995
R:Ziegler, G.; Pansegrau, W.; Strack, B.; Balzer, D.; Kroeger, M.; Kruff, V.; Lank, DNA Seq. 1, 303-327, 1991
A:Title: Nucleotide sequence and organization of genes flanking the transfer origin
A:Reference number: S22992; MUID:92190548; PMID:1665997
A:Accession: S22995
A:Molecule type: DNA
A:Residues: 1-13 <21E>
A:Cross-references: EMBL:X54458; NID:q42656; PIDN:CAA38330.1; PID:q581211
C:Genetics:
A:Genome: plasmid
A:Start codon: TTG

Query Match 27.3% Score 3; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 4.4e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 6 AKK 8

RESULT 8

S47356
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47356
K:Lehner, P.J.

submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47356
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-References: EMBL:Z35680; NID:q527449; PIDN:CAA4749.1; PID:q527450
C:Keywords: T-cell receptor

Query Match 27.4%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 9 DTQ 11

RESULT 9

S47357
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47357
K:Lehner, P.J.

submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47357
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-References: EMBL:Z35681; NID:q527451; PIDN:CAA4750.1; PID:q527452
C:Keywords: T-cell receptor

Query Match 27.4%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 9 DTQ 11

RESULT 10

S47376
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47376
K:Lehner, P.J.

submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47376
A>Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-13 <LEH>
A:Cross-References: EMBL:Z35702; NID:q527497; PIDN:CAA84771.1; PID:q527498
C:Keywords: T-cell receptor

Query Match 27.4%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 9 DTQ 11

RESULT 11

S47377
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47377
K:Lehner, P.J.

submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by
A:Reference number: S47355
A:Accession: S47377
A>Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-13 <LEH>
A:Cross-References: EMBL:Z45706; NID:q527505; PIDN:CAA84775.1; PID:q527506
C:Keywords: T-cell receptor

Query Match 27.4%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 9 DTQ 11

RESULT 12

S47378
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47378
K:Lehner, P.J.

submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by
A:Reference number: S47355
A:Accession: S47378
A>Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-13 <LEH>
A:Cross-References: EMBL:Z45707; NID:q527507; PIDN:CAA84776.1; PID:q527508
C:Keywords: T-cell receptor

Query Match 27.4%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 9 DTQ 11

RESULT 13

S47382
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47382; S47370
K:Lehner, P.J.
submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of Influenza A is dominated by T
 A:Reference number: S47355
 A:Accession: S47382
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-13 <LEH>
 A:Cross-references: EMBL:235687; NID:q527463; FIDN:AA84756.1; PID:q527464; EMBL:235695;
 C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
 III
 DB 9 DTQ 11

RESULT 14
 S47385
 T cell antigen receptor VJ junction beta chain - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05 Nov 1999
 C:Accession: S47385
 A:Reference number: S47385
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-13 <LEH>
 A:Cross-references: EMBL:235705; NID:q527503; FIDN:AA84774.1; PID:q527504
 C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
 III
 DB 9 DTQ 11

RESULT 15
 S47392
 T-cell antigen receptor VJ junction beta chain - human
 C:Species: Homo sapiens (man)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05 Nov-1999
 C:Accession: S47392
 A:Reference number: S47392
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-13 <LEH>
 A:Cross-references: EMBL:235713; NID:q527521; FIDN:AA84782.1; PID:q527522
 C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
 III
 DB 9 DTQ 11

RESULT 16
 A86126
 hypothetical protein Z5883 [imported], Escherichia coli (strain 0157:H7, substrain EDL933)

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
 III
 DB 9 DTQ 11

RESULT 17
 QMVAVV
 mastoparan yellowjacket (Vespula lewisii)
 C:Species: Vespula lewisii
 C:Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 08-Dec-1995
 C:Accession: A01776
 R:Hirai, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.; Fujino, M.; Kitada, C.
 Chem. Pharm. Bull. 27, 1942-1944, 1979
 A:Title: A new mast cell degranulating peptide mastoparan in the venom of Vespula-1
 A:Reference number: A01776; MUID:80155337; PMID:540362
 A:Accession: A01776
 A:Molecule type: protein
 A:Residues: 1-14 <HIR>
 A:Note: the active peptide was also synthesized
 C:Comment: This cytoactive peptide from wasp venom induces mast cell degranulation
 C:Superfamily: mastoparan
 C:Keywords: amidated carboxyl end
 F.14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 27.3% Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
 III
 DB 10 AKK 12

RESULT 18
 OMVHMM
 mastoparan M - hornet (Vespa mandarinia)
 N:Alternate names: mast cell-degranulating peptide
 C:Species: Vespa mandarinia
 C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 08-Dec-1995
 C:Accession: A01777
 R:Hirai, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
 Biomed. Res. 2, 447-449, 1981
 A:Title: A new mast cell degranulating peptide, mastoparan-M, in the venom of the B
 A:Reference number: A01777
 A:Accession: A01777
 A:Molecule type: protein
 A:Residues: 1-14 <HIR>
 C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation
 C:Superfamily: mastoparan
 C:Keywords: amidated carboxyl end; venom
 F.14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
 III
 DB 9 DTQ 11

RESULT 19
 A86126
 hypothetical protein Z5883 [imported], Escherichia coli (strain 0157:H7, substrain EDL933)

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
 III
 DB 9 DTQ 11

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: A86126

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamou, K.; Apos

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A55480; MUID:21074935; PMID:11206551

A:Accession: A86126

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-13 <STH>

A:Cross-references: GB:AF005174; NID:q12519285; PIDN:AAG59469.1; GSPDR:GN00145; UWG

A:Experimental source: Strain 0157:H7, substrain EDL933

C:Genetics:

A:Gene: Z5883

Query Match 27.3% Score 3; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 3.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3

III

DB 8 AKK 10


```

Query Match      27.3% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKK 3
DB      10 AKK 12

RESULT 19
QWVHX
mastoparan X hornet (Vespa xanthoptera)
C:Species: Vespa xanthoptera
C:Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 06-Dec-1995
C:Accession: A01778
Kishitani, Y.; Kowada, M.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
Chem. Pharm. Bull. 27, 1945-1946, 1979
A:Title: A new mast cell degranulating peptide homologous to mastoparan in the venom of
A:Reference number: A01778; MUI0:86155438; PMID:54160
A:Accession: A01778
A:Molecule type: protein
A:Residues: 1-14 <HR>
C:Comment: This cytotoxic peptide from hornet venom induces mast cell degranulation.
C:Superfamily: mastoparan
C:Keywords: amidated carboxyl end
F:14/Modified site: amidated carboxyl end (len) #status experimental

Query Match      27.3% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKK 3
DB      10 AKK 12

RESULT 20
QWVHX
mastoparan C European hornet
C:Species: Vespa crabro (European hornet)
C:Date: 28-Feb-1986 #sequence_revision 26-Feb-1996 #text_change 06-Dec-1995
C:Accession: A01779
R. Argiolas, A.; Pisano, J. J.
J. Biol. Chem. 259, 10106-10111, 1984
A:Title: Isolation and characterization of two new peptides, mastoparan C and crabrolin.
A:Reference number: A52441; MUI0:84289190; PMID:6266393
A:Accession: A01779
A:Molecule type: protein
A:Residues: 1-14 <ARG>
C:Comment: This cytotoxic peptide from hornet venom induces mast cell degranulation.
C:Superfamily: mastoparan
C:Keywords: amidated carboxyl end; venom
F:14/Modified site: amidated carboxyl end (len) #status experimental

Query Match      27.3% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKK 3
DB      10 AKK 12

RESULT 21
S29632
xylan 1,4-beta xylosidase (EC 3.2.1.4) - Thermotoga sp. (strain FJSS-B.1) (fragment)
N:Alternate names: beta-xylosidase
C:Species: Thermotoga sp.
A:Variety: FJSS-B.1
C:Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 18-Jun-1999
C:Accession: S29632
R. Rutter-Smith, L.B.; Daniel, R.M.
Biochim. Biophys. Acta 1156, 167-172, 1993

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A:Title: Thermostable beta-glucosidase and beta-xylosidase from Thermotoga sp. strain
A:Reference number: S29631; MUI0:93152594; PMID:8427876
A:Accession: S29632
A:Molecule type: protein
A:Residues: 1-14 <RUI>
A:Experimental source: strain FJSS-B.1
C:Comment: Although the beta-xylosidase enzyme activity was apparently confirmed for
C:Function:
A:Description: hydrolyzes short chain oligosaccharides and xylobiose to produce D-xylo
A:Note: plays an important role in the relief of end-product inhibition of endoxylan
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match      27.3% Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKK 3
DB      1 AKK 3

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RESULT 22
B34135
DNA-binding protein q - Crithidia fasciculata mitochondrion (fragment)
C:Species: mitochondrion Crithidia fasciculata
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 07-Dec-1999
C:Accession: B34135
R. Tittawella, L.
FEBS Lett. 260, 57-63, 1990
A:Title: Kinetoplast DNA-acquiring proteins from the parasitic protozoan Crithidia
A:Reference number: A54135
A:Accession: B34135
A:Molecule type: protein
A:Residues: 1-14 <IIT>
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SOR6
C:Keywords: mitochondrion

Query Match      27.3% Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKK 3
DB      6 AKK 8

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RESULT 23
PC1215
homeotic protein Egrbx5 - tapeworm (Echinococcus granulosus) (fragment)
C:Species: Echinococcus granulosus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
C:Accession: PC1215
R. Oliver, G.; Vispo, M.; Mailhos, A.; Martinez, C.; Sosa-Pineda, B.; Fiehlitz, W.; Ehr
Gene 121, 337-342, 1992
A:Title: Homeoboxes in flatworms.
A:Reference number: JCI386; MUI0:93077050; PMID:1359988
A:Accession: PC1215
A:Molecule type: DNA
A:Residues: 1-14 <CH>
A:Cross-references: EMBL:X66821
C:Keywords: homeobox

Query Match      27.3% Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches      3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 KER 5
DB      9 KER 11

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RESULT 24
SI4336
Masoparan P. hornet (Vespa basalis)
C:Species: Vespa basalis
C:Date: 19 Mar 1997 #sequence_revision 18-Mar-1997 #text_change 09-Apr-1999
C:Accession: SI4336
R:Ho, C. L.; Huang, L. L.
Biochem. J. 274, 453-456, 1991
A:Title: Structure and biological activities of a new masoparan isolated from the venom
A:Reference number: SI4336; MUID:4174755; PMID:2006909
A:Accession: SI4336
A:Molecule type: protein
A:Residues: 1-14 <DOC>
A:Experimental source: venom
C:Function:
A:Description: possesses a potent hemolytic activity which acts in synergy with the lethal
C:Keywords: amidated carboxyl end; mast cell; venom
F:14/Modified site: amidated carboxyl end (see) ; status experimental

Query Match 27.3%; Score 6; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 10 AKK 12

RESULT 25
PH0135
T-cell receptor beta chain V-D J region MS1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Nov-1991 #sequence_revision 24-Nov-1991 #text_change 10-May-1997
C:Accession: PH0135
R:Marlitz, R.; Howell, M. D.; Jaraquemada, D.; Flierlango, M.; Kiehlert, J.; Brostoff, S.; Lo
J. Exp. Med. 173, 19-24, 1991
A:Title: A myelin basic protein peptide is immunoreactivity cytotoxic T cells in the context
A:Reference number: PH0135; MUID:91086943; PMID:1702117
A:Accession: PH0135
A:Molecule type: mRNA
A:Residues: 1-14 <MAR>
C:Keywords: T-cell receptor

Query Match 27.3%; Score 6; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 11 DTQ 14

RESULT 26
PH1471
T-cell receptor beta chain (clone A24/0844) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Mar-1994 #sequence_revision 16-Mar-1994 #text_change 11-Apr-1995
C:Accession: PH1471
R:Casanova, J. L.; Martinon, F.; Goubetier, H.; Barthelemy, C.; Fournier, A.; Kiehlert,
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of a two class I major histocompatib
A:Reference number: PH1430; MUID:93171e21; PMID:1210111
A:Accession: PH1471
A:Molecule type: mRNA
A:Residues: 1-14 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Support family: immunoglobulin homology
C:Keywords: receptor; T-cell

Query Match 27.3%; Score 6; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 11 DTQ 14

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QY 9 DTQ 11
DB 9 DTQ 11

RESULT 27
PH0765
T-cell receptor beta chain (HL) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0765
R:Casanova, J. L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J. L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility comp
allelle exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0765
A:Molecule type: mRNA
A:Residues: 1-14 <CAS>
A:Cross-references: EXHL:X60859; NID:g51139; PIDN:CAA43249.1; PID:g51140
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 27.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 9 DTQ 11

RESULT 28
PC7079
unidentified 27.2K protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C:Accession: PC7079
R:Tsuaita, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe,
Electrophoresis 21, 1853-1871, 2000
A:Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles
A:Reference number: PC7072
A:Accession: PC7079
A:Molecule type: protein
A:Residues: 1-14 <ISU>
A:Experimental source: strain C57BL/6Cr Slc, male; brain; striatum
C:Keywords: brain

Query Match 27.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
DB 7 KKE 9

RESULT 29
FB3754
Hypothetical protein BB0848 (imported) - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: FB3754
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, K.; Masui, N.; Fujii, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A:Reference number: A91633; MUID:20512582; PMID:11058132
A:Accession: FB3754
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-14 <SLH>
A:Cross references: GNA1001310; GNA1000004; NID:g10173440; PIDN:BA004557.1; GSPDB
A:Experimental source: strain C-125

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C:\Genetools

A:\Genetools

Query Match 27.4% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KDT 10

|||

DB 2 KDT 4

RESULT 40

S02383

Probable membrane antigen C11 - human herpesvirus 4 (fragment)

C:Species: human herpesvirus 4; Epstein-Barr virus

C:Date: 01-Dec-1989 #sequence_revision 6; text_change 06-Feb-1999

C:Accession: S02381

R:Wallis, D.; Cannon, F.

EMBL J. 7; 1191-1196, 1988

A:Title: The expression of novel antigens from the Epstein Barr virus large internal region

A:Reference number: S02381; M010:88296424; PMID:284116

A:Accession: S02381

A:Molecule type: DNA

A:Residues: 1-15 <SWAL>

A:Cross references: EMBL:X07814; NID:059167; EMBL:CAA00761; P11039003

C:Keywords: membrane protein; surface antigen

Query Match 27.4% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KDT 7

|||

DB 1 KDT 13

RESULT 41

A60156

Cellulase (EC 3.2.1.4) - Clostridium histolyticum (fragment)

N:Alternate names: endo-1,4-beta-glucanase

C:Species: Clostridium histolyticum

C:Date: 22-Jan-1993 #sequence_revision 22 Jan 1993 #text_change 22-Nov-1995

C:Accession: A60156

R:Fujino, T.; Sasaki, T.; Ohmiva, K.; Shimizu, S.

Appl. Environ. Microbiol. 56: 1175-1178, 1990

A:Title: Purification and properties of an endo-1,4-beta-glucanase translocated from a Clostridium histolyticum

A:Reference number: A60156; M010:96250587; PMID:2163164

A:Accession: A60156

A:Molecule type: protein

A:Residues: 1-15 <FUD>

C:Function:

A:Description: hydrolysis of 1,4-beta-D-glucan into glucose

A:Pathway: cellulose degradation

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 27.4% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3

|||

DB 1 AKK 15

RESULT 42

PS0450

23K protein p1, mitochondrial - Crithidia fasciculata (fragment)

C:Species: Crithidia fasciculata

C:Date: 03-Feb-1994 #sequence_revision 6; Feb-1994 #text_change 11-Apr-1995

C:Accession: PS0450

R:Tsuigita, A.; Miyatake, N.

submitted to JIPID, April 1995

A:Reference number: PS0268

A:Accession: PS0450

A:Molecule type: protein

A:Residues: 1-15 <TSU>

A:Experimental source: germ. strain Nihonbare

C:Comment: molecular weight 24K, pI 5.3.

Query Match 27.4% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KDT 9

|||

DB 8 KDT 10

RESULT 43

PA0076

fructose-bisphosphate aldolase (EC 4.1.2.13) - fungus (Fusarium sporotrichioides) (f

C:Species: Fusarium sporotrichioides

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C:Accession: PA0076

R:Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JIPID, October 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporot

A:Reference number: PA0051

A:Accession: PA0076

A:Molecule type: protein

A:Residues: 1-15 <CHO>

C:Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match 27.4% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KDT 5

|||

DB 6 KDT 10

RESULT 44

PA0061

protein QF200039 - fungus (Fusarium sporotrichioides) (fragment)

C:Species: Fusarium sporotrichioides

C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001

C:Accession: PA0061

R:Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JIPID, October 1994

A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporot

A:Reference number: PA0051

A:Accession: PA0061

A:Molecule type: protein

A:Residues: 1-15 <CHO>

Query Match 27.4% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KDT 10

|||

DB 11 KDT 13

RESULT 45

A49177

22K protein p1, mitochondrial - Crithidia fasciculata (fragment)

C:Species: Crithidia fasciculata

C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 19-May-1994

C:Accession: A49177; PH1826

R:Tittawella, L.

Exp. Cell Res. 256: 143-151, 1993

A:Title: Identification of DNA binding proteins in the parasitic protozoan Crithidia

A:Reference number: A49177; M010:93245912; PMID:8482355

A:Accession: A49177
A:Molecule type: protein
A:Residues: 1-15 <RT>
C:Species: Thunnus obesus (Bigeye tuna)
C:Comment: This protein binds with mitochondrial DNA.
C:Keywords: DNA binding; Mitochondrion

Query Match 27.3% Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 1 AKK 15

RESULT 36
S77987
cytochrome oxidase (EC 1.9.3.1) chain V (alpha 2) - biotype tuna (fragments)
C:Species: Thunnus obesus (Bigeye tuna)
C:Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 04-Sep-1998
C:Accession: S77987
R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linbet, E.; Lottspeich, F.; Kadenbach, B.
Submitted to the Protein Sequence Database, June 1997
A:Reference number: S77986
A:Accession: S77987
A:Molecule type: protein
A:Residues: 1-8; 9-15 <ARN>
A:Experimental source: heart
C:Genetics:
A:Genome: nuclear
C:Function:
A:Pathway: oxidative phosphorylation; respiratory chain
C:Keywords: electron transfer; membrane associated complex; mitochondrion; inner membrane

Query Match 27.3% Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 7 AKK 9

RESULT 37
PH0764
T-cell receptor alpha chain V region (clone 2F61.V alpha 2) 4) human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH0764
R:Porcellii, S.; Yockey, C.E.; Riedert, M.; Bork, S.
J. Exp. Med. 174, 1-16, 1994
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A:Reference number: PH1750; MCID:94901565; PID:94901565
A:Accession: PH1738
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <POR>

Query Match 27.3% Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERQ 6
DB 5 ERQ 7

RESULT 38
G49655
T-cell receptor beta chain variable region (clone 1) human (fragment)
C:Species: Homo sapiens (man)

C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: G49655; F49655; A49655
R:Grom, A.A.; Thompson, S.D.; Laylink, L.; Passo, M.; Choi, E.; Glass, D.N.
Proc. Natl. Acad. Sci. U.S.A. 90, 11104-11108, 1993
A:Title: Dominant T-cell-receptor beta chain variable region V beta 14- clones in j
A:Reference number: A49655; MCID:94068553; PMID:8248215
A:Accession: G49655
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-15 <GR>
A:Experimental source: hip joint, synovial tissues
A:Note: this was designated clone 1
A:Note: sequence extracted from NCBI backbone (NCBI:P:140453)
A:Accession: F49655
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-15 <GR2>
A:Experimental source: hip joint, synovial tissues
A:Note: sequence extracted from NCBI backbone (NCBI:P:140451)
A:Note: this was designated clone 2
A:Accession: A49655
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-15 <GR0>
A:Experimental source: knee joint, synovial fluid lymphocytes
A:Note: this was designated clone SF-1
A:Note: sequence extracted from NCBI backbone (NCBI:P:140445)
C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 12 DTQ 14

RESULT 39
PH0764
T-cell receptor beta chain (PF2.10.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0764
R:Casanova, J.L.; Romero, P.; Wildmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility compl
Allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0740; MUIB:92078846; PMID:1836010
A:Accession: PH0764
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: EMBL:X60858; NID:q53652; PIDN:CAA43248.1; PID:q53653
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
DB 10 DTQ 12

RESULT 40
S29175
D-galactose-binding lectin V - Axinella polypoides (fragment)
C:Species: Axinella polypoides
C:Date: 19-Mar-1997 #sequence_revision 14-Nov-1997 #text_change 14-Nov-1997
C:Accession: S29175
R:Buck, F.; Leth, C.; Strupat, K.; Bretting, H.
Biochim. Biophys. Acta 1159, 1-8, 1992

A:Title: Comparative investigations on the amino-acid sequences of different isolectins
 A:Reference number: S29172; MUID:91003351; PMID:1390906
 A:Accession: S29175
 A:Molecule type: protein
 A:Residues: 1-15 <BUC>

Query Match 27.3%; Score 2; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EKQ 6

Db 6 EKQ 8

RESULT 41

B24749

C:Species: Bos primigenius taurus (cattle)

C:Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 18-Aug-2009

C:Accession: B24749

R:Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.

Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985

A:Title: Isolation, sequencing, synthesis, and pharmacological characterization of two

A:Reference number: A94074; MUID:26067985; PMID:385519.

A:Accession: B24749

A:Molecule type: Protein

A:Residues: 1-8 <YAN>

C:Superfamily: unassigned animal peptides

C:Keywords: neuropeptide

Query Match 18.2%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

Qy 6 QR 7

Db 6 QR 7

RESULT 42

S37141

C:Species: Erwinia chrysanthemi

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1999

C:Accession: S37141

R:Douville, A.; Ioussaint, A.; Faelen, M.

Submitted to the EMBL Data Library, August 1994

A:Description: Identification of the integration host factor genes of E. chrysanthemi.

A:Reference number: S37139

A:Accession: S37141

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-8 <KQ>

A:Cross-references: EMBL:X74750; NID:q199066; PDB:1AA2/P69.1; PID:4581168

Query Match 18.2%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2

Db 5 AK 6

RESULT 43

A21440

C:Species: Trypanosoma brucei

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Mar-1998

C:Accession: A21440

R:Parsons, M.; Nelson, R.G.; Watkins, K.P.; Arabian, N.

Cell 38, 309-316, 1984

variant surface glycoprotein pSic1 - Trypanosoma brucei (fragment)

A:Title: Trypanosome mRNAs share a common 5' spliced leader sequence.

A:Reference number: A90853; MUID:84282716; PMID:6088073

A:Accession: A21440

A:Molecule type: mRNA

A:Residues: 1-8 <PAR>

A:Title: Trypanosome mRNAs share a common 5' spliced leader sequence.

A:Reference number: A90853; MUID:84282716; PMID:6088073

A:Accession: A21440

A:Molecule type: mRNA

A:Residues: 1-8 <PAR>

A:Cross-references: GB:K02195; NID:q162150; PID:q162151

C:Keywords: glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KE 4

Db 4 KE 5

RESULT 44

PT0323

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C:Accession: PT0323

R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity a

A:Reference number: PT0222; MUID:91108337; PMID:1899102

A:Accession: PT0323

A:Molecule type: DNA

A:Residues: 1-8 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 QR 7

Db 5 QR 6

RESULT 45

148934

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C:Accession: 148934

R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takehashi, N.; Maezaki, Y.; Nadeau,

Mamm. Genome 5, 349-355, 1994

A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.

A:Reference number: 148934; MUID:94319082; PMID:8043949

A:Accession: 148934

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-8 <RES>

A:Cross-references: EMBL:005691; NID:q497010; PID:9642826

Query Match 18.2%; Score 2; DB 2; Length 8;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AK 2

Db 7 AK 8

RESULT 46

A54823

C:Species: Mus musculus (house mouse)

C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999

C:Accession: A54823

olfactory receptor 17 - mouse (fragment)

R.Chess, A.; Simon, I.; Cedar, H.; Axel, R.
Cell 78, 823-834, 1994
A:Title: Allelic inactivation regulates olfactory receptor gene expression.
A:Reference number: A54823; MUID:94373818; PMID:8087849
A:Accession: A54823
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <CHE>

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ER 5
I
DB 2 ER 3

RESULT 47

PT0653
T-cell receptor beta chain V-D-J region (121 nt); mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0653
R.Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991

A:Title: Functional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558

A:Accession: PT0653
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <FEF>
A:Experimental source: day 4 postnatal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ER 5
I
DB 7 ER 8

RESULT 48

148935

apolipoprotein A-II - western wild mouse (fragment)

C:Species: Mus spretus (western wild mouse)
C:Date: 02-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 25-Nov-1999

C:Accession: 148935
R.Ko, M.S.; Ward, X.; Horton, J.H.; Haas, J.; Nakatani, N.; Marzaki, Y.; Nakatani, J.H.
Mamm. Genome 5, 349-355, 1994
A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A:Reference number: 148934; MUID:94319582; PMID:8087849
A:Accession: 148935
A:Status: preliminary; translated from cDNA/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <RES>
A:Cross-references: EMBL:U05692; NID:9457011; PIR:AA004051.1; PDB:4G42827

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
I
DB 7 AK 8

RESULT 49

B54823

olfactory receptor 17 - western wild mouse (fragment)

C:Species: Mus spretus (western wild mouse)

C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C:Accession: B54823
R.Chess, A.; Simon, I.; Cedar, H.; Axel, R.
Cell 78, 823-834, 1994
A:Title: Allelic inactivation regulates olfactory receptor gene expression.
A:Reference number: A54823; MUID:94373818; PMID:8087849
A:Accession: B54823
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <CHE>

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ER 5
I
DB 2 ER 3

RESULT 50

A61597

cytochrome P450 AL-1 - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C:Accession: A61597
R.Shimeno, H.; Toda, A.; Ogata, S.; Naganatsu, A.
Drug Metab. Dispos. 19, 291-297, 1991

A:Title: Purification and aminopyrine monooxygenase activity of liver microsomal cy.
A:Reference number: A61597; MUID:91292910; PMID:1676625

A:Accession: A61597
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <SHI>

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KE 4
I
DB 6 KE 7

Search completed: September 30, 2003, 10:09:41
Job time : 15.4167 secs

107	1	18.2	2	18.2	15	1	FIBA_ANADOL	P22501 anas platyr	180	9.1	8	1	URMV_ORCLI	P82455 orconectes
108	2	18.2	2	18.2	15	1	FIRB_ALBUJO	P24927 abizzia ju	181	9.1	8	1	PLP_PBRNA	P81707 brassica na
109	2	18.2	2	18.2	15	1	LEC2_PSRSC	P24585 psophocarpa	182	9.1	8	1	PPK2_PERAM	P82692 periplaneta
110	2	18.2	15	1	1	1	LEC3_PSRSC	P24583 psophocarpa	183	9.1	8	1	PPK3_PERAM	P82618 periplaneta
111	2	18.2	15	1	1	1	LMA2_LOCM1	P24593 locusta mig	184	9.1	8	1	KPCH_PANBO	P08939 pandalus bo
112	2	18.2	15	1	1	1	MAC1_BAC70	P80972 bacillus th	185	9.1	8	1	KI34_BOVIN	P82929 bos taurus
113	2	18.2	15	1	1	1	MAC2_BAC70	P08835 rhodococcus	186	9.1	8	1	UC20_MAIZE	P80632 zea mays (m
114	2	18.2	15	1	1	1	MIRA_MET16	P22949 melanosara	187	9.1	8	1	UF06_MOUSE	P38644 mus musculus
115	2	18.2	15	1	1	1	MM01_PAT	P81523 rattus norv	188	9.1	8	1	UPA1_HUMAN	P30087 homo sapien
116	2	18.2	15	1	1	1	NE03_SQU10	P50973 pseudonaja	189	9.1	8	1	UPAA_HUMAN	P30096 homo sapien
117	2	18.2	15	1	1	1	NXS2_PSE16	P84287 neorhyncha	190	9.1	8	1	WP1_PERAT	P83195 perkinsus a
118	2	18.2	15	1	1	1	ONE1_CNCMY	P80564 polonata	191	9.1	8	1	AL10_CARMA	P81813 carcinus ma
119	2	18.2	15	1	1	1	PG15_PELAC	P84554 sphincta ol	192	9.1	8	1	AL31_CARMA	P81814 carcinus ma
120	2	18.2	15	1	1	1	R13A_SPLC1	P59553 bacillus st	193	9.1	8	1	ALC1_CHURE	P82678 chlamydomon
121	2	18.2	15	1	1	1	RS10_BAC51	P59561 bacillus st	194	9.1	8	1	BS43_SERPL	P83375 seriatia pl
122	2	18.2	15	1	1	1	RS4C_BAC51	P59662 bacillus st	195	9.1	8	1	BOK_CLOPA	P81337 clostridium
123	2	18.2	15	1	1	1	RS6_BAC51	P19647 bacterioph	196	9.1	8	1	CCAP_CARMA	P38556 carcinus ma
124	2	18.2	15	1	1	1	TERM_BPM2	P83447 clostridium	197	9.1	8	1	CUNO_CONGE	P05486 conus geogr
125	2	18.2	15	1	1	1	TH1_CLOPA	P83623 zea mays (m	198	9.1	8	1	CUNO_CONVE	P05487 conus stria
126	2	18.2	15	1	1	1	UC17_MAIZE	P80626 zea mays (m	199	9.1	8	1	DI1_NEPNO	P24916 nephrops no
127	2	18.2	15	1	1	1	UC20_MAIZE	P81705 pinus plac	200	9.1	8	1	UNF1_LUCM1	P16339 locusta mig
128	2	18.2	15	1	1	1	UC27_MAIZE	P81673 pinus plac	201	9.1	8	1	DSIP_RABIT	P01158 oryctolagus
129	2	18.2	15	1	1	1	UNCL_PINES	P84439 metarhizium	202	9.1	8	1	FAR1_CALVO	P41857 calliphora
130	2	18.2	15	1	1	1	UNCL_PINES	P73237 marquellia	203	9.1	8	1	FAR2_CALVO	P41857 calliphora
131	2	18.2	15	1	1	1	UC12_METAN	P80907 mehandact	204	9.1	8	1	FAR2_PANRE	P41873 panagrellus
132	2	18.2	15	1	1	1	UC12_METAN	P44926 atylus alb	205	9.1	8	1	FAR3_CALVO	P41858 calliphora
133	2	18.2	15	1	1	1	UC12_METAN	P44926 atylus alb	206	9.1	8	1	FAR3_PANRE	P83276 macrobrachi
134	2	18.2	15	1	1	1	UC12_METAN	P25412 libellula a	207	9.1	8	1	FAR3_PENMO	P83318 penaeus mon
135	2	18.2	15	1	1	1	UC12_METAN	P25424 melolonth	208	9.1	8	1	FAR4_CALVO	P41859 calliphora
136	2	18.2	15	1	1	1	UC12_METAN	P44555 tabacus atr	209	9.1	8	1	FAR4_PENMO	P83319 penaeus mon
137	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	210	9.1	8	1	FAR5_ASCSU	P43170 ascaris suu
138	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	211	9.1	8	1	FAR5_ASCSU	P41860 calliphora
139	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	212	9.1	8	1	FAR5_CALVO	P82661 panagrellu
140	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	213	9.1	8	1	FAR5_PANRE	P83320 penaeus mon
141	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	214	9.1	8	1	FAR5_PENMO	P41861 calliphora
142	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	215	9.1	8	1	FAR6_CALVO	P83279 macrobrachi
143	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	216	9.1	8	1	FAR6_MACRS	P41862 calliphora
144	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	217	9.1	8	1	FAR7_CALVO	P41862 calliphora
145	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	218	9.1	8	1	FAR8_MACRS	P83281 macrobrachi
146	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	219	9.1	8	1	FAR8_MACRS	P43172 ascaris suu
147	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	220	9.1	8	1	FAR9_ASCSU	P41865 calliphora
148	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	221	9.1	8	1	FAR9_ASCSU	P41868 calliphora
149	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	222	9.1	8	1	FAR9_ASCSU	P41868 calliphora
150	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	223	9.1	8	1	FAR9_ASCSU	P38495 callinectes
151	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	224	9.1	8	1	FAR9_ASCSU	P19346 erythrocebu
152	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	225	9.1	8	1	FAR9_ASCSU	P19344 papio anubi
153	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	226	9.1	8	1	FAR9_ASCSU	P19343 papio hamad
154	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	227	9.1	8	1	FAR9_ASCSU	P19342 theropithe
155	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	228	9.1	8	1	FAR9_ASCSU	P80159 treponema h
156	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	229	9.1	8	1	FAR9_ASCSU	P83350 sarcophaga
157	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	230	9.1	8	1	FAR9_ASCSU	P82992 rhodopseu
158	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	231	9.1	8	1	FAR9_ASCSU	P83058 bombina var
159	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	232	9.1	8	1	FAR9_ASCSU	P08945 litorea aur
160	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	233	9.1	8	1	FAR9_ASCSU	P08946 phyllomedu
161	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	234	9.1	8	1	FAR9_ASCSU	P31799 locusta mig
162	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	235	9.1	8	1	FAR9_ASCSU	P29177 bos taurus
163	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	236	9.1	8	1	FAR9_ASCSU	P19853 clypeaster
164	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	237	9.1	8	1	FAR9_ASCSU	P19852 clypeaster
165	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	238	9.1	8	1	FAR9_ASCSU	P12481 human immu
166	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	239	9.1	8	1	FAR9_ASCSU	P34966 cavia porce
167	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	240	9.1	8	1	FAR9_ASCSU	P04277 homo sapien
168	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	241	9.1	8	1	FAR9_ASCSU	P41492 sarcophaga
169	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	242	9.1	8	1	FAR9_ASCSU	P42995 bufo regula
170	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	243	9.1	8	1	FAR9_ASCSU	P23879 cyprinus ca
171	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	244	9.1	8	1	FAR9_ASCSU	P42998 eisensta foe
172	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	245	9.1	8	1	FAR9_ASCSU	P80027 octopus vul
173	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	246	9.1	8	1	FAR9_ASCSU	P82878 oryctolagus
174	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	247	9.1	8	1	FAR9_ASCSU	P42994 rala clav
175	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	248	9.1	8	1	FAR9_ASCSU	P43000 squalus aca
176	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	249	9.1	8	1	FAR9_ASCSU	P81179 diaprepes a
177	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	250	9.1	8	1	FAR9_ASCSU	P83360 lycopersico
178	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	251	9.1	8	1	FAR9_ASCSU	P82691 periplaneta
179	2	18.2	15	1	1	1	UC12_METAN	P81815 carcinus ma	252	9.1	8	1	FAR9_ASCSU	P82003 bombyx mori

253	1	9.1	9	1	RE42_LITRC	P82075	litoria rub	326	1	9.1	10	1	MOSQ_CLYVA	P19962	clypeaster
254	1	9.1	9	1	SAMP_MUSCA	P19095	mustelus ca	327	1	9.1	10	1	NO40_TOBAC	P55962	nicotiana t
255	1	9.1	9	1	SAP_STOXA	P24047	stomopneute	328	1	9.1	10	1	OPP2_BOVIN	P11180	bos taurus
256	1	9.1	9	1	TAL1_PICJA	P17440	pichia jadi	329	1	9.1	10	1	PAP1_PARMA	P81863	pardachirus
257	1	9.1	9	1	TAL1_PICJA	P17442	pichia jadi	330	1	9.1	10	1	PNEU_HUMAN	P22103	homo sapien
258	1	9.1	9	1	TRC1_CALVO	P41517	calliphora	331	1	9.1	10	1	PNEU_HUMAN	P22196	rattus norv
259	1	9.1	9	1	TRC1_LOCMI	P16223	locusta miq	332	1	9.1	10	1	PORB_MEITH	P80901	melanobact
260	1	9.1	9	1	TRP4_LEUMA	P81736	leucophaea	333	1	9.1	10	1	PPCK_FASHE	P80525	fasciola he
261	1	9.1	9	1	UF04_MOUSE	P38640	mus muscu.u	334	1	9.1	10	1	PVK_LOCM1	P83382	locusta mig
262	1	9.1	9	1	UHA2_HUMAN	P40429	homo sapien	335	1	9.1	10	1	Q2OB_COMTE	P80465	comamonas t
263	1	9.1	9	1	ULAE_HUMAN	P31932	homo sapien	336	1	9.1	10	1	Q2OG_COMTE	P80466	comamonas t
264	1	9.1	9	1	ULAE_HUMAN	P31934	homo sapien	337	1	9.1	10	1	RL16_ACHLA	P29221	acholeptasm
265	1	9.1	9	1	UN19_CLOPA	P81355	clostridium	338	1	9.1	10	1	RRPL_PHODY	P35946	phocine dis
266	1	9.1	9	1	UPA3_HUMAN	P30889	homo sapien	339	1	9.1	10	1	RT02_BOVIN	P82923	bos taurus
267	1	9.1	9	1	UPA6_HUMAN	P30992	homo sapien	340	1	9.1	10	1	SLAP_BACTG	P49325	bacillus th
268	1	9.1	9	1	UPA7_HUMAN	P30993	homo sapien	341	1	9.1	10	1	TEMK_RANTE	P56923	rana tempor
269	1	9.1	9	1	XYLA_STRSU	P19149	stieptomyce	342	1	9.1	10	1	TKL2_LOCM1	P16224	locusta mig
270	1	9.1	9	1	YBEK_AZOV1	P25825	azotobacter	343	1	9.1	10	1	TKL3_LOCM1	P30249	locusta mig
271	1	9.1	10	1	AEGL_AGRAE	P83465	agropyre ae	344	1	9.1	10	1	TKL4_LOCM1	P30250	locusta mig
272	1	9.1	10	1	AH1_PROUSE	P29261	prunus seio	345	1	9.1	10	1	TKNB_CHICK	P19851	gallus gall
273	1	9.1	10	1	ARHX_LOCM1	P81626	locusta miq	346	1	9.1	10	1	TKNB_ONCMY	P28500	oncorhynch
274	1	9.1	10	1	AL19_CARMA	P81422	carcinus ma	347	1	9.1	10	1	TKNB_RANCA	P22689	rana catesb
275	1	9.1	10	1	AMPN_HELAM	P81731	helicoverpa	348	1	9.1	10	1	TKNB_RANCI	P29135	rana ridibu
276	1	9.1	10	1	ANG1_BOTJA	P10581	bothrops ja	349	1	9.1	10	1	TKNB_RANCA	P22690	rana catesb
277	1	9.1	10	1	ANG1_BOVIN	P30317	bos taurus	350	1	9.1	10	1	TKNB_PIG	P01292	sus scrofa
278	1	9.1	10	1	ANG1_CHICK	P30318	gallus gall	351	1	9.1	10	1	TKN_PHYBI	P08610	phyllomedus
279	1	9.1	10	1	APE_CARGI	P83474	capnocytoph	352	1	9.1	10	1	TKS1_AEDAE	P42634	aedes aegypt
280	1	9.1	10	1	BPP2_BOVIN	P30422	bothrops in	353	1	9.1	10	1	TKU2_UREUN	P40752	urechis uni
281	1	9.1	10	1	BPP2_BOVIN	P30422	bothrops ja	354	1	9.1	10	1	TMOF_AEDAE	P19425	aedes aegypt
282	1	9.1	10	1	BPP6_BOVIN	P30426	bothrops in	355	1	9.1	10	1	TP15_NICPL	P19118	nicotiana p
283	1	9.1	10	1	BPP_VIPAS	P31451	viperia asp	356	1	9.1	10	1	TRP5_LEUMA	P81737	leucophaea
284	1	9.1	10	1	BRK_ONCMY	P30671	oncorhynch	357	1	9.1	10	1	TRP6_LEUMA	P81738	leucophaea
285	1	9.1	10	1	CA12_LITCI	P62086	litoria cit	358	1	9.1	10	1	TRP7_LEUMA	P81739	leucophaea
286	1	9.1	10	1	CAER_LITXA	P56264	litoria xan	359	1	9.1	10	1	TRP8_LEUMA	P81740	leucophaea
287	1	9.1	10	1	CARL_SHEEP	P83205	ovis aries	360	1	9.1	10	1	TRP9_LEUMA	P81741	leucophaea
288	1	9.1	10	1	COXH_ONCMY	P80331	oncorhynch	361	1	9.1	10	1	UH05_RAT	P36573	rattus norv
289	1	9.1	10	1	COXK_ONCMY	P80342	oncorhynch	362	1	9.1	10	1	UHA3_HUMAN	P40930	homo sapien
290	1	9.1	10	1	COXO_RAT	P80342	rattus norv	363	1	9.1	10	1	UPA2_HUMAN	P30088	homo sapien
291	1	9.1	10	1	COXQ_HUO-B	P80342	rattus norv	364	1	9.1	10	1	UPA4_HUMAN	P30090	homo sapien
292	1	9.1	10	1	COXQ_PABIT	P80346	cryptolagus	365	1	9.1	10	1	UPA5_HUMAN	P30091	homo sapien
293	1	9.1	10	1	EST1_LACTA	P83758	lactobacill	366	1	9.1	10	1	UPA8_HUMAN	P30094	homo sapien
294	1	9.1	10	1	ESTA_SCHGA	P81012	schizaphis	367	1	9.1	10	1	UPA9_HUMAN	P30095	homo sapien
295	1	9.1	10	1	FAR2_PENMO	P83317	penaeus mon	368	1	9.1	10	1	UPA1_HUMAN	P32118	homo sapien
296	1	9.1	10	1	FAR5_MACRS	P83278	macrobrachi	369	1	9.1	10	1	UPA6_HUMAN	P32080	homo sapien
297	1	9.1	10	1	FAR6_PANRE	P82560	panagrellus	370	1	9.1	10	1	UPA7_HUMAN	P34990	homo sapien
298	1	9.1	10	1	FAR7_MACRS	P83280	macrobrachi	371	1	9.1	10	1	UPH3_MORMO	P17339	morganelia
299	1	9.1	10	1	FAR8_CALVO	P43867	calliphora	372	1	9.1	10	1	UXA2_CHLTR	P38003	chlamydia t
300	1	9.1	10	1	FAR9_LOCM1	P38553	locusta miq	373	1	9.1	10	1	UXB1_YEAST	P99012	saccharomyc
301	1	9.1	10	1	FAR1_MASSE	P18523	maduca sex	374	1	9.1	10	1	VEG6_BACSU	P80699	bacillus su
302	1	9.1	10	1	FAR1_MASSE	P42540	mytilus ed	375	1	9.1	10	1	ANGT_CRIGE	P09037	crinia geor
303	1	9.1	10	1	FAR1_MASSE	P42540	mytilus ed	376	1	9.1	10	1	ASL1_BACSF	P83146	bacteroides
304	1	9.1	10	1	FAR1_MASSE	P42540	mytilus ed	377	1	9.1	10	1	ASL1_BACSF	P83146	bacteroides
305	1	9.1	10	1	GAJU_HUMAN	P02158	homo sapien	378	1	9.1	10	1	BPP3_BOVIN	P30423	bothrops in
306	1	9.1	10	1	GLEM_HUMAN	P02728	homo sapien	379	1	9.1	10	1	BPP4_BOVIN	P30424	bothrops in
307	1	9.1	10	1	GONI_ALUM1	P37041	alligator m	380	1	9.1	10	1	BPPB_AGRHA	P01021	agkistrodon
308	1	9.1	10	1	GONI_CHEPR	P80677	chelyosoma	381	1	9.1	10	1	BPPB_AGRHA	P01021	agkistrodon
309	1	9.1	10	1	GONI_CLIPA	P81749	clupea pall	382	1	9.1	10	1	CA21_LITCI	P42562	agkistrodon
310	1	9.1	10	1	GONI_PETMA	P64378	petromyzon	383	1	9.1	10	1	CA22_LITCI	P82087	litoria cit
311	1	9.1	10	1	GONI_PETMA	P80678	chelyosoma	384	1	9.1	10	1	CA31_LITCI	P82088	litoria cit
312	1	9.1	10	1	GONI_PETMA	P37043	gallus gall	385	1	9.1	10	1	CA32_LITCI	P82090	litoria cit
313	1	9.1	10	1	GONI_PETMA	P20367	oncorhynch	386	1	9.1	10	1	CA41_LITCI	P82091	litoria cit
314	1	9.1	10	1	GONI_PETMA	P30948	petromyzon	387	1	9.1	10	1	CA42_LITCI	P82092	litoria cit
315	1	9.1	10	1	GONI_SQUA1	P27429	squalus aca	388	1	9.1	10	1	CEP1_ACHFU	P22790	achatina fu
316	1	9.1	10	1	GRP_RANCI	P23260	rana ridibu	389	1	9.1	10	1	COR2_PERAM	P11496	periplaneta
317	1	9.1	10	1	GS09_BACSU	P60243	bacillus su	390	1	9.1	10	1	COXA_CANFA	P99501	canis fami
318	1	9.1	10	1	HTF1_RMMI	P81110	romalea mic	391	1	9.1	10	1	CS15_BACSU	P81095	bacillus su
319	1	9.1	10	1	HTF2_ARMH	P11385	carausius m	392	1	9.1	10	1	CX5A_CONAL	P58848	conus aulic
320	1	9.1	10	1	HTF3_RLZE	P16353	heliopsis z	393	1	9.1	10	1	CX5B_CONAL	P58849	conus aulic
321	1	9.1	10	1	HTF4_NAUCI	P10939	nauphoeta c	394	1	9.1	10	1	CX11_CONNR	P58807	conus marmo
322	1	9.1	10	1	HTF5_JAHAI	P14596	telanus atr	395	1	9.1	10	1	ES1_RAT	P81350	clostridium
323	1	9.1	10	1	LARA_JATMC	P13270	jatropha mu	396	1	9.1	10	1	FAK6_PENNO	P56571	rattus norv
324	1	9.1	10	1	LPK2_LOCM1	P21144	leucophaea	397	1	9.1	10	1	FAK9_CALVO	P83321	penaeus mon
325	1	9.1	10	1	LSK2_LEUMA	P41488	locusta miq	398	1	9.1	10	1	HS70_PINPS	P81672	pinus pinas

394	1	9.1	11	1	LAGB_ONCMY	P4518 caccorhynch	472	1	9.1	12	1	UR2B_CATCO	P04559 catostomus
400	1	9.1	11	1	LPW_THETH	P0524 thermus the	473	1	9.1	12	1	UR2B_CYPCA	P04561 cyprinus ca
401	1	9.1	11	1	LSK_LEUMA	P0428 leucophaea	474	1	9.1	12	1	UR2_GILMI	P01147 gillichthys
402	1	9.1	11	1	LSKP_PERAM	P3685 periplaneta	475	1	9.1	12	1	UR2_POLSP	P81022 polyodon sp
403	1	9.1	11	1	MHI_KLEPN	P89580 klebsiella	476	1	9.1	12	1	UR2_SCYCA	P35490 scyllorhinu
404	1	9.1	11	1	MLG_THETS	P41989 theromyzon	477	1	9.1	12	1	V14K_WSSV	P82006 white spot
405	1	9.1	11	1	MGRN_HUMAN	P01163 homo sapien	478	1	9.1	12	1	V23K_WSSV	P82005 white spot
406	1	9.1	11	1	NUHM_CANFA	P42520 canis fami	479	1	9.1	12	1	V25K_WSSV	P82004 white spot
407	1	9.1	11	1	PKK_PERAM	P41437 periplaneta	480	1	9.1	12	1	XYLA_STRVN	P14405 streptomyce
408	1	9.1	11	1	RAN_KANI	P0635 rana pipien	481	1	9.1	13	1	ACT7_SOYBN	P15987 glycine max
409	1	9.1	11	1	RELI_LITRU	P5274 litoria rub	482	1	9.1	13	1	ADFB_TENMO	P83109 tenebrio mo
410	1	9.1	11	1	RK2_PONAR	P4234 conspoholis	483	1	9.1	13	1	AH4_PROSE	P29262 pinus sero
411	1	9.1	11	1	RK2_PONAR	P4179 chandipara	484	1	9.1	13	1	HLAC_STRGR	P81173 streptomyce
412	1	9.1	11	1	RS3_ONCMY	P8328 caccorhynch	485	1	9.1	13	1	RUMI_PSEGU	P42991 pseudophryn
413	1	9.1	11	1	TEPI_PROVO	P41341 proteus vi	486	1	9.1	13	1	BP37_LEUMA	P81754 leucophaea
414	1	9.1	11	1	TINI_HOPTI	P82631 hoplobatr	487	1	9.1	13	1	BPPI_BOTJA	P01030 bothrops ja
415	1	9.1	11	1	TINI_HOPTI	P82634 hoplobatr	488	1	9.1	13	1	CE71_LITEF	P82051 litoria ewi
416	1	9.1	11	1	TKC2_CALVO	P41518 calliphora	489	1	9.1	13	1	CHEP_PARID	P42718 parapolybia
417	1	9.1	11	1	TKN1_PSECU	P42986 pseudophryn	490	1	9.1	13	1	CPI_APLCA	O10998 aplysia cal
418	1	9.1	11	1	TKN1_GREPN	P82026 peroteia i	491	1	9.1	13	1	CRBL_ICASP	P17237 icaria sp.
419	1	9.1	11	1	TKN1_GREPN	P06612 peroteia i	492	1	9.1	13	1	CRBL_VESMA	P17232 vespa manda
420	1	9.1	11	1	TKN2_PSECU	P42987 pseudophryn	493	1	9.1	13	1	CRBL_VESTR	P17231 vespa tropi
421	1	9.1	11	1	TKN2_PSECU	P06616 peroteia i	494	1	9.1	13	1	CRBL_VESTR	P17231 vespa tropi
422	1	9.1	11	1	TKN3_PSECU	P42948 pseudophryn	495	1	9.1	13	1	CXA2_CONGE	P01520 conus geogr
423	1	9.1	11	1	TKN4_PSECU	P42989 pseudophryn	496	1	9.1	13	1	CXAA_CONST	P28878 conus stria
424	1	9.1	11	1	TKN5_PSECU	P42990 pseudophryn	497	1	9.1	13	1	CXLA_CONNR	P58810 conus marmo
425	1	9.1	11	1	TKNA_CHICK	P59850 galus gall	498	1	9.1	13	1	E121_LITRU	P82097 litoria rub
426	1	9.1	11	1	TKNA_GAUMC	P26498 gadus morhu	499	1	9.1	13	1	E122_LITRU	P82098 litoria rub
427	1	9.1	11	1	TKNA_BOESE	P01290 equus cabai	500	1	9.1	13	1	EP65_HUMAN	P54963 homo sapien
428	1	9.1	11	1	TKNA_ONCMY	P28499 caccorhynch							
429	1	9.1	11	1	TKNA_RANCA	P28486 rana catesb							
430	1	9.1	11	1	TKNA_SCYTA	P41333 scyllorhinu							
431	1	9.1	11	1	TKN_PHYFU	P05615 physciaemus							
432	1	9.1	11	1	UF05_MOUSE	P36643 mus musculu							
433	1	9.1	11	1	ULAG_HUMAN	P41933 homo sapien							
434	1	9.1	12	1	CALM_TECTH	P05555 tetrahymena							
435	1	9.1	12	1	CD14_LITXA	P56245 litoria xan							
436	1	9.1	12	1	CD14_LITXA	P56246 litoria xan							
437	1	9.1	12	1	CXA2_CONGE	P05993 conus imper							
438	1	9.1	12	1	CXSF_CONIE	P56846 conus texti							
439	1	9.1	12	1	PA31_CALVO	P41869 calliphora							
440	1	9.1	12	1	E121_SARBU	P83349 sarcophaga							
441	1	9.1	12	1	PREL_LITIN	P82021 litoria int							
442	1	9.1	12	1	GRAR_RANRO	P40734 rana rufoa							
443	1	9.1	12	1	HCY1_CAKRA	P83176 carcinus ma							
444	1	9.1	12	1	HEPI_BACSE	P83054 bacteroides							
445	1	9.1	12	1	LICH_BACSE	P82507 bacillus li							
446	1	9.1	12	1	LMT1_LORM	P22395 locusta miq							
447	1	9.1	12	1	LASK_LORM	P47733 locusta miq							
448	1	9.1	12	1	N440_LITLA	P22426 lotus japon							
449	1	9.1	12	1	N440_SEBRI	P24359 sordaria to							
450	1	9.1	12	1	N040_SRYAN	P55946 glycine max							
451	1	9.1	12	1	NIDM_CANFA	P54713 canis fami							
452	1	9.1	12	1	OPS3_DROAVI	P7645 drosophila							
453	1	9.1	12	1	PA21_MICPEM	P25072 micropus fu							
454	1	9.1	12	1	PA2B_VIPBO	P31859 vipera beti							
455	1	9.1	12	1	PKK4_PERAM	P82619 periplaneta							
456	1	9.1	12	1	PKK4_PERAM	P82690 periplaneta							
457	1	9.1	12	1	PSP3_FHYTA	P80662 physcomitre							
458	1	9.1	12	1	PKR2_FERAM	P41555 periplaneta							
459	1	9.1	12	1	RFL_QJNSP	P58805 conus spur							
460	1	9.1	12	1	TA10_EREME	P01371 tremella me							
461	1	9.1	12	1	LN2_HOPTI	P42652 hoplobatr							
462	1	9.1	12	1	TINI_HOPTI	P82631 hoplobatr							
463	1	9.1	12	1	TKN1_KASMA	P88613 kassina mac							
464	1	9.1	12	1	TKN2_KASMA	P88614 kassina mac							
465	1	9.1	12	1	TKN_KASSE	P08611 kassina sen							
466	1	9.1	12	1	TM2A_MEIMA	P80652 methanosar							
467	1	9.1	12	1	UKA2_HUMAN	P41144 homo sapien							
468	1	9.1	12	1	GLAL_MOUSE	P99032 mus musculu							
469	1	9.1	12	1	UN19_CICPA	P81359 ciostriidiam							
470	1	9.1	12	1	UP01_CABEL	P57954 caccorhabd							
471	1	9.1	12	1	UR2A_CATCO	P54958 catostomus							

ALIGNMENTS

RESULT 1																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
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AC Q46490;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 40S ribosomal protein S19 (Fragment)
 GN RPSS OR RPS19
 OS Clover yellow edge phytoplasm
 OC Bacteria; Firmicutes; Mollicutes; Actinobacteriales
 OC Actinobacteriales; Mollicutes; Actinobacteriales
 OC NCBI_TaxID=35775;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:94350802; PubMed:5071196;
 RA Gundersen C.E., Lee I.M., Reiner S.A., Davis R.P., Kinoshita J.L.;
 RT "Phylogeny of mycoplasma-like organisms (Mycoplasmas): a basis for
 their classification."
 RI J. Bacteriol. 176:5244-5254(1994)
 CC -!- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S15 THAT BINDS STRONGLY
 CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
 CC
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 CC
 DR FMH1: L27019; AAA83940.1;
 DR HAMAP: MF_035311; 1;
 DR InterPro: IPR002222; Ribosomal_S19
 DR PROSITE: PS00323; RIBOSOMAL_S19; PARTIAL
 DR Ribosomal protein; rRNA-binding
 FT N-TER
 FT N-TER
 SQ SEQUENCE 12 AA; 1409 MW; 40C478EF833AA3 CRC64;
 Query Match 27.3%; Score 3; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.2e-03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKK 3
 Db 3 AKK 5
 RESULT 4
 ID LPAA_P0001 STANDARD; PRI: 14 AA
 AC P01411;
 DT 15-DEC-1998 (Rel. 37, Created)
 DE 15-DEC-1998 (Rel. 37, Last sequence update)
 DE 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Lipid A-associated protein (Fragment)
 OS Porphyromonas gingivalis (Bacteroides classis)
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Porphyromonadaceae; Porphyromonadaceae
 CC NCBI_TaxID=837;
 RN [1]
 RP SEQUENCE
 RX STRAIN-W50; PubMed:9846747;
 RA Sharp L., Poole S., Reddi K., Fletcher J., Nair S., Wilson M.,
 RA Curtis M., Henderson B., Tabona P.
 RT "A lipid A-associated protein of Porphyromonas gingivalis, derived
 RT from the haemagglutinating domain of the R1 protease gene family, is
 RT a potent stimulator of interleukin 6 synthesis."
 RL Microbiology 144:3019-3026(1998)
 CC -!- FUNCTION: IS ASSOCIATED WITH LIPID A, A PHOSPHORYLATED GLYCOLIPID
 CC THAT ANCHORS THE LIPOLYSACCHARIDE TO THE OUTER MEMBRANE OF THE
 CC CELL.
 CC VARIANT 12 12 G -> F
 FT N-TER 13 13

SQ SEQUENCE 13 AA; 1346 MW; 38EA796EAF6A3AB7 CRC64;
 Query Match 27.3%; Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.1e-03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 KDT 10
 Db 8 KDT 10
 RESULT 4
 ID MAST_VESPA STANDARD; PRI: 14 AA
 AC P21654;
 DT 01-MAY-1991 (Rel. 18, Created)
 DE 01-MAY-1991 (Rel. 18, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mastoparan B.
 OS Vespa basalis (Hornet).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=7444;
 RN [1]
 RP SEQUENCE
 RC TISSUE-Venom;
 RX MEDLINE-91174755; PubMed-206909;
 RA Lo C.-L., Hwang L.-L.;
 RT "Structure and biological activities of a new mastoparan isolated
 RT from the venom of the hornet Vespa basalis."
 RI Biochem. J. 274:453-456(1991).
 CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
 CC that couple to phospholipase C.
 CC PIR: S14336; S14336.
 DR Mast cell degranulation; Amidation
 FT MCD_RES 14 14
 FT SEQUENCE 14 AA; 1613 MW; D35944CA193A19A2 CRC64;
 Query Match 27.3%; Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.2e-03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKK 5
 Db 10 AKK 12
 RESULT 5
 ID MAST_VESCR STANDARD; PRI: 14 AA
 AC P01516;
 DT 21-JUL-1986 (Rel. 01, Created)
 DE 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mastoparan C.
 OS Vespa crabro (European hornet).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=7445;
 RN [1]
 RP SEQUENCE
 RC TISSUE-Venom;
 RX MEDLINE-84289390; PubMed-6206053;
 RA Argolas A., Pisano J.J.;
 RT "Isolation and characterization of two new peptides, mastoparan C and
 RT crabrolin, from the venom of the European hornet, Vespa crabro."
 RI J. Biol. Chem. 259:10106-10111(1984).
 CC -!- FUNCTION: Mast cell degranulating peptide. Activates G proteins
 CC that couple to phospholipase C.
 CC PIR: A01779; QMVHP2.
 DR Mast cell degranulation; Amidation.
 FT N-TER 12 12 G -> F
 FT N-TER 13 13

```

FT MDL_RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA: 1508 MW: 5500676.056AE1B7 79664.

Query Match: 27.9% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 10 AKK 12

RESULT 6
MAST_VESPA
ID MAST_VESPA STANDARD: PRI: 14 AA.
AC P01514
DT 21-JUL-1986 (Rel. 01, Created)
DI 21-JUL-1986 (Rel. 01, Last sequence update)
DE Mastoparan M (Mast cell degranulating peptide)
OS Vespa manducaria (Hornet)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
CX NCBI_TaxID=7446;
RN 1;
RP SEQUENCE AND SYNTHESIS.
RC TISSUE: Venom.
RX MEDLINE=80155338; PubMed=540463;
RA Hirai Y., Yasuhara T., Yoshida H., Nakajima T.;
RT "A new mast cell degranulating peptide homologous to mastoparan in
RL Chem. Pharm. Bull. 27:1942-1943(1979).
OC 1- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
DR PIR: AC1776; QMVAW.
DR PDB: 107N; 20-JUN-01.
KW Mast cell degranulating peptide; 3D-structure.
FT MDL_RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA: 1480 MW: 4760674.026AD7B00DD CRC64.

Query Match: 27.9% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 10 AKK 12

RESULT 7
MAST_VESMA
ID MAST_VESMA STANDARD: PRI: 14 AA.
AC P04205
DT 20-MAR-1987 (Rel. 04, Created)
DI 20-MAR-1987 (Rel. 04, Last sequence update)
DE Mastoparan M (Mast cell degranulating peptide)
OS Vespa manducaria (Hornet)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
CX NCBI_TaxID=7446;
RN 1;
RP SEQUENCE.
RC TISSUE: Venom.
RA Hirai Y., Yasuhara T., Yoshida H., Nakajima T.;
RT "A new mast cell degranulating peptide homologous to mastoparan in
RL Biomed. Res. 2:447-449(1981).
OC 1- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
DR PIR: AC1777; QMVHM.

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KW Mast cell degranulation; Amidation.
FT MDL_RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA: 1480 MW: 485476CA1D7B00DD CRC64.

Query Match: 27.9% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 10 AKK 12

RESULT 8
MAST_VESXA
ID MAST_VESXA STANDARD: PRI: 14 AA.
AC P01515
DT 21-JUL-1986 (Rel. 01, Created)
DI 21-JUL-1986 (Rel. 01, Last sequence update)
DE Mastoparan X (MP-X)
OS Vespa xanthoptera (Japanese hornet)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
CX NCBI_TaxID=7448;
RN 1;
RP SEQUENCE.
RC TISSUE: Venom.
RX MEDLINE=80155338; PubMed=540463;
RA Hirai Y., Kuwada M., Yasuhara T., Yoshida H., Nakajima T.;
RT "A new mast cell degranulating peptide homologous to mastoparan in
RL Chem. Pharm. Bull. 27:1945-1946(1979).
OC 1- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
DR PIR: AC1778; QMVHX.
DR PDB: 1A13; 16-FEB-99.
KW Mast cell degranulation; Amidation; 3D-structure.
FT MDL_RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA: 1509 MW: 57506D7AA7AB0DD CRC64.

Query Match: 27.9% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 10 AKK 12

RESULT 9
KNN_RANMA
ID KNN_RANMA STANDARD: PRI: 14 AA.
AC P40531
DT 01-FEB-1995 (Rel. 01, Created)
DI 01-FEB-1995 (Rel. 01, Last sequence update)
OC 1- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
DR PIR: AC1779; QMVHXX.
DR PDB: 1A13; 16-FEB-99.
KW Mast cell degranulation; Amidation; 3D-structure.
FT MDL_RES 14 14 AMIDATION.
SQ SEQUENCE 14 AA: 1509 MW: 57506D7AA7AB0DD CRC64.

Query Match: 27.9% Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 10 AKK 12

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DE Rana margaritae (Chinese frog).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranidae; Rana.
 OX NCBI_TaxID=121156;
 RN [1]
 RP Kunitzmaradin.
 RC TISSUE: Skin secretion;
 RX MEDLINE=90026452; PubMed=280554;
 RA Tang Y.Q., Tian S.H., Wu S.X., Hua J., Wu D.F., Zhao E.M., Lu Y.A.,
 RA Zhu Y.Q., Zou G., Tsou K.;
 RT *Isolation and structure of kunitzmaradin, a new tachykinin from the
 RT skin of Chinese frog Rana margaritae*.
 RL Sci. China, Ser. B, Chem. Life Sci. Earth Sci. 42(5): 579(1999).
 RN [2]
 RP SYNTHESIS.
 RX MEDLINE=92253600; PubMed=2140887;
 RA Lu Y.A., Peng J.L., Zhu Y.Q., Wu S.X., Tang Y.Q., Tian S.H., Zou G.,
 RA *Synthesis and biological activity of a new frog skin peptide,
 RA kunitzmaradin*.
 RL Sci. China, Ser. B, Chem. Life Sci. Earth Sci. 43(7): 177(1996).
 CC *FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOLVE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC *SUBCELLULAR LOCATION: Secreted.
 CC *TISSUE SPECIFICITY: Skin.
 CC *SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DE INTERPRO: IPR002040; Tachykinin.
 DR PROSITE: PS00267; TACHYKININ_1
 KW Amphibia; defense peptide; Tachykinin; Neuropeptide; Acylation.
 FT MDS RES 14 14 AMIDATION
 SQ SEQUENCE 14 AA: 1617 MW: 1459.668 Da; 16730 Da; CR64;
 Query Match 27.4% Score 3; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.2e-03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKK 3
 DB 7 AKK 9
 RESULT 19
 CXXLTHDB
 ID CXXLTHDB STANDARD; PRI: 15 AA;
 AC P80978;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Cytochrome c oxidase polypeptide γ subunit (fragment)
 OS Thomas goby (Bigeye tuna)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Eupercaria; Neoclinostei;
 CC Acanthomorpha; Acanthopterygii; Perciformes; Scombridae;
 CC Scombridae; Thunnus.
 OX NCBI_TaxID=8241;
 RN [1]
 RP SEQUENCE.
 RC TISSUE: Heart;
 RX MEDLINE=97454291; PubMed=9430465;
 RA Arnold S., Lee I., Kim M., Song E., Fisher D., Felleman E.,
 RA Kadenbach B.;
 RT *The subunit structure of cytochrome oxidase from tuna heart and
 RT liver*.
 RL Eur. J. Biochem. 248:99-103(1997).
 CC *FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC *CATALYTIC ACTIVITY: 4 ferrioxochrome + 2 H⁺ + 4 ferrioxochrome
 CC + 2 H₂O;
 CC *SUBCELLULAR LOCATION: Mitochondrion inner membrane
 DR ECR: S77987; S77987.

KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 1
 FT NON_CONS 8
 FT NON_TER 9
 FT NON_TER 15
 SQ SEQUENCE 15 AA: 1696 MW: 4240.966 Da; 4240.966 Da; CR64;
 Query Match 27.4% Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e-03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKK 3
 DB 7 AKK 9
 RESULT 11
 GR78_HORSE
 ID GR78_HORSE STANDARD; PRI: 15 AA;
 AC P16392;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE 78 kDa glucose-regulated protein (GRP 78) (Immunoglobulin heavy chain
 DE binding protein) (Bip) (Fragment).
 GN HSPAS OR GRP78
 OS Equus caballus (Horse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90147817; PubMed=1689155;
 RA Oblas B., Hoyd N.D., Luben-Narod J., Reyes V.E., Leeman S.E.;
 RT *Isolation and identification of a polypeptide in the Hsp 70 family
 RT that binds substance P*.
 RL Biochem. Biophys. Res. Commun. 166:978-983(1990).
 CC *FUNCTION: Probably plays a role in facilitating the assembly of
 CC multimeric protein complexes inside the ER.
 CC *SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
 CC *SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
 DE INTERPRO: IPR01023; HSP70.
 DR PROSITE: PS00247; HSP70_1; PARTIAL.
 DR PROSITE: PS00329; HSP70_2; PARTIAL.
 DR PROSITE: PS00365; HSP70_3; PARTIAL.
 KW ATP-binding; Endoplasmic reticulum.
 FT NON_TER 15
 SQ SEQUENCE 15 AA: 1647 MW: 81190.210 Da; 81190.210 Da; CR64;
 Query Match 27.4% Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.2e-03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KKE 4
 DB 5 KKE 7
 RESULT 12
 ACTCAPMA
 ID ACTCAPMA STANDARD; PRI: 8 AA;
 AC P80709;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Actin (Fragment).
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 CC Eubranchia; Portunidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6757;
 RN [1]
 RP SEQUENCE.
 RA Lachaise F., Sureau G., Carpentier G., Granjeon E., Webster S.,

RA Bagdasarian D.:
 RT "A transaldolase. An enzyme implicated in crab steroidogenesis".
 RL Eukaryote 5:23-32(1996).
 CC -1- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
 IN VARIOUS TYPES OF CELL MOTILITY AND ARE UNUSUALLY OVERLY EXPRESSED
 IN ALL EUKARYOTIC CELLS.
 CC -2- SUBCELLULAR LOCATION: CYTOSOLSMIC.
 CC -3- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PT OF THIS PROTEIN IS:
 6.8. ACTS MW IS: 46 kDa.
 CC -4- SIMILARITY: Belongs to the actin family.
 DR InterPro: IPR004001; Actin.
 DR PROSITE: PS00400; Actin-like.
 DR PROSITE: PS00406; ACTINS 1; PARTIAL.
 DR PROSITE: PS00432; ACTINS 2; PARTIAL.
 DR PROSITE: PS01132; ACTINS_ACT LIKE; PARTIAL.
 KW Structural protein.
 FT NON_TER : 1
 FT NON_TER : 8
 SQ SEQUENCE 8 AA: 976 MW: 1424035AB2FAABX CR 04:
 Query Match 18.2% Score 2: DB 1: Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 RK 8
 DB 7 RK 8
 RESULT 14
 NS1_MYCTD
 ID NS1_MYCTD STANDARD: P51: 8 AA.
 AC P15507
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuropeptide B.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovidae;
 CC Bovidae; Bovidae; Bos.
 CC NCBI_TaxID:9911;
 RN 1;
 RP SEQUENCE.
 RX MEDLINE-86067985; PubMed-3865155.
 RA Yang H, Yip J, Pratta W, Majumdar A, Gupta P
 RT "Isolation, sequencing, synthesis, and pharmacological
 characterization of two brain neuropeptides that modulate the action
 of morphine."
 RL Proc Natl Acad Sci USA 82:1000-1004, 1985.
 CC -1- FUNCTION: MODULATES THE ACTION OF MORPHINE.
 DR PIR: R24749; R24749.
 KW Neuropeptide; Amidation.
 FT MODRES : 8 B AMIDATION
 SQ SEQUENCE 8 AA: 1082 MW: 870416377b36729 CR 04:
 Query Match 18.2% Score 2: DB 1: Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 QR 7
 DB 6 QR 7
 RESULT 14
 NS1_MYCTD
 ID NS1_MYCTD STANDARD: P51: 8 AA.
 AC P81152
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE 30 kDa non secretory protein 3 (Fragment).
 OS Mycobacterium tuberculosis
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 CC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 CC NCBI_TaxID-1773;
 RN 1;
 RP SEQUENCE.
 RC STRAIN-H37RV;
 RA Prasad H.K., Annamanna P.S.;
 RS Submitted (DEC-1997) to the SWISS-PROT data bank.
 CC -1- CAUTION: We are unable to find this protein in the translation of
 the genome of strain H37RV.
 FT NON_TER : 1
 FT NON_TER : 8
 SQ SEQUENCE 8 AA: 819 MW: 8840430B19C0C2D2 CR 64:
 Query Match 18.2% Score 2: DB 1: Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AK 2
 DB 7 AK 8
 RESULT 15
 RS1_ERWCH
 ID RS1_ERWCH STANDARD: PRT: 8 AA.
 AC P37985;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE 30S ribosomal protein S1 (Fragment).
 CC RPSA
 OS Erwinia chrysanthemi.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Pectobacterium.
 CC NCBI_TaxID-556;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN-3937;
 RA Eschillie A., Toussaint A., Faclen M.;
 RL Submitted (AUG-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: BINDS MRNA; THUS FACILITATING RECOGNITION OF THE
 INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT
 SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
 CC -2- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC EMBL: X74750; CAA52769.1;
 DR PIR: S37141; S37141.
 KW Ribosomal protein; Repeat; RNA-binding.
 FT NON_TER : 1
 SQ SEQUENCE 8 AA: 837 MW: 9E18733DC5B339CD CR 64:
 Query Match 18.2% Score 2: DB 1: Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AK 2
 DB 5 AK 6
 RESULT 16
 RS7_MYC11

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ID RS7_MYCIT STANDARD: PRT: 8 AA.
AC E33564;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S7 (Fragment).
GN RPS3.
OS Mycobacterium intracellulare.
OC Bacteria; Actinobacteriales; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
CX NCBI_TaxID=1767;
FN [1]
SE SEQUENCE FROM N.A.
MEDLINE=94197130; PubMed=8451117;
NAIR J., Kouse D.A., Morris S.L.;
RT "Nucleotide sequence analysis of the ribosomal S12 gene of
RT Mycobacterium intracellulare."
RL Nucleic Acids Res. 21:1039-1049(1993).
CC -!- FUNCTION: One of the primary rRNA binding proteins. It binds
CC directly to 16S rRNA where it nucleates assembly of the head
CC domain of the 30S subunit. Is located at the subunit interface
CC close to the decoding center, probably blocks exit of the E-site
CC tRNA (by similarity).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
CC and S11 (by similarity).
CC -!- SIMILARITY: BELONGS TO THE S/P FAMILY OF RIBOSOMAL PROTEINS.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation;
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.sib.ch/
CC or send an email to license@isb.sib.ch).
CC
DR EMBL: L08171; AAA25376.1;
DR PIR: S35538; S35538.
DR HAMAP: MF_00480; 1;
DR InterPro: IPR000235; Ribosomal_S7.
DR PROSITE: PS00052; RIBOSOMAL_S7; PARTIAL.
KW Ribosomal protein; rRNA-binding; rRNA binding.
FT INIT_MET 0 0 BY SIMILARITY.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 850 MW; 632761c768732417 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KK 8
DB 2 KK 3

RESULT 17
UH09_RAT STANDARD: PRT: 8 AA.
ID UH09_RAT
AC P56575;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Unknown protein from 2D-page of heart tissue (Spot 49) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CX NCBI_TaxID=101116;
FN [1]
SE SEQUENCE.
RC STRAIN-Histar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheller C., Kozlitz-Zachrasek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED P1 OF THIS UNKNOWN

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CC PROTEIN IS: 8.9, ITS MW IS: 42 kDa.
FT NON_TER 8
SQ SEQUENCE 8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ER 5
DB 2 ER 3

RESULT 18
COXE_IH00R STANDARD: PRT: 9 AA.
ID COXE_IH00R
AC P80575;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Cytochrome c oxidase polypeptide via (EC 1.9.3.1) (Fragment).
OS Thunnus obesus (Bigeye tuna).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
CX NCBI_TaxID=8241;
FN [1]
SE SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=97454291; PubMed=9310466;
RA Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
RA Kadenbach B.;
RT "The subunit structure of cytochrome-c oxidase from tuna heart and
RT liver."
RC Eur. J. Biochem. 248:99-103(1997).
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
DR PIR: S77984; S77984.
DR InterPro: IPR001349; COX6A.
DR PROSITE: PS01329; COX6A; PARTIAL.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1146 MW; 62E072C9CB0776DB CRC64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KE 4
DB 1 KE 2

RESULT 19
HUTU_KLEAE STANDARD: PRT: 9 AA.
ID HUTU_KLEAE
AC P12381;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Urocanate hydratase (EC 4.2.1.49) (Urocanase) (Imidazolonepropionate
DE hydrolase) (Fragment).
GN HUTU.
OS Klebsiella aerogenes.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Klebsiella.

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DR NCBI_TaxID-28451;
DR L;
DR SEQUENCE FROM N.A.
DR MEDLINE-86198018; PubMed-2643345;
RA Newkirk A.J., Baldauf S.A., Hudspeeth M.E.S., Bender R.A.;
RT "Bidirectional promoter in the hnf (P) region of the histidine
RT utilization (huf) operons from Klebsiella aerogenes.";
RL J. Bacteriol. 170:2240-2246(1988).
RL [2]
DR SEQUENCE FROM N.A.
DR MEDLINE-90368611; PubMed-2203754;
RA Schwacha A., Bender R.A.;
RT "Nucleotide sequence of the gene encoding the repressor for the
RT histidine utilization genes of Klebsiella aerogenes.";
RL J. Bacteriol. 172:5477-5483(1990)
CC -1- CATALYTIC ACTIVITY: 3-(5-oxo-4,5-dihydroxy-2H-imidazol-4-yl)propanoate + urocanate -> H2O.
CC -1- COFACTOR: Binds 1 NAD per subunit (By similarity).
CC -1- PATHWAY: Histidine degradation; Second step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE UROCANASE FAMILY.
CC
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CC
CC -----
DR EMBL; M19665; AAA25078.1;
DR EMBL; M34604; AAA25076.1;
DR HAMAP; MF_00577; 1.
DR InterPro: IPR000193; Urocanase.
DR PROSITE; PS01233; UROCANASE; PARTIAL.
KW Histidine metabolism; Lyase; NAD.
FT N/N-TER 9
FT N/N-TER 9
SQ SEQUENCE 9 AA: 1240 MW: 97604156.426605 CRC64:
-----
Query Match 18.2%, Score 21, DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RQ 6
DB 7 RQ 8

RESULT: 20
LMT32XMI
ID LMT32XMI STANDARD; PRT; 9 AA
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DE 01-NOV-1995 (Rel. 32, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamytroptin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Phryganea;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locustina
DX NCBI_TaxID-7004;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;
RA Schoofs L., Holman G.M., Hayes T.K., Naeffels R.D., Kochansky J.P.,
RA de Loof A.;
RT "Isolation, identification and synthesis of locustamytroptin III and
RT IV, two additional neuropeptides of Locusta migratoria; members of the
RT locustamytroptin peptide family.";
RL Insect Biochem. Mol. Biol. 22:447-452(1992).
CC -1- FUNCTION: POTENT MEDIATOR OF VISCERAL MUSCLE CONTRACTIONS
CC (MYOTROPIC ACTIVITY).
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
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DR

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DR PIR; A61620; A61620;
DR InterPro: IPR001484; Pyrokinin.
DR PROSITE; PS00539; PYROKININ; 1.
KW Neuropeptide; Amidation; Pyrokinin.
FT MOD_RES 5
FT MOD_RES 5 AMIDATION.
SQ SEQUENCE 9 AA: 1140 MW: 05AE1772C9D776C6 CRC64:
-----
Query Match 18.2%, Score 21, DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RQ 6
DB 1 RQ 2

RESULT 21
LPCA_STAAC
ID LPCA_STAAC STANDARD; PRT; 9 AA.
AC P36884;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Chloramphenicol resistance leader peptide.
OS Staphylococcus aureus, and
OS Staphylococcus aureus.
OC Plasmid pSCS6, Plasmid pSCS7, Plasmid pUB112, and Plasmid pIP501.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID-1280, 1311;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-S. aureus; STRAIN-436; PLASMID-pSCS7;
RX MEDLINE-92021652; PubMed-1929326;
RA Schwarz S., Cardoso M.;
RT "Nucleotide sequence and phylogeny of a chloramphenicol
RT acetyltransferase encoded by the plasmid pSCS7 from Staphylococcus
RT aureus.";
RL Antimicrob. Agents Chemother. 35:1551-1556(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES-S. aureus; PLASMID-pSCS6;
RX MEDLINE-92388047; PubMed-1517170;
RA Cardoso M., Schwarz S.;
RT "Nucleotide sequence and structural relationships of a
RT chloramphenicol acetyltransferase encoded by the plasmid pSCS6 from
RT Staphylococcus aureus.";
RL J. Appl. Bacteriol. 72:289-293(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES-S. aureus; PLASMID-pUB112;
RX MEDLINE-86581739; PubMed-3865770;
RA Brueckner R., Matzura H.;
RT "Regulation of the inducible chloramphenicol acetyltransferase gene
RT of the Staphylococcus aureus plasmid pUB112.";
RL EMBO J. 4:2295-2300(1985).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES-S. agalactiae; PLASMID-pIP501;
RX MEDLINE-91096867; PubMed 1461942;
RA Zieu-Cuot P., de Guespdes G., Horaud T.;
RT "Nucleotide sequence of the chloramphenicol resistance determinant of
RT the streptococcal plasmid pIP501.";
RL Plasmid 28:272-276(1992).
CC
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CC
CC -----
DR EMBL; M58515; AAA26612.1;

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ER EMBL: M58516; AA16528.1; ...
 DR EMBL: X02872; CAA26630.1; ...
 DR EMBL: X60827; CAA43217.1; ...
 DR EMBL: X65462; CAA46454.1; ...
 DR F01: B24362; B24362.
 DR PIR: S10494; S30494.
 KW Leader peptide: Antibiotic resistance: fusidic acid.
 SQ SEQUENCE 9 AA: 1074 MW: 562CA5AA95B55517664;
 Query Match 18.2% Score 2: DB 1: Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 KK 3
 DE 2 KK 3
 RESULT 24
 RS10_SERMA STANDARD: PRT: 9 AA
 AC 066936;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S10 (fragment)
 GN RPS1
 OS Serratia marcescens.
 CC Bacteria: Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Serratia.
 QX NCBI_TaxID: 615;
 RN 11;
 RP SEQUENCE FROM N.A.
 RA Nardani S.M., Lindahl L., Zengel J.M.;
 RC Submitted (APR-1998) to the EMBL/Genbank/DDBJ databases.
 CC 1 FUNCTION: Involved in the binding of tRNA to the ribosomes (by similarity).
 CC 1 SIMILARITY: BELONGS TO THE S10 FAMILY OF RIBOSOMAL PROTEINS.
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 CC ER F01: AF058451; AAC24294.1;
 DR HAMAP: M00598; ...
 DR UNIPROT: P6021848; Ribosomal_S10; ...
 DR PROSITE: P500361; RIBOSOMAL_S10; ...
 KW Ribosomal protein.
 FT NON_TER 9
 FT NON_TER 9
 SQ SEQUENCE 9 AA: 1214 MW: DE0943 04103400 3601.
 Query Match 18.2% Score 2: DB 1: Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 QK 7
 DE 4 QK 5
 RESULT 25
 RT13_RCVIN STANDARD: PRT: 9 AA
 AC PR2926;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitochondrial 28S ribosomal protein S13 (S13.2) (fragment).
 GN MRPS13.

OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 QX NCBI_TaxID: 9913;
 RN 11;
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=2127644; PubMed 11279123;
 RA Koe E.C., Burkhardt W., Blackburn K., Moseley A., Spremulli L.L.;
 PT "The small subunit of the mammalian mitochondrial ribosome: identification of the full complement of ribosomal proteins present.";
 RL J. Biol. Chem. 276:19363-19374(2001).
 CC 1 SUBUNIT: Component of the mitochondrial ribosome small subunit (28S) which comprises a 12S rRNA and about 30 distinct proteins.
 CC 1 SUBCELLULAR LOCATION: Mitochondrial.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 9
 FT NON_TER 9
 SQ SEQUENCE 9 AA: 1032 MW: D44ID73776DB05B9 CRC64;
 Query Match 18.2% Score 2: DB 1: Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AK 2
 DE 1 AK 9
 RESULT 24
 THYF_PIG STANDARD: PRT: 9 AA
 AC P01255;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Thymic factor.
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 QX NCBI_TaxID: 9623;
 RN 11;
 RP SEQUENCE.
 RX MEDLINE=74024571; PubMed 914862;
 RA Pless J.-M., Dardenne M., Biouquart Y., Bach J.-F.;
 RT "Structural study of circulating thymic factor: a peptide isolated from pig serum. II. Amino acid sequence.";
 RL J. Biol. Chem. 262:8645-8647(1977).
 CC 1 MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
 DR PIR: A01521; YEPG.
 KW Pyrrolidone carboxylic acid.
 FT MGO_RES 3
 FT MGO_RES 3
 SQ SEQUENCE 9 AA: 879 MW: D5U0B87866C5B33D CRC64;
 Query Match 18.2% Score 2: DB 1: Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AK 4
 DE 2 AK 3
 RESULT 25
 CLAD_HUMAN STANDARD: PRT: 9 AA
 ID CLAD_HUMAN
 AC P33929;
 DT 31-JUL-1993 (Rel. 26, Created)
 DT 31-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 43, Last annotation update)
 DE Unknown protein from 20-page of liver tissue (Spot 106) (fragment).


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Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
DB 9 AK 10

RESULT 33
PSRF_JAPAN
ID PSRF_JAPAN STANDARD; PRI: 1; AA:
AC Q03367;
DI 01-JUN-1994 (Rel. 29, Created)
DI 01-JUN-1994 (Rel. 29, Last sequence update)
DI 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cytochrome b559 beta subunit (PSII reaction center subunit VI)
DE (Fragment).
GN PSBF.
OS Capsicum annuum (bell pepper).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiales; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID:4072;
KN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:cv. Camuyo; TISSUE:Fruit; and Leaf;
RX MEDLINE:94099270; PubMed:1463853;
RA Kunitz M., Camara R., Weil J.-H., Schmitz R.;
RT "The psbL gene from bell pepper (Capsicum annuum): plastid KNA
RT editing also occurs in non-photosynthetic chlamyoplasts.";
RL Plant Mol. Biol. 20:1185-1188(1992).
CC -!- FUNCTION: This b-type cytochrome is tightly associated with the
CC reaction center of photosystem II and possibly is part of the
CC water oxidation complex.
CC -!- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
CC -!- SIMILARITY: Belongs to the psbL / psbF family.

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EMBL: X65570; CAA46549.1;
DB PIR: S28055;
DB BAMAP: MF_006433;
DB InterPro: IPR006216;
DB PROSITE: PS00537; CYTOCHROME b559, LAMINAR
KW Chloroplast; Photosystem II; Homo; Electron transport; Transmembrane;
FT NON-TER 1
FT TRANSMEM 41
FT DOMAIN 6 10
FT SEQUENCE 10 AA; 1180 MW; 817D0F5AD6E659 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 QR 7
DB 9 QR 10

RESULT 34
RCA_PINS
ID RCA_PINS STANDARD; PRI: 1; AA:
AC R81084;
DI 15-JUL-1998 (Rel. 36, Created)
DI 15-JUL-1998 (Rel. 36, Last sequence update)
DI 16-OCT-2001 (Rel. 40, Last annotation update)

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DE Probable ribulose biphosphate carboxylase/oxygenase activase (Rubisco
DE activase) (RA) (Water stress responsive protein 4) (fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID:71647;
KN [1]
RP SEQUENCE.
RC TISSUE:Needle;
RX MEDLINE:98418576; PubMed:9747804;
RA Costa P., Bahrman N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit responsive proteins in maritime pine.";
RL Plant Mol. Biol. 38:587-596(1998).
DI 121;
RP SEQUENCE.
RC TISSUE:Needle;
RX MEDLINE:99274088; PubMed:10344291;
RA Costa P., Pionneau C., Baw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- FUNCTION: ACTIVATION OF RUBISCO (RUBULOSE-1,5-BISPHOSPHATE
CC CARBOXYLASE/OXYGENASE; EC 4.1.1.39) INVOLVES THE ATP-DEPENDENT
CC CARBOXYLATION OF THE EPSILON-AMINO GROUP OF LYSINE LEADING TO A
CC CARBAMATE STRUCTURE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Chloroplast stroma (By similarity).
CC -!- INDUCTION: By water stress.
CC -!- SIMILARITY: BELONGS TO THE RUBISCO ACTIVASE FAMILY.
KW Chloroplast; ATP-binding.
FT NON-TER 1
FT NON-TER 10 30
FT SEQUENCE 10 AA; 1171 MW; C0A506D2C72B1EA6 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
DB 9 AK 10

RESULT 35
SP34_DICMU
ID SP34_DICMU STANDARD; PRI: 10 AA:
AC P81545;
DI 15-JUL-1999 (Rel. 48, Created)
DI 15-JUL-1999 (Rel. 48, Last sequence update)
DI 15-JUL-1999 (Rel. 48, Last annotation update)
DE Surface protein P34 (fragment).
GN P34.
OS Dictyostelium mucoroides (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
OX NCBI_TaxID:31287;
KN [1]
RP SEQUENCE.
RC STRAIN:DM 7;
RA Schreiner S.J.;
RT "Characterization of a surface protein in macrocysts of Dictyostelium
RL mucoroides.";
RL Submitted (NOV 1998) to the SWISS-PROT data bank.
CC -!- FUNCTION: THIS PROTEIN IS PRESENT IN THE MACROCYST PRIMARY WALL
CC WHICH IS PRODUCED BY AMOEBAE DURING THE ONSET OF SEXUAL
CC REPRODUCTION.
CC -!- SUBCELLULAR LOCATION: MACROCYST PRIMARY WALL.
KW Cell wall.
FT NON-TER 10 10
FT SEQUENCE 10 AA; 1190 MW; 1B6A707AA3345B50 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      8 KD 9
DB      6 KD 7

RESULT 36
SPL_HAIR:
ID SPL_HAIR0 STANDARD: PRI: 10 AA.
AC Q0997.
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Serine proteinase inhibitor (Fragment).
OS Halocynthia roretzi (sea squirt).
OC Eukaryota; Metazoa; Chordata; Branchiata; Ascidiacea;
OC Stolidobranchia; Pyruidae; Halocynthia.
ON NCBI_TaxID:7729;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph;
RX MEDLINE:96321313; PubMed:87929255;
RA Shishikura F., Abe F., Ohtake S.-I., Tanaka K.
RT "Purification and characterization of a 58,000 Da proteinase
RT inhibitor from the hemolymph of a solitary ascidian, Halocynthia
RT roretzi".
RC Comp. Biochem. Physiol. 114B:1-9(1996).
CC 1- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
CC 1- SUBUNIT: MONOMER.
CC 1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro: IPR000215; Serpin.
DR PROSITE: PS00284; SERPIN, PARTIAL.
KW Serpin; Serine protease inhibitor; Glycyl-protein; Plasma.
FT NTER 10 10
SQ SEQUENCE 10 AA: 1104 MW: 4225730187AA; CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KK 3
DB      11
      2 KK 3

RESULT 37
SYK_CAMP
ID SYK_CAMP STANDARD: PRI: 10 AA.
AC Q46464.
DT 15-DEC-1992 (Rel. 37, Created)
DT 15-DEC-1992 (Rel. 37, Last sequence update)
DT 24-FEB-2003 (Rel. 41, Last annotation update)
DE Lysyl-tRNA synthetase (EC 6.1.1.6) (lysine tRNA ligase) (lysRS)
DE (Fragment).
DE LYSS.
OS Campylobacter upsaliensis.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Campylobacteraceae; Campylobacter.
ON NCBI_TaxID:28680;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN+ATCC 43954;
RX MEDLINE-97149302; PubMed-8996110;
RA Bourke B., Rashid S.T., Bingham H.L., Chan V.L.
RT "Characterization of Campylobacter upsaliensis for and its
RT localization in a highly conserved region of the Campylobacter
RT genome".
RC Gene 183:219-224(1996).
CC 1- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) -> AMP + diphosphate
CC + L-lysyl-tRNA(Lys).
CC 1- COFACTOR: Binds 3 magnesium ions per subunit (by similarity).
CC 1- SUBUNIT: Homodimer (by similarity).
CC 1- SUBCELLULAR LOCATION: Cytoplasmic.

-1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC
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DR EMBL: L77076; AAB41442.1;
DR HAMAP: MF_00252; 1.
DR InterPro: IPR006195; tRNA_Ligase-II.
DR PROSITE: PS50862; AA_tRNA_LIGASE-II; PARTIAL.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
KW Metal-binding; Magnesium.
FT NTER 1 1
SQ SEQUENCE 10 AA: 1218 MW: 9CEA46AB13372B05 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 KE 4
DB      11
      6 KE 7

RESULT 38
TKNL_SCYCA
ID TKNL_SCYCA STANDARD: PRI: 10 AA.
AC P08508;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Scyllorhynchin I.
OS Scyllorhynchus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhynchus.
ON NCBI_TaxID:7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE-86192829; PubMed:2422058;
RA Conlon J.M., Deacon C.F., O'Toole L., Thim L.;
RT "Scyllorhynchin I and II: two novel tachykinins from dogfish gut.";
RI FEBS Lett. 200:111-116(1986).
RN [2]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE-93292508; PubMed-7685693;
RA Waudh D., Wang Y., Hazon N., Halment R.J., Conlon J.M.;
RT "Primary structures and biological activities of substance-P-related
RT peptides from the brain of the dogfish, Scyllorhynchus canicula.";
RI Eur. J. Biochem. 214:469-474(1993).
CC 1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR: A24867; A24867.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10
SQ SEQUENCE 10 AA: 1219 MW: D0602D6B59C33AA9 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AK 2
11
1 AK 2

DB

RESULT 39

TKS2_AEDAE STANDARD: PRI: 10 AA.

AC P42635;
D1 01-NOV-1995 (Rel. 32, Created)
D2 01-NOV-1995 (Rel. 32, Last sequence update)
D3 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sialokinin II.
DS Aedes aegypti (Yellowfever Mosquito)
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Neotera; Culicoidae; Aedes.
GX NCBI_TaxID:71159;
RN 111
RP SEQUENCE.
RC STRAIN:Kochofolter; TISSUE:Salivary gland;
RX MEDLINE:54195119; PubMed:6278454;
RA Champagne G.E., Ribeiro J.M.G.;
RT *Sialokinin I and II: vasodilatory tachykinins from the yellow fever
RT mosquito Aedes aegypti.*
RL Proc. Natl. Acad. Sci. U.S.A. 91:148 142(1994).
CC 1- FUNCTION: VASODILATORY PEPTIDE MAY ACTIVATE MACROPHAGES AT THE
CC SITE OF FEEDING.
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
DR PIR, B49581; B49581.
DR InterPro: IPR02040; Tachykinin.
DK PROSITE: PS0267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MATURES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 1146 MW: 3277;cdhcvvvaav tpsv;
Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DI 10
11
1 DI 2

DB

RESULT 40

TKU1_UREN STANDARD: PRI: 10 AA.

AC P40751;
D1 01-FEB-1995 (Rel. 31, Created)
D2 01-FEB-1995 (Rel. 31, Last sequence update)
D3 15-SEP-2003 (Rel. 42, Last annotation update)
DE Greckistachykinin I.
DS Urechis unicinctus.
OS Eukaryota; Metazoa; Echinura; Xenophora; Chordata; Tachis.
GX NCBI_TaxID:6442;
RN 111
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE:Ventral nerve cord;
RX MEDLINE:93236558; PubMed:8476412;
RA Ikeda T., Minakata H., Nomoto K., Kikuta T., Buzarska Y.,
RT *Two novel tachykinin-related neuropeptides in the echinoid worm,
RT Urechis unicinctus.*
RL Biochem. Biophys. Res. Commun. 192:1-6(1993).
CC 1- FUNCTION: CONTRACTILE ACTION ON THE INNER TROPHAR BODY WALL,
CC MUSCLE OF THE ANIMAL.
CC 1- SUBCELLULAR LOCATION: Secreted.
CC 1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MATURES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 1177 MW: 3631;cdvcpvavav tpsv;
Query Match 18.2%; Score 2; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RQ 6
11
2 RQ 8

DB

RESULT 41

UXA6_CHELR STANDARD: PRI: 10 AA.

AC P38007;
D1 01-OCT-1994 (Rel. 30, Created)
D2 01-OCT-1994 (Rel. 30, Last sequence update)
D3 30-MAY-2000 (Rel. 39, Last annotation update)
DE Unknown protein from 20-page from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
GX NCBI_TaxID:813;
RN 111
RP SEQUENCE.
RC STRAIN:L2/434/B-1;
RA Bini L., Santucci A., Maqi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christianen G., Birkelund S., Vitreou E., Ratti G.,
RA Pallini V.;
RL Submitted (SSP-1994) to the SWISS-PROT data bank.
CC 1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.44; ITS MW IS: 38.6 KDa.
DR SIOGA 2DPAGE; P38307;
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1243 MW: DAD39A33304H5339 CRC64;
Query Match 18.2%; Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KK 4
1
7 KK 8

DB

RESULT 42

ASL2_HACSE STANDARD: PRI: 11 AA.

AC P81147;
D1 28-FEB-2003 (Rel. 41, Created)
D2 28-FEB-2003 (Rel. 41, Last sequence update)
D3 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acharan sulfate lyase 2 (EC 4.2.2.1) (Fragment).
OS Bacteroides stercoris.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
GX NCBI_TaxID:46506;
RN 111
RP SEQUENCE, FUNCTION, ENZYME REGULATION, AND SUBUNIT.
RC STRAIN:HJ-15;
RX MEDLINE:2123019; PubMed:11422884;
RA Kim B.T., Hong S.W., Kim W.-S., Kim Y.-S., Kim D.-H.;
RT *Purification and characterization of acharan sulfate lyases, two
RT novel heparinases, from Bacteroides stercoris HJ-15.*;
RL Eur. J. Biochem. 268:2635-2641(2001).
CC 1- FUNCTION: Degrades acharan sulfate and, to a lesser extent,
CC heparin and heparan sulfate
CC 1- ENZYME REGULATION: Inhibited by cupric ion, nitrogen and lead.
CC 1- Activated by reducing agents, such as DL-dithiothreitol and 2-
CC mercaptoethanol.
CC 1- SUBUNIT: Monomer.
CC 1- PTM: The N-terminus is blocked.
CC 1- MISCELLANEOUS: Has an isoelectric point of 8.6. Its optimum pH is
CC 7.2 and optimum temperature 45 degrees Celsius.
KW Lyase; Heparin-binding;
FT NON_TER 1 11
SQ NON_TER 11 11

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SQ SEQUENCE 11 AA: 1195 MW: 179089707AA451A1C6W54;
Query Match 18.2% Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QK 1
DB 10 QK 11

RESULT 43
BRK_MSCFL
ID BRK_MSCFL STANDARD: PRT; 11 AA;
AC P12757;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Meqascoliaflavins ((Thr6)bradykinin-Lys-Ala) (Contains: Bradykinin like
peptide ((Thr6)bradykinin)).
OS Meqascolia flavitrons (Garden dagger wasp) (Sociality wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
NC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Scelionidae;
OX Scelionidae; Meqascolia.
NX NCBI_TaxID:7437;
RN 1;
RP SEQUENCE;
TX TISSUE-Venom;
RA Yashara T., Mantel P., Nakajima T., Park J.;
RT *Two kins isolated from an extract of the venom reservoirs of the
solitary wasp Meqascolia flavitrons.
RE Toxicon 25:527-535(1987).
RN 12;
RP SEQUENCE;
RA Nakajima T., Park J., Yashara T., Mantel P.;
RT *Two kins isolated from the venom of Meqascolia flavitrons.
RE Toxicon 26:334-34(1989).
OC FUNCTION: Both proteins have bradykinin like although lower
activities (e.g. smooth muscle contraction).
NC SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs
CX SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
DE PIR, B26744; B26744.
KW Bradykinin; Vasodilator.
FT PEPTIDE 1 11
FT PEPTIDE 1 5
SQ SEQUENCE 11 AA: 1273 MW: 1486743G61A7A7C654;

Query Match 18.2% Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 QK 8
DB 9 QK 10

RESULT 44
NXSN_PSEFL
ID NXSN_PSEFL STANDARD: PRT; 11 AA;
AC P59472;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Short neurotoxin N1 (Alpha neurotoxin) (Friedman)
OS Pseudonaja textilis (Eastern Brown Snake)
OC Eukaryota; Metazoa; Chordata; Chelonia; Vertebrata; Euteleostomi;
NC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OX Elapidae; Acanthophiinae; Pseudonaja.
NX NCBI_TaxID:8674;
RN 1;
RP SEQUENCE, AND MASS SPECTROMETRY.

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TISSUE-Venom;
MEDLINE-99449692; PubMed-19518793;
RA Gong N.L., Arumugam A., Jayaseelan K.;
RT *Postsynaptic short chain neurotoxins from Pseudonaja textilis: cDNA
cloning, expression and protein characterization.
RL Eur. J. Biochem. 265:982-989(1999).
CC FUNCTION: Lethal neurotoxin, binds and inhibits nicotinic
acetylcholine receptors (nAChR).
CC SUBCELLULAR LOCATION: Secreted.
CC TISSUE SPECIFICITY: Expressed by the venom gland.
CC MASS SPECTROMETRY: MW-6236; METHOD-Electrospray.
CC MISCELLANEOUS: LD(50) is 0.84 mg/kg by intravenous injection.
CX SIMILARITY: Belongs to the snake toxin family.
DE InterPro: IPR003571; Snake toxin.
DE ProSite: PS00272; SNAKE_TOXIN; PARTIAL.
KW Toxin; Neurotoxin; Postsynaptic neurotoxin;
KW Acetylcholine receptor inhibitor; Multigene family.
FT UNSURE 3
FT NCN_IER 11 11
SQ SEQUENCE 11 AA: 1315 MW: 0D1EF0C81B58732B CRC64;

Query Match 18.2% Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DI 10
DB 9 DI 10

RESULT 45
PKCL_CARMO
ID PKCL_CARMO STANDARD: PRT; 11 AA;
AC PB2584;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinnin-1 (3am-PK-1) (EXPRL-Amide).
OS Caracus murens (Indian stick insect).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
NC Neoptera; Orthopteroidea; Phasmatoidea; Euphasmida; Phasmatoidea;
OX Heteronemidae; Caracus.
NX NCBI_TaxID:7622;
RN 11;
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
TX TISSUE-Corpora cardiaca.
RA Predel R., Kellner K., Garde G.;
RT *Myotropic neuropeptides from the retrocerebral complex of the stick
insect, Caracus murens (Phasmatoidea: Lonchodidae).
RL Eur. J. Entomol. 96:275-278(1999).
CC FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
(MYOINOTROPIC ACTIVITY).
CC MASS SPECTROMETRY: MW-1235; METHOD-MALDI.
CX SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DE InterPro: IPR01484; Pyrokinnin.
DE ProSite: PS00539; PYROKININ; FALSE_NEG.
KW Neuropeptide; Amidation; Pyrokinnin.
FT MOD_RES 11 11
FT AMIDATION.
SQ SEQUENCE 11 AA: 1236 MW: 2BFA5225BB46C1A8 CRC64;

Query Match 18.2% Score 2; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IQ 11
DB 5 IQ 5

RESULT 46
PQOC_PSEFL
ID PQOC_PSEFL STANDARD: PRT; 11 AA;
AC P55173;

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RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE: Intestine;
 RX MEDLINE: 91254337; PubMed: 2043143;
 RA Kozawa H., Hino J., Minamino N., Kandawa K., Matsuo H.;
 RT "Isolation of four novel tachykinins from frog (*Rana catesbeiana*)
 RI brain and intestine."
 RL Biochem. Biophys. Res. Commun. 177:585-595(1991)
 RN [2]
 RP SEQUENCE.
 RC TISSUE: Intestine;
 RX MEDLINE: 94023216; PubMed: 8210506;
 RA Kandawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
 RI "Four novel tachykinins in frog (*Rana catesbeiana*) brain and
 RL intestine."
 RL Regul. Pept. 46:81-88(1993).
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -1- SURCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
 DR PIR: D61031; D61033.
 DR InterPro: IPR002040; Tachykinin.
 DR PROSITE: PS00267; TACHYKININ; FALSE NEG.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD_RES 11 11
 SQ SEQUENCE 11 AA: 1350 MW: 3A34256C9943807 CRC64;

Query Match 18.2% Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e-04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 ER 5
 DB 5 ER 6

RESULT 50
 TRN_ELEM:
 ID TRN_ELEM STANDARD PRI 11 AA.
 AC P01293;
 BI 21-JUN-1986 (Rel. 01, Created)
 DI 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Eledoisin.
 OS Eledone moschata (Musk octopus) (*Loligo muschata*), and
 OS Eledone cirrosa (Curled octopus) (*Eledone cirrosa*).
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Nautilus; Nautilus.
 OC Octapodiformes; Octopoda; Incirrata; Oct. 4 subcl. Eledone.
 OX NCBI_TaxID=6641, 102876;
 RN [1]
 RP SEQUENCE.
 RA Anastasi A., Erspamer V.;
 RI "The isolation and amino acid sequence of eledoisin, the active
 RT endocapside of the posterior salivary glands of *Eledone*."
 RL Arch. Biochem. Biophys. 101:56-65(1963)
 CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES.
 CC -1- SURCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: SKIN.
 CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY
 DR PIR: A01561; EOCC.
 DR PIR: B01561; EOCC.
 DR PDH: IMXQ; 18-FEB-03.
 DR InterPro: IPR002040; Tachykinin
 DR PROSITE: PS00267; TACHYKININ; 1.
 KW Tachykinin; Neuropeptide; Amidation; L-tyrosyl-L-homocysteine acid;
 FT MOD_RES 11 11
 SQ SEQUENCE 11 AA: 1206 MW: 5700702559C9AA; CRC64;

Query Match 18.2% Score 2; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e-04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 KD 9
 DB 4 KD 5

Search completed: September 10, 2003, 10:25:58
 Job time : 8.25 secs

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OM protein - protein search, using SW model

Ref. 001
September 30, 2003, 10:00:04, Search Time 41.6557 seconds
(wait time 0.194606s)
89.639 Million operations/sec.

Title: US-09-787-443-2

1 : 40005 1.94 rad

Sequence: ; AKKERQKDTQ 11

Score and Rating: 0-100

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 2215 pword

Total number of hits satisfying chosen parameters: 3459

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 sorted: 10.8

Database :

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phage.*
- 10: sp.plant.*
- 11: sp.rodent.*
- 12: sp.virus.*
- 13: sp.vtebrate.*
- 14: sp.unclassified.*
- 15: sp.virus.*
- 16: sp.bacteriophage.*
- 17: sp.archaea.*

Prod. No. is the number of results produced by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match	Length	DB	Description
1	4	36.4	11	4	Q9Y4Z2
2	4	36.4	11	15	Q9Y4W4
3	4	36.4	15	2	Q5A9W4
4	4	36.4	15	2	Q5A9V5
5	3	27.3	8	4	Q15495
6	3	27.3	10	2	P83162
7	3	27.3	11	4	Q9H4H5
8	3	27.3	11	6	Q9Y4W5
9	3	27.3	12	2	Q8V1X8
10	3	27.3	12	76	Q25174
11	3	27.3	13	2	Q55044
12	3	27.3	13	4	Q9H4C1
13	3	27.3	13	6	Q9Y4K5
14	3	27.3	13	8	Q9Y4H5
15	3	27.3	13	8	Q9Y4K4
16	3	27.3	13	8	Q9Y4H6
17	3	27.3	13	8	Q9Y4H2
18	3	27.3	13	8	Q9Y4H3
19	3	27.3	13	8	Q9Y4H4
20	3	27.3	13	8	Q9Y4H1
21	3	27.3	13	8	Q9Y4H7
22	3	27.3	13	8	Q9Y4H8
23	3	27.3	13	8	Q9Y4H9
24	3	27.3	13	8	Q9Y4H0
25	3	27.3	13	8	Q9Y4H6
26	3	27.3	13	8	Q9Y4H7
27	3	27.3	13	8	Q9Y4H8
28	3	27.3	13	8	Q9Y4H9
29	3	27.3	13	8	Q9Y4H0
30	3	27.3	13	8	Q9Y4H6
31	3	27.3	13	8	Q9Y4H7
32	3	27.3	13	8	Q9Y4H8
33	3	27.3	13	8	Q9Y4H9
34	3	27.3	13	8	Q9Y4H0
35	3	27.3	13	8	Q9Y4H6
36	3	27.3	13	8	Q9Y4H7
37	3	27.3	13	8	Q9Y4H8
38	3	27.3	13	8	Q9Y4H9
39	3	27.3	13	8	Q9Y4H0
40	3	27.3	13	8	Q9Y4H6
41	3	27.3	13	8	Q9Y4H7
42	3	27.3	13	8	Q9Y4H8
43	3	27.3	13	8	Q9Y4H9
44	3	27.3	13	8	Q9Y4H0
45	3	27.3	13	8	Q9Y4H6
46	3	27.3	13	8	Q9Y4H7
47	3	27.3	13	8	Q9Y4H8
48	3	27.3	13	8	Q9Y4H9
49	3	27.3	13	8	Q9Y4H0
50	3	27.3	13	8	Q9Y4H6
51	3	27.3	13	8	Q9Y4H7
52	3	27.3	13	8	Q9Y4H8
53	3	27.3	13	8	Q9Y4H9
54	3	27.3	13	8	Q9Y4H0
55	3	27.3	13	8	Q9Y4H6
56	3	27.3	13	8	Q9Y4H7
57	3	27.3	13	8	Q9Y4H8
58	3	27.3	13	8	Q9Y4H9
59	3	27.3	13	8	Q9Y4H0
60	3	27.3	13	8	Q9Y4H6
61	3	27.3	13	8	Q9Y4H7
62	3	27.3	13	8	Q9Y4H8
63	3	27.3	13	8	Q9Y4H9
64	3	27.3	13	8	Q9Y4H0
65	3	27.3	13	8	Q9Y4H6
66	3	27.3	13	8	Q9Y4H7
67	3	27.3	13	8	Q9Y4H8
68	3	27.3	13	8	Q9Y4H9
69	3	27.3	13	8	Q9Y4H0
70	3	27.3	13	8	Q9Y4H6
71	3	27.3	13	8	Q9Y4H7
72	3	27.3	13	8	Q9Y4H8
73	3	27.3	13	8	Q9Y4H9
74	3	27.3	13	8	Q9Y4H0
75	3	27.3	13	8	Q9Y4H6
76	3	27.3	13	8	Q9Y4H7
77	3	27.3	13	8	Q9Y4H8
78	3	27.3	13	8	Q9Y4H9
79	3	27.3	13	8	Q9Y4H0
80	3	27.3	13	8	Q9Y4H6
81	3	27.3	13	8	Q9Y4H7
82	3	27.3	13	8	Q9Y4H8
83	3	27.3	13	8	Q9Y4H9
84	3	27.3	13	8	Q9Y4H0
85	3	27.3	13	8	Q9Y4H6
86	3	27.3	13	8	Q9Y4H7
87	3	27.3	13	8	Q9Y4H8
88	3	27.3	13	8	Q9Y4H9
89	3	27.3	13	8	Q9Y4H0
90	3	27.3	13	8	Q9Y4H6
91	3	27.3	13	8	Q9Y4H7
92	3	27.3	13	8	Q9Y4H8
93	3	27.3	13	8	Q9Y4H9
94	3	27.3	13	8	Q9Y4H0
95	3	27.3	13	8	Q9Y4H6
96	3	27.3	13	8	Q9Y4H7
97	3	27.3	13	8	Q9Y4H8
98	3	27.3	13	8	Q9Y4H9
99	3	27.3	13	8	Q9Y4H0
100	3	27.3	13	8	Q9Y4H6

Q944k6 bryopsis sp.
Q944k3 bryopsis sp.
Q81761 hepatitis c
Q81794 hepatitis c
Q81784 hepatitis c
Q81778 hepatitis c
Q81787 hepatitis c
Q81775 hepatitis c
Q81767 hepatitis c
Q81758 hepatitis c
Q81800 hepatitis c
Q81745 hepatitis c
Q81781 hepatitis c
Q81769 hepatitis c
Q81773 hepatitis c
Q81799 hepatitis c
Q81786 hepatitis c
Q81798 hepatitis c
Q81763 hepatitis c
Q81764 hepatitis c
Q81796 hepatitis c
Q81791 hepatitis c
Q81762 hepatitis c
Q81790 hepatitis c
Q81783 hepatitis c
Q81789 hepatitis c
Q81797 hepatitis c
Q81795 hepatitis c
Q81782 hepatitis c
Q81790 hepatitis c
Q81771 hepatitis c
Q81772 hepatitis c
Q81792 hepatitis c
Q81777 hepatitis c
Q84415 escherichia
Q56750 western x p
Q46291 canadian pc
Q811y9 chiroccid
Q15998 homo sapien
Q94wx8 manduca sex
Q9cs58 mus musculus
P82831 rana luteiv
Q9kel4 bacillus ha
Q94r48 bacillus fi
Q47612 escherichia
Q9ure0 saccharomyc
Q9ucc7 homo sapien
Q9unc2 homo sapien
Q81zk0 homo sapien
Q94wu4 crithidia f
Q94wv3 axinella po
Q9sq16 oryza sativ
Q9qwk2 rattus norv
Q65643 human herpe
Q9r7t2 escherichia
Q9agp4 arthrobacte
Q93zk0 planktothri
Q69485 klebsiella
Q93sr0 staphylococ
Q93258 synechococ
Q85r33 lactobacill
Q56429 thermus te
Q9r9e0 bacillus su
Q45889 clostridium
Q945r0 shigella dy
Q51594 escherichia
Q53790 streptococ

90	2	18.2	9	2	Q80M55	Q80M55	zebra mays (m
91	2	18.2	9	3	Q80M59	Q80M59	mus musculus
92	2	18.2	9	4	Q80M64	Q80M64	mus musculus
93	2	18.2	9	5	Q80M68	Q80M68	human herpe
94	2	18.2	9	6	Q80M72	Q80M72	human herpe
95	2	18.2	9	7	Q80M76	Q80M76	human herpe
96	2	18.2	9	8	Q80M80	Q80M80	human herpe
97	2	18.2	9	9	Q80M84	Q80M84	human herpe
98	2	18.2	9	10	Q80M88	Q80M88	human herpe
99	2	18.2	9	11	Q80M92	Q80M92	human herpe
100	2	18.2	9	12	Q80M96	Q80M96	human herpe
101	2	18.2	9	13	Q80M100	Q80M100	human herpe
102	2	18.2	9	14	Q80M104	Q80M104	human herpe
103	2	18.2	9	15	Q80M108	Q80M108	human herpe
104	2	18.2	9	16	Q80M112	Q80M112	human herpe
105	2	18.2	9	17	Q80M116	Q80M116	human herpe
106	2	18.2	9	18	Q80M120	Q80M120	human herpe
107	2	18.2	9	19	Q80M124	Q80M124	human herpe
108	2	18.2	9	20	Q80M128	Q80M128	human herpe
109	2	18.2	9	21	Q80M132	Q80M132	human herpe
110	2	18.2	9	22	Q80M136	Q80M136	human herpe
111	2	18.2	9	23	Q80M140	Q80M140	human herpe
112	2	18.2	9	24	Q80M144	Q80M144	human herpe
113	2	18.2	9	25	Q80M148	Q80M148	human herpe
114	2	18.2	9	26	Q80M152	Q80M152	human herpe
115	2	18.2	9	27	Q80M156	Q80M156	human herpe
116	2	18.2	9	28	Q80M160	Q80M160	human herpe
117	2	18.2	9	29	Q80M164	Q80M164	human herpe
118	2	18.2	9	30	Q80M168	Q80M168	human herpe
119	2	18.2	9	31	Q80M172	Q80M172	human herpe
120	2	18.2	9	32	Q80M176	Q80M176	human herpe
121	2	18.2	9	33	Q80M180	Q80M180	human herpe
122	2	18.2	9	34	Q80M184	Q80M184	human herpe
123	2	18.2	9	35	Q80M188	Q80M188	human herpe
124	2	18.2	9	36	Q80M192	Q80M192	human herpe
125	2	18.2	9	37	Q80M196	Q80M196	human herpe
126	2	18.2	9	38	Q80M200	Q80M200	human herpe
127	2	18.2	9	39	Q80M204	Q80M204	human herpe
128	2	18.2	9	40	Q80M208	Q80M208	human herpe
129	2	18.2	9	41	Q80M212	Q80M212	human herpe
130	2	18.2	9	42	Q80M216	Q80M216	human herpe
131	2	18.2	9	43	Q80M220	Q80M220	human herpe
132	2	18.2	9	44	Q80M224	Q80M224	human herpe
133	2	18.2	9	45	Q80M228	Q80M228	human herpe
134	2	18.2	9	46	Q80M232	Q80M232	human herpe
135	2	18.2	9	47	Q80M236	Q80M236	human herpe
136	2	18.2	9	48	Q80M240	Q80M240	human herpe
137	2	18.2	9	49	Q80M244	Q80M244	human herpe
138	2	18.2	9	50	Q80M248	Q80M248	human herpe
139	2	18.2	9	51	Q80M252	Q80M252	human herpe
140	2	18.2	9	52	Q80M256	Q80M256	human herpe
141	2	18.2	9	53	Q80M260	Q80M260	human herpe
142	2	18.2	9	54	Q80M264	Q80M264	human herpe
143	2	18.2	9	55	Q80M268	Q80M268	human herpe
144	2	18.2	9	56	Q80M272	Q80M272	human herpe
145	2	18.2	9	57	Q80M276	Q80M276	human herpe
146	2	18.2	9	58	Q80M280	Q80M280	human herpe
147	2	18.2	9	59	Q80M284	Q80M284	human herpe
148	2	18.2	9	60	Q80M288	Q80M288	human herpe
149	2	18.2	9	61	Q80M292	Q80M292	human herpe
150	2	18.2	9	62	Q80M296	Q80M296	human herpe
151	2	18.2	9	63	Q80M300	Q80M300	human herpe
152	2	18.2	9	64	Q80M304	Q80M304	human herpe
153	2	18.2	9	65	Q80M308	Q80M308	human herpe
154	2	18.2	9	66	Q80M312	Q80M312	human herpe
155	2	18.2	9	67	Q80M316	Q80M316	human herpe
156	2	18.2	9	68	Q80M320	Q80M320	human herpe
157	2	18.2	9	69	Q80M324	Q80M324	human herpe
158	2	18.2	9	70	Q80M328	Q80M328	human herpe
159	2	18.2	9	71	Q80M332	Q80M332	human herpe
160	2	18.2	9	72	Q80M336	Q80M336	human herpe
161	2	18.2	9	73	Q80M340	Q80M340	human herpe
162	2	18.2	9	74	Q80M344	Q80M344	human herpe
163	2	18.2	9	75	Q80M348	Q80M348	human herpe
164	2	18.2	9	76	Q80M352	Q80M352	human herpe
165	2	18.2	9	77	Q80M356	Q80M356	human herpe
166	2	18.2	9	78	Q80M360	Q80M360	human herpe
167	2	18.2	9	79	Q80M364	Q80M364	human herpe
168	2	18.2	9	80	Q80M368	Q80M368	human herpe
169	2	18.2	9	81	Q80M372	Q80M372	human herpe
170	2	18.2	9	82	Q80M376	Q80M376	human herpe
171	2	18.2	9	83	Q80M380	Q80M380	human herpe
172	2	18.2	9	84	Q80M384	Q80M384	human herpe
173	2	18.2	9	85	Q80M388	Q80M388	human herpe
174	2	18.2	9	86	Q80M392	Q80M392	human herpe
175	2	18.2	9	87	Q80M396	Q80M396	human herpe
176	2	18.2	9	88	Q80M400	Q80M400	human herpe
177	2	18.2	9	89	Q80M404	Q80M404	human herpe
178	2	18.2	9	90	Q80M408	Q80M408	human herpe
179	2	18.2	9	91	Q80M412	Q80M412	human herpe
180	2	18.2	9	92	Q80M416	Q80M416	human herpe
181	2	18.2	9	93	Q80M420	Q80M420	human herpe
182	2	18.2	9	94	Q80M424	Q80M424	human herpe
183	2	18.2	9	95	Q80M428	Q80M428	human herpe
184	2	18.2	9	96	Q80M432	Q80M432	human herpe
185	2	18.2	9	97	Q80M436	Q80M436	human herpe
186	2	18.2	9	98	Q80M440	Q80M440	human herpe
187	2	18.2	9	99	Q80M444	Q80M444	human herpe
188	2	18.2	9	100	Q80M448	Q80M448	human herpe
189	2	18.2	9	101	Q80M452	Q80M452	human herpe
190	2	18.2	9	102	Q80M456	Q80M456	human herpe
191	2	18.2	9	103	Q80M460	Q80M460	human herpe
192	2	18.2	9	104	Q80M464	Q80M464	human herpe
193	2	18.2	9	105	Q80M468	Q80M468	human herpe
194	2	18.2	9	106	Q80M472	Q80M472	human herpe
195	2	18.2	9	107	Q80M476	Q80M476	human herpe
196	2	18.2	9	108	Q80M480	Q80M480	human herpe
197	2	18.2	9	109	Q80M484	Q80M484	human herpe
198	2	18.2	9	110	Q80M488	Q80M488	human herpe
199	2	18.2	9	111	Q80M492	Q80M492	human herpe
200	2	18.2	9	112	Q80M496	Q80M496	human herpe
201	2	18.2	9	113	Q80M500	Q80M500	human herpe
202	2	18.2	9	114	Q80M504	Q80M504	human herpe
203	2	18.2	9	115	Q80M508	Q80M508	human herpe
204	2	18.2	9	116	Q80M512	Q80M512	human herpe
205	2	18.2	9	117	Q80M516	Q80M516	human herpe
206	2	18.2	9	118	Q80M520	Q80M520	human herpe
207	2	18.2	9	119	Q80M524	Q80M524	human herpe
208	2	18.2	9	120	Q80M528	Q80M528	human herpe
209	2	18.2	9	121	Q80M532	Q80M532	human herpe
210	2	18.2	9	122	Q80M536	Q80M536	human herpe
211	2	18.2	9	123	Q80M540	Q80M540	human herpe
212	2	18.2	9	124	Q80M544	Q80M544	human herpe
213	2	18.2	9	125	Q80M548	Q80M548	human herpe
214	2	18.2	9	126	Q80M552	Q80M552	human herpe
215	2	18.2	9	127	Q80M556	Q80M556	human herpe
216	2	18.2	9	128	Q80M560	Q80M560	human herpe
217	2	18.2	9	129	Q80M564	Q80M564	human herpe
218	2	18.2	9	130	Q80M568	Q80M568	human herpe
219	2	18.2	9	131	Q80M572	Q80M572	human herpe
220	2	18.2	9	132	Q80M576	Q80M576	human herpe
221	2	18.2	9	133	Q80M580	Q80M580	human herpe
222	2	18.2	9	134	Q80M584	Q80M584	human herpe
223	2	18.2	9	135	Q80M588	Q80M588	human herpe
224	2	18.2	9	136	Q80M592	Q80M592	human herpe
225	2	18.2	9	137	Q80M596	Q80M596	human herpe
226	2	18.2	9	138	Q80M600	Q80M600	human herpe
227	2	18.2	9	139	Q80M604	Q80M604	human herpe
228	2	18.2	9	140	Q80M608	Q80M608	human herpe
229	2	18.2	9	141	Q80M612	Q80M612	human herpe
230	2	18.2	9	142	Q80M616	Q80M616	human herpe
231	2	18.2	9	143	Q80M620	Q80M620	human herpe
232	2	18.2	9	144	Q80M624	Q80M624	human herpe
233	2	18.2	9	145	Q80M628	Q80M628	human herpe
234	2	18.2	9	146	Q80M632	Q80M632	human herpe
235	2	18.2	9	147	Q80M636	Q80M636	human herpe
236	2	18.2	9	148	Q80M640	Q80M640	human herpe
237	2	18.2	9	149	Q80M644	Q80M644	human herpe
238	2	18.2	9	150	Q80M648	Q80M648	human herpe
239	2	18.2	9	151	Q80M652	Q80M652	human herpe
240	2	18.2	9	152	Q80M656	Q80M656	human herpe
241	2	18.2	9	153	Q80M660	Q80M660	human herpe
242	2	18.2	9	154	Q80M664	Q80M664	human herpe
243	2	18.2	9	155	Q80M668	Q80M668	human herpe
244	2	18.2	9	156	Q80M672	Q80M672	human herpe
245	2	18.2	9	157	Q80M676	Q80M676	human herpe
246	2	18.2	9	158	Q80M680	Q80M680	human herpe
247	2	18.2	9	159	Q80M684	Q80M684	human herpe
248	2	18.2	9	160	Q80M688	Q80M688	human herpe
249	2	18.2	9	161	Q80M692	Q80M692	human herpe
250	2	18.2	9	162	Q80M696	Q80M696	human herpe
251	2	18.2	9	163	Q80M700	Q80M700	human herpe
252	2	18.2	9	164	Q80M704	Q80M704	human herpe
253	2	18.2	9	165	Q80M708	Q80M708	human herpe
254	2	18.2	9	166	Q80M712	Q80M712	human herpe
255	2	18.2	9	167	Q80M716	Q80M716	human herpe
256	2	18.2	9	168	Q80M720	Q80M720	human herpe

236	2	18.2	10	10	Q9S926	Q9S926 glycolic max	309	2	18.2	11	7	077911	077911 oreochromis
237	2	18.2	10	10	Q8LP17	Q8LP17 zua rays (m	310	2	18.2	11	8	Q8MEL7	Q8MEL7 sida hooker
238	2	18.2	10	10	Q9S936	Q9S936 beta vulgar	311	2	18.2	11	8	Q8MAZ1	Q8MAZ1 maripa pani
239	2	18.2	10	10	P82937	P82937 hordeum vul	312	2	18.2	11	8	Q8MB19	Q8MB19 willsonia hu
240	2	18.2	10	10	P82938	P82938 hordeum vul	313	2	18.2	11	8	Q8MBM2	Q8MBM2 laquaria p
241	2	18.2	10	10	P82434	P82434 ruscocoria l	314	2	18.2	11	8	Q8MB58	Q8MB58 seddera hlr
242	2	18.2	10	10	Q9QVFB	Q9QVFB mus sp. pro	315	2	18.2	11	8	Q8MAZ3	Q8MAZ3 maripa repe
243	2	18.2	10	11	Q9QVFB	Q9QVFB mus sp. pro	316	2	18.2	11	8	Q8MES5	Q8MES5 abelmoschus
244	2	18.2	10	11	Q9QVFB	Q9QVFB mus sp. pro	317	2	18.2	11	8	Q8MEP0	Q8MEP0 hibiscus pe
245	2	18.2	10	11	Q9QVFB	Q9QVFB mus sp. pro	318	2	18.2	11	8	Q8MES1	Q8MES1 alyogyne pi
246	2	18.2	10	11	Q9QVFB	Q9QVFB mus sp. pro	319	2	18.2	11	8	Q8MEP3	Q8MEP3 hibiscus no
247	2	18.2	10	11	Q9QVFB	Q9QVFB mus sp. pro	320	2	18.2	11	8	Q8MBE1	Q8MBE1 ipomoea alb
248	2	18.2	10	11	Q9QVFB	Q9QVFB mus sp. pro	321	2	18.2	11	8	Q8MEP7	Q8MEP7 hibiscus dr
249	2	18.2	10	11	Q9QVFB	Q9QVFB mus sp. pro	322	2	18.2	11	8	Q8MEP7	Q8MEP7 hibiscus dr
250	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	323	2	18.2	11	8	Q8MEP9	Q8MEP9 pavonia has
251	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	324	2	18.2	11	8	Q8MB77	Q8MB77 odonellia h
252	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	325	2	18.2	11	8	Q8MEH0	Q8MEH0 hibiscus co
253	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	326	2	18.2	11	8	Q8MES3	Q8MES3 alyogyne cr
254	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	327	2	18.2	11	8	Q8MB79	Q8MB79 aniseia arg
255	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	328	2	18.2	11	8	Q8MB97	Q8MB97 merremia pe
256	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	329	2	18.2	11	8	Q8MEP5	Q8MEP5 hibiscus mi
257	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	330	2	18.2	11	8	Q8MEH1	Q8MEH1 hibiscus ca
258	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	331	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
259	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	332	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
260	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	333	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
261	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	334	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
262	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	335	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
263	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	336	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
264	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	337	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
265	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	338	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
266	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	339	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
267	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	340	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
268	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	341	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
269	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	342	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
270	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	343	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
271	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	344	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
272	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	345	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
273	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	346	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
274	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	347	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
275	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	348	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
276	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	349	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
277	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	350	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
278	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	351	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
279	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	352	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
280	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	353	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
281	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	354	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
282	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	355	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
283	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	356	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
284	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	357	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
285	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	358	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
286	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	359	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
287	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	360	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
288	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	361	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
289	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	362	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
290	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	363	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
291	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	364	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
292	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	365	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
293	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	366	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
294	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	367	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
295	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	368	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
296	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	369	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
297	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	370	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
298	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	371	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
299	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	372	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
300	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	373	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
301	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	374	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
302	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	375	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
303	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	376	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
304	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	377	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
305	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	378	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
306	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	379	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
307	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	380	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti
308	2	18.2	10	12	Q9QVFB	Q9QVFB mus sp. pro	381	2	18.2	11	8	Q8MEH7	Q8MEH7 fioria viti

QY 11 SIMILARITY: BELONGS TO THE RUBISCO, SMALL SUBUNIT FAMILY.
 KW Photosynthesis; Carbon dioxide fixation; Photorespiration; Lyase;
 KW Oxidoreductase; Monooxygenase; Calvin cycle;
 FT NON_TER 10
 SQ SEQUENCE 10 AA: 1322 MW: 84422Da; 132767.1; 136764;

Query Match 27.3%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KER 5
 DB 6 KER 8
 ID 11
 AC Q9H4H5 PRELIMINARY; PRT; 11 AA.
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE 5361120.2 (Novel Helicase C-terminal domain and SNF2 N-terminal
 DE domains containing protein) (Fragment).
 GN h629ELL1.3
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homin
 OC NCBI_TaxID 9606;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Score 0.3
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A051659; CAC17164.2;
 FT NON_TER 11
 FT NON_TER 11
 SQ SEQUENCE 11 AA: 1420 MW: 565232Da; 142615.4; 14674;

Query Match 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
 DB 2 KKE 5
 ID 11
 AC Q9H4H5 PRELIMINARY; PRT; 11 AA.
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 25 kDa protein P25, peptide P4 (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa;
 OC Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID-9913;
 RN 11
 RP SEQUENCE.
 RA MEDLINE: 91372400; PubMed:1909472;
 RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
 RA Shiratsuchi A., Uchida T., Imahori K.
 XT *A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
 RT Ser/Thr-pro kinase (TPK II) from tau protein kinase fractions.*;
 RL FEBS Lett. 289:37-43(1991).
 FT NON_TER 11
 FT NON_TER 11
 SQ SEQUENCE 11 AA: 1276 MW: 147215Da; 1476AA; 14674;

Query Match 27.3%; Score 3; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 7.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KER 5
 DB 1 KER 4
 ID 11
 AC Q8VLX8 PRELIMINARY; PRT; 12 AA.
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Lysyl-tRNA synthetase (Fragment).
 GN LYSS.
 OS Thermus thermophilus.
 OC Bacteria; Deihnococcus Thermus; Deinococci; Thermales; Thermaceae;
 OC Thermus.
 OC NCBI_TaxID-274;
 RN 11
 RP SEQUENCE FROM N.A.
 RA STRA:N-K18;
 RA Spada S., Pembroke J., Wall J.C.;
 RT "Cloning and characterisation of the *czrB* metal cation efflux protein
 RT from *T. thermophilus*.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ307316; CAC83721.1;
 KW Aminoacyl tRNA synthetase.
 FT NON_TER 11
 SQ SEQUENCE 12 AA: 1327 MW: 502433Da; 1327ECDDb13 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
 DB 4 KKE 6
 ID 11
 AC Q25179 PRELIMINARY; PRT; 12 AA.
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical Protein HP0429.
 GN HP0429.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
 OC Helicobacteraceae; Helicobacter.
 OC NCBI_TaxID=210;
 RN 11
 RP SEQUENCE FROM N.A.
 RA STRAIN-26695 / ATCC 700392;
 RA MEDLINE: 97334467; PubMed:9252185;
 RA Tomb J.-F., White O., Kerlavage A.R., Klenk H.-P., Gill S., Dougherty B.A.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Kirkness E.F., Peterson S.,
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Glodek A.,
 RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
 RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
 RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen *Helicobacter*
 RT *pylori*.";
 RL Nature 388:539-547(1997).
 DR EMBL: AF005559; AAC07512.1;
 DR TIGR: HP0429.

K0 Bystochetis protein: Complete proteome.
SQ SEQUENCE 12 AA: 1375 MW: 20959A845215538 CRC64:

Query Match 27.3% Score 3; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4

DL 6 KKE 8

RESULT 10

Q55094 PRELIMINARY: PRT: 13 AA.

AC Q55094.

DT 01-NOV-1996 (TRENBLREL: 01, Created)

DT 01-NOV-1996 (TRENBLREL: 01, Last sequence update)

DT 01-NOV-1998 (TRENBLREL: 08, Last annotation update)

DE Allophycocyanin (Fragment).

GN APCB.

OS Bystochetis sp.

OC Bacteria; Cyanobacteria; Charococcales; Synechocystis

OX NCBI_TaxID:1143;

RN [1]

RZ SEQUENCE FROM N.A.

XX MEDLINE:96236188; PubMed:9787495;

RA Brass S.; Ernst A.; Rger P.;

RT *An insertion element prevents physiological synthesis in NZ fixing

RI Synechocystis sp. strain B-8422.

RL Appl. Environ. Microbiol. 62:1464-1468 (1996).

DR EMBL:176084; AAC41532.1;

FT NON_TER

SQ SEQUENCE 13 AA: 1451 MW: 611917916057766 CRC64:

Query Match

Best Local Similarity 27.3% Score 3; DB 13; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKE 5

DL 9 KKE 11

RESULT 11

Q59401

AC Q59401 PRELIMINARY: PRT: 13 AA.

DT 01-MAR-2001 (TRENBLREL: 16, Created)

DT 01-MAR-2001 (TRENBLREL: 16, Last sequence update)

DT 01-DEC-2001 (TRENBLREL: 19, Last annotation update)

DE Anotopoletin-ZB (Fragment).

GN ANOTOPOLETIN-ZB.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Euteleostomi; Euteleostomi

OX NCBI_TaxID:9606;

RN [1]

RZ SEQUENCE FROM N.A.

XX MEDLINE:20424111; PubMed:19647173;

RA Mezquita J.; Mezquita P.; Monserat J.; Mezquita P.; Francine V.;

RA Villanosa X.; Mezquita C.;

RZ *Genomic structure and alternative splicing of ankyrin and related in

RI ZB.

RE Biochem. Biophys. Res. Commun. 277:445-451 (2001).

DR EMBL:AJ289780; CAC08179.1;

FT NON_TER

SQ SEQUENCE 13 AA: 1548 MW: 35435050456024964.

Query Match

Best Local Similarity 27.3% Score 3; DB 13; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KKE 5

DL 9 KKE 11

QY 2 KKE 4
DL 6 KKE 8

RESULT 12

Q574K5 PRELIMINARY: PRT: 13 AA.

AC Q574K5.

DT 01-MAY-2000 (TRENBLREL: 13, Created)

DT 01-MAY-2000 (TRENBLREL: 13, Last sequence update)

DT 01-MAY-2000 (TRENBLREL: 13, Last annotation update)

DE PSH (Fragment).

GN PSH.

OS Bryopsis sp. C.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;

OC Bryopsidaceae; Bryopsis.

OX NCBI_TaxID:103780;

RN [1]

RZ SEQUENCE FROM N.A.

RP STRAIN VARIOUS STRAINS;

RA Krellwitz E.C.; Kowalik K.V.; Manos P.S.;

RT *Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North

RI Atlantic and Caribbean based on coding and Non-coding sequences of the

RI Chloroplast psbB operon.;

RI Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL:AF170407; AAC56846.1;

DR EMBL:AF170383; AAC56798.1;

DR EMBL:AF170384; AAC56800.1;

DR EMBL:AF170385; AAC56802.1;

DR EMBL:AF170386; AAC56804.1;

DR EMBL:AF170387; AAC56806.1;

DR EMBL:AF170388; AAC56808.1;

DR EMBL:AF170389; AAC56810.1;

DR EMBL:AF170392; AAC56812.1;

DR EMBL:AF170391; AAC56814.1;

DR EMBL:AF170392; AAC56816.1;

DR EMBL:AF170393; AAC56818.1;

DR EMBL:AF170394; AAC56820.1;

KW Chloroplast.

FT NON_TER

SQ SEQUENCE 13 AA: 1366 MW: 2031687A2E93A338 CRC64:

Query Match

Best Local Similarity 27.3% Score 3; DB 8; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KKE 10

DL 7 KKE 9

RESULT 13

Q57HSC PRELIMINARY: PRT: 13 AA.

AC Q57HSC.

DT 01-MAY-2000 (TRENBLREL: 13, Created)

DT 01-MAY-2000 (TRENBLREL: 13, Last sequence update)

DE PSH (Fragment).

GN PSH.

OS Bryopsis sp. B.

OC Chloroplast.

OC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;

OC Bryopsidaceae; Bryopsis.

OX NCBI_TaxID:103780;

RN [1]

RZ SEQUENCE FROM N.A.

RA Kowalik K.V.; Kowalik K.V.; Manos P.S.;

RT *Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North

RI Atlantic and Caribbean based on coding and Non-coding sequences of the

RT Chloroplast psbB Operon.
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF170404; AAD56844.1;
 KW Chloroplast.
 FT NON-TER 13 13
 SQ SEQUENCE 13 AA: 1351 MW: 20316A502E3A6A00 10000

Query Match 27.3% Score 3; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KDT 10

LD 1

LD 7 KDT 9

RESULT 14

Q9T4K4

AC Q9T4K4 PRELIMINARY; PRT: 13 AA.

DT 01-MAY-2000 (TRENBLREL, 13, Created)

DT 01-MAY-2000 (TRENBLREL, 13, Last sequence update)

DT 01-MAY-2000 (TRENBLREL, 13, Last annotation update)

DE PSB (Fragment).

GN PSB.

OS Bryopsis sp. B.

OC Chloroplast.

CC Eukaryota; Viridiplantae; Chlorophyta; Ulvophyceae; Caulerpaceae;

CC Bryopsidaceae; Bryopsis.

OX NCBI_TaxID:103785;

RN 11

RP SEQUENCE FROM N.A.

RC STRAIN VARIANTS STRAINS:

RA Kreilwitz E.C., Kowalik K.V., Manos P.S.;

RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North

AT Atlantic and Caribbean based on Coding and Non-coding sequences of the

RT Chloroplast psbB Operon."

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF170405; AAD56842.1;

DR EMBL: AF170406; AAD56843.1;

DR EMBL: AF170407; AAD56844.1;

DR EMBL: AF170408; AAD56845.1;

DR EMBL: AF170409; AAD56846.1;

DR EMBL: AF170410; AAD56847.1;

DR EMBL: AF170411; AAD56848.1;

DR EMBL: AF170412; AAD56849.1;

DR EMBL: AF170413; AAD56850.1;

DR EMBL: AF170414; AAD56851.1;

DR EMBL: AF170415; AAD56852.1;

DR EMBL: AF170416; AAD56853.1;

DR EMBL: AF170417; AAD56854.1;

DR EMBL: AF170418; AAD56855.1;

DR EMBL: AF170419; AAD56856.1;

DR EMBL: AF170420; AAD56857.1;

DR EMBL: AF170421; AAD56858.1;

DR EMBL: AF170422; AAD56859.1;

DR EMBL: AF170423; AAD56860.1;

DR EMBL: AF170424; AAD56861.1;

DR EMBL: AF170425; AAD56862.1;

DR EMBL: AF170426; AAD56863.1;

DR EMBL: AF170427; AAD56864.1;

DR EMBL: AF170428; AAD56865.1;

DR EMBL: AF170429; AAD56866.1;

DR EMBL: AF170430; AAD56867.1;

DR EMBL: AF170431; AAD56868.1;

DR EMBL: AF170432; AAD56869.1;

DR EMBL: AF170433; AAD56870.1;

DR EMBL: AF170434; AAD56871.1;

DR EMBL: AF170435; AAD56872.1;

DR EMBL: AF170436; AAD56873.1;

DR EMBL: AF170437; AAD56874.1;

DR EMBL: AF170438; AAD56875.1;

DR EMBL: AF170439; AAD56876.1;

DR EMBL: AF170440; AAD56877.1;

DR EMBL: AF170441; AAD56878.1;

DR EMBL: AF170442; AAD56879.1;

DR EMBL: AF170443; AAD56880.1;

DR EMBL: AF170444; AAD56881.1;

DR EMBL: AF170445; AAD56882.1;

DR EMBL: AF170446; AAD56883.1;

DR EMBL: AF170447; AAD56884.1;

DR EMBL: AF170448; AAD56885.1;

DR EMBL: AF170449; AAD56886.1;

DR EMBL: AF170450; AAD56887.1;

DR EMBL: AF170451; AAD56888.1;

DR EMBL: AF170452; AAD56889.1;

DR EMBL: AF170453; AAD56890.1;

DR EMBL: AF170454; AAD56891.1;

DR EMBL: AF170455; AAD56892.1;

DR EMBL: AF170456; AAD56893.1;

DR EMBL: AF170457; AAD56894.1;

DR EMBL: AF170458; AAD56895.1;

DR EMBL: AF170459; AAD56896.1;

DR EMBL: AF170460; AAD56897.1;

DR EMBL: AF170461; AAD56898.1;

DR EMBL: AF170462; AAD56899.1;

DR EMBL: AF170463; AAD56900.1;

DR EMBL: AF170464; AAD56901.1;

DR EMBL: AF170465; AAD56902.1;

DR EMBL: AF170466; AAD56903.1;

DR EMBL: AF170467; AAD56904.1;

DR EMBL: AF170468; AAD56905.1;

DR EMBL: AF170469; AAD56906.1;

DR EMBL: AF170470; AAD56907.1;

DR EMBL: AF170471; AAD56908.1;

DR EMBL: AF170472; AAD56909.1;

DR EMBL: AF170473; AAD56910.1;

DR EMBL: AF170474; AAD56911.1;

DR EMBL: AF170475; AAD56912.1;

DR EMBL: AF170476; AAD56913.1;

DR EMBL: AF170477; AAD56914.1;

DR EMBL: AF170478; AAD56915.1;

DR EMBL: AF170479; AAD56916.1;

DR EMBL: AF170480; AAD56917.1;

DR EMBL: AF170481; AAD56918.1;

DR EMBL: AF170482; AAD56919.1;

DR EMBL: AF170483; AAD56920.1;

DR EMBL: AF170484; AAD56921.1;

DR EMBL: AF170485; AAD56922.1;

DR EMBL: AF170486; AAD56923.1;

DR EMBL: AF170487; AAD56924.1;

DR EMBL: AF170488; AAD56925.1;

DR EMBL: AF170489; AAD56926.1;

DR EMBL: AF170490; AAD56927.1;

DR EMBL: AF170491; AAD56928.1;

DR EMBL: AF170492; AAD56929.1;

DR EMBL: AF170493; AAD56930.1;

DR EMBL: AF170494; AAD56931.1;

DR EMBL: AF170495; AAD56932.1;

DR EMBL: AF170496; AAD56933.1;

DR EMBL: AF170497; AAD56934.1;

DR EMBL: AF170498; AAD56935.1;

DR EMBL: AF170499; AAD56936.1;

DR EMBL: AF170500; AAD56937.1;

DR EMBL: AF170501; AAD56938.1;

DR EMBL: AF170502; AAD56939.1;

DR EMBL: AF170503; AAD56940.1;

DR EMBL: AF170504; AAD56941.1;

DR EMBL: AF170505; AAD56942.1;

DR EMBL: AF170506; AAD56943.1;

DR EMBL: AF170507; AAD56944.1;

DR EMBL: AF170508; AAD56945.1;

DR EMBL: AF170509; AAD56946.1;

DR EMBL: AF170510; AAD56947.1;

DR EMBL: AF170511; AAD56948.1;

DR EMBL: AF170512; AAD56949.1;

DR EMBL: AF170513; AAD56950.1;

DR EMBL: AF170514; AAD56951.1;

DR EMBL: AF170515; AAD56952.1;

DR EMBL: AF170516; AAD56953.1;

DR EMBL: AF170517; AAD56954.1;

DR EMBL: AF170518; AAD56955.1;

DR EMBL: AF170519; AAD56956.1;

DR EMBL: AF170520; AAD56957.1;

DR EMBL: AF170521; AAD56958.1;

DR EMBL: AF170522; AAD56959.1;

DR EMBL: AF170523; AAD56960.1;

DR EMBL: AF170524; AAD56961.1;

DR EMBL: AF170525; AAD56962.1;

DR EMBL: AF170526; AAD56963.1;

DR EMBL: AF170527; AAD56964.1;

DR EMBL: AF170528; AAD56965.1;

DR EMBL: AF170529; AAD56966.1;

DR EMBL: AF170530; AAD56967.1;

DR EMBL: AF170531; AAD56968.1;

DR EMBL: AF170532; AAD56969.1;

DR EMBL: AF170533; AAD56970.1;

DR EMBL: AF170534; AAD56971.1;

DR EMBL: AF170535; AAD56972.1;

DR EMBL: AF170536; AAD56973.1;

DR EMBL: AF170537; AAD56974.1;

DR EMBL: AF170538; AAD56975.1;

DR EMBL: AF170539; AAD56976.1;

DR EMBL: AF170540; AAD56977.1;

DR EMBL: AF170541; AAD56978.1;

DR EMBL: AF170542; AAD56979.1;

DR EMBL: AF170543; AAD56980.1;

DR EMBL: AF170544; AAD56981.1;

DR EMBL: AF170545; AAD56982.1;

DR EMBL: AF170546; AAD56983.1;

DR EMBL: AF170547; AAD56984.1;

DR EMBL: AF170548; AAD56985.1;

DR EMBL: AF170549; AAD56986.1;

DR EMBL: AF170550; AAD56987.1;

DR EMBL: AF170551; AAD56988.1;

DR EMBL: AF170552; AAD56989.1;

DR EMBL: AF170553; AAD56990.1;

DR EMBL: AF170554; AAD56991.1;

DR EMBL: AF170555; AAD56992.1;

DR EMBL: AF170556; AAD56993.1;

DR EMBL: AF170557; AAD56994.1;

DR EMBL: AF170558; AAD56995.1;

DR EMBL: AF170559; AAD56996.1;

DR EMBL: AF170560; AAD56997.1;

DR EMBL: AF170561; AAD56998.1;

DR EMBL: AF170562; AAD56999.1;

DR EMBL: AF170563; AAD57000.1;

DR EMBL: AF170564; AAD57001.1;

DR EMBL: AF170565; AAD57002.1;

DR EMBL: AF170566; AAD57003.1;

DR EMBL: AF170567; AAD57004.1;

DR EMBL: AF170568; AAD57005.1;

DR EMBL: AF170569; AAD57006.1;

DR EMBL: AF170570; AAD57007.1;

DR EMBL: AF170571; AAD57008.1;

DR EMBL: AF170572; AAD57009.1;

DR EMBL: AF170573; AAD57010.1;

DR EMBL: AF170574; AAD57011.1;

DR EMBL: AF170575; AAD57012.1;

DR EMBL: AF170576; AAD57013.1;

DR EMBL: AF170577; AAD57014.1;

DR EMBL: AF170578; AAD57015.1;

DR EMBL: AF170579; AAD57016.1;

DR EMBL: AF170580; AAD57017.1;

DR EMBL: AF170581; AAD57018.1;

DR EMBL: AF170582; AAD57019.1;

DR EMBL: AF170583; AAD57020.1;

DR EMBL: AF170584; AAD57021.1;

DR EMBL: AF170585; AAD57022.1;

DR EMBL: AF170586; AAD57023.1;

DR EMBL: AF170587; AAD57024.1;

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QC Bryopsidaceae: Bryopsis.
CX NCBI_TaxID=103784;
FN
RP SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS;
RA Kreilwitz E.C., Kowalik K.V., Marcus P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
AT Atlantic and Caribbean based on Coding and Non-coding Sequences of the
RT Chloroplast psbB Operon."
RE Submitted (JUL-1999) to the EMBL/GenBank/TrEMBL databases
DR EMBL: AF170415; AAD56862.1;
DR EMBL: AF170408; AAD56848.1;
DR EMBL: AF170409; AAD56850.1;
DR EMBL: AF170410; AAD56852.1;
DR EMBL: AF170411; AAD56854.1;
DR EMBL: AF170412; AAD56856.1;
DR EMBL: AF170414; AAD56860.1;
KW Chloroplast.
FT NON-TER
SQ SEQUENCE 13 AA: 1366 MW: 26516874259-AAA+48-46-44;
      27.3% Score 3; DB 12; Length 13;
      Best Local Similarity 100.0%; Pred. No. 8.5e+03;
      Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KDT 10
DB
  III
  7 KDT 9

RESULT 18
Q914K3
ID Q914K3 PRELIMINARY: PRT: 13 AA.
AC Q914K3
DT 01 MAY-2000 (TrEMBLrel. 13; Created)
DT 01 MAY-2000 (TrEMBLrel. 13; Last sequence update)
DT 01 JUN-2001 (TrEMBLrel. 17; Last annotation update)
DE PSBH (Fragment).
GN PSBH
GS Bryopsis sp. E.
OS Chloroplast.
OC Eukaryota: Viridiplantae: Chlorophyta: Chlorophyceae: Bryopsidaceae: Bryopsis.
CX NCBI_TaxID=103788;
FN
RP SEQUENCE FROM N.A.
RC STRAIN-95-05-23, 96-07-03, 95-12-23, 95-12-23, 95-12-23, and 96-08-03.
RA Kreilwitz E.C., Kowalik K.V., Marcus P.S.;
RT "Phylogenetic Study of Bryopsis (Chlorophyta) from the Western North
AT Atlantic and Caribbean based on Coding and Non-coding Sequences of the
RT Chloroplast psbB Operon."
RE Submitted (JUL-1999) to the EMBL/GenBank/TrEMBL databases.
DR EMBL: AF170380; AAD56792.1;
DR EMBL: AF170381; AAD56793.1;
DR EMBL: AF170373; AAD56778.1;
DR EMBL: AF170375; AAD56782.1;
DR EMBL: AF170376; AAD56784.1;
DR EMBL: AF170377; AAD56786.1;
DR EMBL: AF170378; AAD56788.1;
KW Chloroplast.
FT NON-TER
SQ SEQUENCE 13 AA: 1366 MW: 26516874259-AAA+48-46-44;
      27.3% Score 3; DB 12; Length 13;
      Best Local Similarity 100.0%; Pred. No. 8.5e+03;
      Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KDT 10
DB
  III
  7 KDT 9

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 19
Q61761
ID Q61761 PRELIMINARY: PRT: 13 AA.
AC Q61761
DT 01-NOV-1996 (TrEMBLrel. 01; Created)
DT 01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22; Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses: ssRNA positive-strand viruses, no DNA stage: Flaviviridae;
CX Hepacivirus.
CX NCBI_TaxID=11104;
FN
RP SEQUENCE FROM N.A.
RC STRAIN D3;
RX MEDLINE-92279243; PubMed-117578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
AT Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
DE -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84842; AAA45679.1;
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON-TER
SQ SEQUENCE 13 AA: 1572 MW: 464F97E1A42FC763 CRC64;
      27.3% Score 3; DB 12; Length 13;
      Best Local Similarity 100.0%; Pred. No. 8.5e+03;
      Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8
DB
  III
  8 QRK 10

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 20
Q81794
ID Q81794 PRELIMINARY: PRT: 13 AA.
AC Q81794
DT 01-NOV-1996 (TrEMBLrel. 01; Created)
DT 01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22; Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses: ssRNA positive-strand viruses, no DNA stage: Flaviviridae;
CX Hepacivirus.
CX NCBI_TaxID=11104;
FN
RP SEQUENCE FROM N.A.
RC STRAIN-IND5;
RX MEDLINE-92279243; PubMed-117578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus."
AT Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
DE -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84854; AAA45711.1;
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON-TER
SQ SEQUENCE 13 AA: 1572 MW: 464F97E1A42FC763 CRC64;
      27.3% Score 3; DB 12; Length 13;
      Best Local Similarity 100.0%; Pred. No. 8.5e+03;
      Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KDT 10
DB
  III
  7 KDT 9

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 6 QRK 8
DB 111
8 QRK 10

RESULT 21
Q81784
ID Q81784 PRELIMINARY: PRT: 13 AA.
AC Q81784
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-21;
RX MEDLINE:92279243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84845; AAA45701.1;
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW: 4649791442FC763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8
DB 111
8 QRK 10

RESULT 22
Q81778
ID Q81778 PRELIMINARY: PRT: 13 AA.
AC Q81778
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SW3;
RX MEDLINE:92279243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84850; AAA45695.1;
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.

QY 6 QRK 8
DB 111
8 QRK 10

RESULT 23
Q81787
ID Q81787 PRELIMINARY: PRT: 13 AA.
AC Q81787
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Z6;
RX MEDLINE:92279243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84862; AAA45704.1;
DR InterPro: IPR002522; HCV_capsid;
DR Pfam: PF01543; HCV_capsid; 1;
KW Polyprotein.
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW: 4649791442FC763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8
DB 111
8 QRK 10

RESULT 24
Q81775
ID Q81775 PRELIMINARY: PRT: 13 AA.
AC Q81775
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SA7;
RX MEDLINE:92279243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A

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CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84852; AAA45693.1; -.
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER 13
SQ SEQUENCE 13 AA: 1572 MW: 46497E1A42FC763 CRC64.

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 9
DB 8 QRK 10

RESULT 25
Q81767 PRELIMINARY; PRT; 13 AA.
AC Q81767;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN HK5;
RX MEDLINE-92279243; PubMed-1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RI "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84849; AAA45685.1; -.
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER 13
SQ SEQUENCE 13 AA: 1572 MW: 46497E1A42FC763 CRC64.

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8
DB 8 QRK 10

RESULT 26
Q81798 PRELIMINARY; PRT; 13 AA.
AC Q81798;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-SAL1;
RX MEDLINE-92279243; PubMed-1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RI "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84858; AAA45715.1; -.
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER 13
SQ SEQUENCE 13 AA: 1572 MW: 46497E1A42FC763 CRC64.

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8
DB 8 QRK 10

RESULT 27
Q81774 PRELIMINARY; PRT; 13 AA.
AC Q81774;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SAL1;
RX MEDLINE-92279243; PubMed-1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RI "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84860; AAA45692.1; -.
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER 13
SQ SEQUENCE 13 AA: 1572 MW: 46497E1A42FC763 CRC64.

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8
DB 8 QRK 10

RESULT 28
Q81766 PRELIMINARY; PRT; 13 AA.
AC Q81766;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

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Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 6 QPK 8
DB 111
8 QPK 10

RESULT 32
Q81765 ID Q81765 PRELIMINARY: PRT; 13 AA.
AC Q81765
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US11;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992);
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M44865; AAA45717; 1.
DR InterPro: IPR002522; HCV_capsid; 1.
DR Pfam: PF01543; HCV_capsid; 1.
KW Non_Ter.
FT NON_TER.
SQ SEQUENCE 13 AA: 1572 MW: 464797E1A42FC763 CRC64;

Query Match: 27.3% Score 3; DB 12: Length 13;
Best local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 6 QPK 8
DB 111
8 QPK 10

RESULT 33
Q81765 ID Q81765 PRELIMINARY: PRT; 13 AA.
AC Q81765
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US4;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992);
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M44865; AAA45683; 1.
DR InterPro: IPR002522; HCV_capsid; 1.

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DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER.
SQ SEQUENCE 13 AA: 1572 MW: 464797E1A42FC763 CRC64;

Query Match: 27.3% Score 3; DB 12: Length 13;
Best local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 6 QPK 8
DB 111
8 QPK 10

RESULT 34
Q81765 ID Q81765 PRELIMINARY: PRT; 13 AA.
AC Q81765
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992);
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M44865; AAA45698; 1.
DR InterPro: IPR002522; HCV_capsid; 1.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER.
SQ SEQUENCE 13 AA: 1557 MW: 464CF7E1A42FC763 CRC64;

Query Match: 27.3% Score 3; DB 12: Length 13;
Best local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 6 QPK 8
DB 111
8 QPK 10

RESULT 35
Q81765 ID Q81765 PRELIMINARY: PRT; 13 AA.
AC Q81765
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=US;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;

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BL      Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC      1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC      LIPIDPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC      PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC      PROTEIN C AND MRNA (BY SIMILARITY).
DR      EMBL: M84856; AAA45687.1; .
DR      InterPro: IPR002522; HCV_capsid; 1;
DR      Pfam: PF01543; HCV_capsid; 1;
KW      Polyprotein.
FT      NON_TER
SQ      SEQUENCE 13 AA: 1559 MW: 465403.1; AA421704; 19304;

Query Match 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 QKK 8
DB      8 QKK 10

RESULT 46
Q81773
ID      Q81773 PRELIMINARY; PRI: 13 AA.
AC      Q81773;
DT      01-NOV-1996 (TrEMBLrel. 01; Created)
DI      01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DE      01-NOV-2002 (TrEMBLrel. 22; Last annotation update)
DE      Genome polyprotein (Fragment).
GN      POLYPROTEIN.
OS      Hepatitis C virus.
OC      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
CC      Hepacivirus.
CX      NCBI_TaxId:11103;
KW      NON_TER
SQ      SEQUENCE FROM N.A.
RC      STRAIN-S9;
RX      MEDLINE-92279243; PubMed-1317578;
RA      Bakh J., Purcell R.H., Miller R.H.;
RT      *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RT      Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC      1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC      LIPIDPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC      PROTEIN C AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC      PROTEIN C AND MRNA (BY SIMILARITY).
DR      EMBL: M84856; AAA45691.1; .
DR      InterPro: IPR002522; HCV_capsid; 1;
DR      Pfam: PF01543; HCV_capsid; 1;
KW      Polyprotein.
FT      NON_TER
SQ      SEQUENCE 13 AA: 1572 MW: 464976.1; AA421704; 19304;

Query Match 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 QKK 8
DB      8 QKK 10

RESULT 47
Q81799
ID      Q81799 PRELIMINARY; PRI: 13 AA.
AC      Q81799;
DT      01-NOV-1996 (TrEMBLrel. 01; Created)
DI      01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DE      01-OCT-2002 (TrEMBLrel. 22; Last annotation update)
DE      Genome polyprotein (Fragment).
GN      POLYPROTEIN.
OS      Hepatitis C virus.
OC      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
CC      Hepacivirus.

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CX      NCBI_TaxId:11103;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-T10;
RX      MEDLINE-92279243; PubMed-1317578;
RA      Bakh J., Purcell R.H., Miller R.H.;
RT      *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RT      Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC      1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC      LIPIDPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC      PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC      PROTEIN C AND MRNA (BY SIMILARITY).
DR      EMBL: M84843; AAA45716.1; .
DR      InterPro: IPR002522; HCV_capsid; 1;
DR      Pfam: PF01543; HCV_capsid; 1;
KW      Polyprotein.
FT      NON_TER
SQ      SEQUENCE 13 AA: 1572 MW: 464976.1; AA421704; 19304;

Query Match 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 QKK 8
DB      8 QKK 10

RESULT 48
Q81786
ID      Q81786 PRELIMINARY; PRI: 13 AA.
AC      Q81786;
DT      01-NOV-1996 (TrEMBLrel. 01; Created)
DI      01-NOV-1996 (TrEMBLrel. 01; Last sequence update)
DE      01-OCT-2002 (TrEMBLrel. 22; Last annotation update)
DE      Genome polyprotein (Fragment).
GN      POLYPROTEIN.
OS      Hepatitis C virus.
OC      Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
CC      Hepacivirus.
CX      NCBI_TaxId:11103;
KW      NON_TER
SQ      SEQUENCE FROM N.A.
RC      STRAIN-25;
RX      MEDLINE-92279243; PubMed-1317578;
RA      Bakh J., Purcell R.H., Miller R.H.;
RT      *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RT      Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC      1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC      LIPIDPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC      PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC      PROTEIN C AND MRNA (BY SIMILARITY).
DR      EMBL: M84828; AAA45703.1; .
DR      InterPro: IPR002522; HCV_capsid; 1;
DR      Pfam: PF01543; HCV_capsid; 1;
KW      Polyprotein.
FT      NON_TER
SQ      SEQUENCE 13 AA: 1572 MW: 464976.1; AA421704; 19304;

Query Match 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 QKK 8
DB      8 QKK 10

RESULT 49
Q81788
ID      Q81788 PRELIMINARY; PRI: 13 AA.
AC      Q81788;
DT      01-NOV-1996 (TrEMBLrel. 01; Created)

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DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN 28;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84839; AAA45705.1; -
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW POLYPROTEIN
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW; 464F7E1A42FC763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8
DB 8 QRK 10

RESULT 40
Q81763 PRELIMINARY; PRT; 13 AA.
AC Q81763;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DK9;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84851; AAA45682.1; -
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW POLYPROTEIN
FT NON_TER
SQ SEQUENCE 13 AA: 1572 MW; 464F97E1A42FC763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8
DB 8 QRK 10

RESULT 41
Q81764 PRELIMINARY; PRT; 13 AA.
AC Q81764;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DK9;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84837; AAA45713.1; -
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW POLYPROTEIN
FT NON_TER
SQ SEQUENCE 13 AA: 1571 MW; 464D1DE1A42FC763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QRK 8
DB 8 QRK 10

RESULT 42
Q81796 PRELIMINARY; PRT; 13 AA.
AC Q81796;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Genome polyprotein (Fragment)
GN POLYPROTEIN
OS Hepatitis C virus
OC Viruses; ssRNA positive strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus
OX NCBI_TaxID=11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S52;
RX MEDLINE=92279243; PubMed=1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84837; AAA45713.1; -
DR InterPro: IPR002522; HCV_capsid.
DR Pfam: PF01543; HCV_capsid; 1.
KW POLYPROTEIN
FT NON_TER
SQ SEQUENCE 13 AA: 1571 MW; 464D1DE1A42FC763 CRC64;

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Query Match: 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GRK 8
DB 8 GRK 10

RESULT 44
Q81762
ID Q81762 PRELIMINARY; PRT: 13 AA.
AC Q81762
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DK12;
RX MEDLINE:92279243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992);
CC [1] SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84864; AAA45708.1;
DK InterPro: IPR002522; HCV_capsid;
KW Polyprotein.
FT NON_TER 13
SEQUENCE 13 AA: 1572 MW: 464597E1A42FC763 CRC64;

Query Match: 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GRK 8
DB 8 GRK 10

RESULT 44
Q81762
ID Q81762 PRELIMINARY; PRT: 13 AA.
AC Q81762
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DK12;
RX MEDLINE:92279243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992);
CC [1] SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
PROTEIN C AND MRNA (BY SIMILARITY).

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DR EMBL: M84864; AAA45680.1;
DK InterPro: IPR002522; HCV_capsid;
KW Polyprotein.
FT NON_TER 13
SEQUENCE 13 AA: 1572 MW: 464597E1A42FC763 CRC64;

Query Match: 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GRK 8
DB 8 GRK 10

RESULT 45
Q81790
ID Q81790 PRELIMINARY; PRT: 13 AA.
AC Q81790
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DK12;
RX MEDLINE:92279243; PubMed:1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT *Sequence analysis of the 5' noncoding region of hepatitis C virus.*;
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992);
CC [1] SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
PROTEIN C AND MRNA (BY SIMILARITY).
DR EMBL: M84864; AAA45707.1;
DK InterPro: IPR002522; HCV_capsid;
KW Polyprotein.
FT NON_TER 13
SEQUENCE 13 AA: 1571 MW: 4540DE1A42FC763 CRC64;

Query Match: 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GRK 8
DB 8 GRK 10

RESULT 46
Q81783
ID Q81783 PRELIMINARY; PRT: 13 AA.
AC Q81783
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_TaxID:11103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DK6;
RX MEDLINE:92279243; PubMed:1317578;

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RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPID-PROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
CC EMBL: M84830; AAA45700.1; .
DR InterPro: IPR002522; HCV_capsid; 1.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SC SEQUENCE 13 AA: 1572 MW: 464F97E1A42FC763 CRC64:

Query Match 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPK 8
DB 8 QPK 10

RESULT 47
Q81789 PRELIMINARY: PRT: 13 AA.
AC Q81789;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_taxID-11103;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN DK11;
RX MEDLINE 92279243; PubMed-1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPID-PROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
CC EMBL: M84831; AAA45706.1; .
DR InterPro: IPR002522; HCV_capsid; 1.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SC SEQUENCE 13 AA: 1572 MW: 464F97E1A42FC763 CRC64:

Query Match 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPK 8
DB 8 QPK 10

RESULT 48
Q81797 PRELIMINARY: PRT: 13 AA.
AC Q81797;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.

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OC Viruses; ssRNA positive strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_taxID-11103;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN SA10;
RX MEDLINE 92279244; PubMed-1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPID-PROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
CC EMBL: M84844; AAA45714.1; .
DR InterPro: IPR002522; HCV_capsid; 1.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SC SEQUENCE 13 AA: 1572 MW: 464F97E1A42FC763 CRC64:

Query Match 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPK 8
DB 8 QPK 10

RESULT 49
Q81795 PRELIMINARY: PRT: 13 AA.
AC Q81795;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Genome polyprotein (Fragment).
GN POLYPROTEIN.
OS Hepatitis C virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Hepacivirus.
OX NCBI_taxID-11103;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN-IN08;
RX MEDLINE 92279244; PubMed-1317578;
RA Bukh J., Purcell R.H., Miller R.H.;
RT "Sequence analysis of the 5' noncoding region of hepatitis C virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946(1992).
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPID-PROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA (BY SIMILARITY).
CC EMBL: M84853; AAA45712.1; .
DR InterPro: IPR002522; HCV_capsid; 1.
DR Pfam: PF01543; HCV_capsid; 1.
KW Polyprotein.
FT NON_TER
SC SEQUENCE 13 AA: 1572 MW: 464F97E1A42FC763 CRC64:

Query Match 27.3%; Score 3; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QPK 8
DB 8 QPK 10

RESULT 50
Q81782 PRELIMINARY: PRT: 13 AA.
AC Q81782;

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AT ORF782;
 GI 51 NOV-1996 (TRENBLER1_01, Created)
 GI 51 NOV-1996 (TRENBLER1_01, Last sequence update)
 DT 01 OCT-2002 (TRENBLER1_22, Last annotation update)
 DE Genome polyprotein (Fragment).
 GN POLYPROTEIN
 GS Hepatitis C virus.
 OC Hepatitis C virus.
 OC VIRUSES: ssRNA positive-strand viruses, no RNA stage: Flaviviridae.
 OC Hepacivirus.
 CX NCBI TaxID: 11103;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN JS3;
 RX MEDLINE 92279243; PubMed-137578;
 RA Bokk S, Purcell R.H., Miller F.H.;
 RT "Sequence analysis of the 5' noncoding region of hepatitis C virus";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:442-446(1992).
 CC -1 SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
 CC GLYCOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
 CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
 CC PROTEIN C AND RNA (BY SIMILARITY).
 CC PMID: 804857; AAA56991;
 DR InterPro: IPR002522; HCV_capsid
 DR Pfam: PF01543; HCV_capsid; 1.
 KW polyprotein.
 FT Non-ter. 13 13
 SQ SEQUENCE 13 AA: 1572 MW: 464576.646250476013

Query Match 27.3% Score 31.10 E-05 Sequences 13
 Best local similarity 100.0% Pct. No. Hsp(s)
 Matches 33 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 1 QPK #
 IL 1
 H QPK 10

Search completed: September 30, 2003, 11:07:05
 Job time: 47.6667 secs

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CM protein - protein search, using SW-BLAST

Run on: September 30, 2003, 10:07:03, Search type: BLASTS, Sequences (without alignment)
99,341 Million ref., updates/sec

Title: US-09-787-443-2

Perfect score: 11

Sequence: 1 AKKERQKKUQ 11

Scoring table: GILGO

Gapop 50.0, Gapext 60.0

Searched: 3287.7 seqs, 4231058 residues

Word size: 0

Total number of hits satisfying chosen parameters: 75359

Minimum hit seq length: 8

Maximum hit seq length: 15

Post-processing: Listing first 500 summaries

Database: Issued Patents AA.*
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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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8	4	36.4	12	1	US-08-548-940-147
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15	4	36.4	13	2	US-08-747-187-77
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277	3	27.3	9	3	US-09-112-226-173	Sequence 179, App	350	3	27.3	9	4	US-09-839-542B-3379	Sequence 3379, Ap
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279	3	27.3	9	3	US-09-112-226-184	Sequence 181, App	352	3	27.3	9	4	US-09-839-542B-3461	Sequence 3461, Ap
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283	3	27.3	9	3	US-09-112-226-188	Sequence 185, App	356	3	27.3	9	4	PCT-US91-07506-37	Sequence 37, Appl
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285	3	27.3	9	3	US-09-112-226-190	Sequence 190, App	358	3	27.3	9	5	PCT-US93-12679-33	Sequence 33, Appl
286	3	27.3	9	3	US-09-112-226-191	Sequence 191, App	359	3	27.3	9	5	PCT-US95-00147-39	Sequence 39, Appl
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290	3	27.3	9	3	US-09-217-352-03	Sequence 203, App	363	3	27.3	9	5	US-08-103-490A-8	Sequence 8, Appl
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ALIGNMENTS

RESULT 1
US-08-159-339A-989
Sequence 989, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kuber, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Esteban
TITLE OF INVENTION: HLA Binding peptides and Their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 29-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993

APPLICATION NUMBER: US 08/185,448
 FILING DATE: 08-AUG-1993
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 REFERENCE/DOCKET NUMBER: 0185-23 30-00000005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 TELEX:
 INFORMATION FOR SEQ ID NO: 989:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE TYPE: peptide
 US-08 159-339A-989

Query Match 36.4% Score 4; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KSRQ 6
 DB 4 KSRQ 7

RESULT 2
 US 08-185-448-5
 Sequence 5; Application: US/05185448
 Patent No. 5580747

GENERAL INFORMATION:
 APPLICANT: SULTZ, JOHN W.
 APPLICANT: WHITE, DOUGLAS H.
 TITLE OF INVENTION: NON-RADIOLACTIVE KINASE
 TITLE OF INVENTION: PHOSPHATASE AND PHOSPHATASE ASSAY
 NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
 ADDRESSEE: ANDRUS, SCOTLAND, STARK & SAWALL
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 ZIP: 53202

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: BALUOLIO Release #1.0, VOLS 1-2
 SOFTWARE: #1125

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/185,448
 FILING DATE: 21-JAN-1994
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/794,428
 FILING DATE: 12-NOV-1991

ATTORNEY/AGENT INFORMATION:
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TELEX: 26832 ANDSTARK
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 FEATURE TYPE: peptide

NAME/KEY: Binding-site
 LOCATION: 1
 OTHER INFORMATION: /label= LABEL
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 OTHER INFORMATION: DETECTION TAG"
 US-08-185-448-5

Query Match 46.4% Score 4; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KSRK 8
 DB 3 KSRK 6

RESULT 3
 US 08-476-405A-10

Sequence 10; Application US/08476405A
 Patent No. 5776459
 GENERAL INFORMATION:
 APPLICANT: Vandenberg, Arthur A.

TITLE OF INVENTION: Method of Treatment Using TCR VBeta5 Peptides
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Connective Therapeutics, Inc.
 STREET: 3400 West Bayshore Road
 CITY: Palo Alto
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 COUNTRY: USA
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COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent: Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/476,405A
 FILING DATE:
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/059,020
 FILING DATE: 16-MAR-1993

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/755,612
 FILING DATE: 16-JUL-1991

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/708,022
 FILING DATE: 31-MAY-1991

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/554,529
 FILING DATE: 19-JUL-1990

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/467,577
 FILING DATE: 19-JAN-1990

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/352,804
 FILING DATE: 19-JUL-1989

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REFERENCE/DOCKET NUMBER: #86-P15
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-843-2800
 TELEFAX: 415-843-2899

INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE TYPE: peptide

US-08 476-405A-10

Query Match 36.4%, Score 47, DB 1, Length 11:
 Best Local Similarity 100.0%, Pred No. 1, 2e-02
 Matches 4: Conservative 0; Mismatches 0; Gaps 0

QY 4 BRQR 7
 DB 7 BRQR 10

RESULT 4
 US-08 476-405A-11
 : Sequence 11, Application US/847443A
 : Patent No. 5776459
 : GENERAL INFORMATION:
 : APPLICANT: Vandenberg, Arthur A.
 : TITLE OF INVENTION: Method of Treatment Using The Vis-25 Peptides
 : NUMBER OF SEQUENCES: 27
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Connective Therapeutics, Inc.
 : STREET: 1400 West Bayshore Road
 : CITY: Palo Alto
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/476-405A
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/069,120
 FILING DATE: 16-MAR-1993

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/708,612
 FILING DATE: 16-JUL-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/708,622
 FILING DATE: 31-MAY-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/708,622
 FILING DATE: 19-JUL-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/708,622
 FILING DATE: 19-JAN-1990
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/708,622
 FILING DATE: 19-JUL-1991

ATTORNEY/AGENT INFORMATION:
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 REFERENCE/DOCKET NUMBER: 886,116
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-843-2800
 TELEFAX: 415-843-2899
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08 476-405A-11

Query Match 36.4%, Score 47, DB 1, Length 11:
 Best Local Similarity 100.0%, Pred No. 1, 2e-02
 Matches 4: Conservative 0; Mismatches 0; Gaps 0

QY 4 BRQR 7

DB 1111 / BRQR 10

RESULT 5
 US-08 747-137-63
 : Sequence 69, Application US/08747117
 : Patent No. 5945014
 : GENERAL INFORMATION:
 : APPLICANT: VEN, Richard C.K.
 : TITLE OF INVENTION: NON-CROSSESLINKED PROTEIN PARTICLES FOR
 : TITRATION OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
 : NUMBER OF SEQUENCES: 184
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Townsend and Townsend and Crew LLP
 : STREET: Two Embarcadero Center, 8th Floor
 : CITY: San Francisco
 : STATE: CA
 : COUNTRY: USA
 : ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/747,137
 FILING DATE: 12-NOV-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/212,546
 FILING DATE: 14-MAR-1994

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/069,831
 FILING DATE: 01-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/959,560
 FILING DATE: 13-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/641,720
 FILING DATE: 15-JAN-1991

ATTORNEY/AGENT INFORMATION:
 NAME: Apple, Randolph T.
 REGISTRATION NUMBER: 36,429
 REFERENCE/DOCKET NUMBER: 016167 00384005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-576-0200
 INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amide acid
 STRANDEDNESS: not relevant
 TOPOLOGY: not relevant
 US-08-747-137-63

Query Match 36.4%, Score 47, DB 2, Length 11:
 Best Local Similarity 100.0%, Pred No. 1, 7e-02
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 5 BRQR 6
 DB 3 BRQR 6

RESULT 6
 US-09-100-930A-10
 : Sequence 10, Application US/29100910A
 : Patent No. 6248549
 : GENERAL INFORMATION:
 : APPLICANT: Van Eyk, Jennifer E.
 : APPLICANT: Mak, Alan S.
 : APPLICANT: Cote, Graham P.
 : TITLE OF INVENTION: Methods of Modulating Muscle Contraction

```
FILE REFERENCE: 1997-021-03US
CURRENT APPLICATION NUMBER: US/09/100,945A
CURRENT FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/950,478
PRIOR FILING DATE: 1997-06-24
PRIOR APPLICATION NUMBER: 60/959,595
PRIOR FILING DATE: 1998-06-16
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 10
LENGTH: 11
TYPE: PRT
ORGANISM: Unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)...(11)
OTHER INFORMATION: Residues 424 to 435 of chicken gizzard caldesmon
NAME/KEY: PEPTIDE
LOCATION: (11)
OTHER INFORMATION: Targeted Ser phosphorylating acid
US-09-100 930A 10

Query Match 36.48: Score 4: DB 1: Length 11:
Best Local Similarity 100.0%: Pred. No. 1.7e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKKE 4
DB 7 AKKE 10

RESULT 7
US-08-156-552A 18
Sequence 18: Application US/58-552A
Patent No. 5726155
GENERAL INFORMATION:
APPLICANT: Bokoch, Gary M
TITLE OF INVENTION: REGULATION OF OXIDATIVE PEROXIDE USING
TITLE OF INVENTION: DMG-DERIVED PEPTIDES AND ANALOGS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, 10550 N.
SECRET: 19666 No. 5726155th Inter. U.S. Pat. App. #
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/156,552A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,944
FILING DATE: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Logan, Adell C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: SCHF 491.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-09-100 930A 10

Query Match 36.48: Score 4: DB 1: Length 11:
Best Local Similarity 100.0%: Pred. No. 1.7e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKKE 4
DB 7 AKKE 10

RESULT 7
US-08-156-552A 18
Sequence 18: Application US/58-552A
Patent No. 5726155
GENERAL INFORMATION:
APPLICANT: Bokoch, Gary M
TITLE OF INVENTION: REGULATION OF OXIDATIVE PEROXIDE USING
TITLE OF INVENTION: DMG-DERIVED PEPTIDES AND ANALOGS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, 10550 N.
SECRET: 19666 No. 5726155th Inter. U.S. Pat. App. #
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/156,552A
FILING DATE: 15-NOV-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/102,944
FILING DATE: 02-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Logan, Adell C.
REGISTRATION NUMBER: 33,950
REFERENCE/DOCKET NUMBER: SCHF 491.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear

FILE REFERENCE: 1997-021-03US
CURRENT APPLICATION NUMBER: US/09/100,945A
CURRENT FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/950,478
PRIOR FILING DATE: 1997-06-24
PRIOR APPLICATION NUMBER: 60/959,595
PRIOR FILING DATE: 1998-06-16
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 10
LENGTH: 11
TYPE: PRT
ORGANISM: Unknown
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)...(11)
OTHER INFORMATION: Residues 424 to 435 of chicken gizzard caldesmon
NAME/KEY: PEPTIDE
LOCATION: (11)
OTHER INFORMATION: Targeted Ser phosphorylating acid
US-09-100 930A 10

Query Match 36.48: Score 4: DB 1: Length 12:
Best Local Similarity 100.0%: Pred. No. 1.9e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 RKDI 10
DB 9 RKDI 12

RESULT 8
US-08-548-540-147
Sequence 147: Application US/58548540
Patent No. 5733731
GENERAL INFORMATION:
APPLICANT: Schatz, Peter J.
APPLICANT: Cull, Milard G.
APPLICANT: Miller, Jeff F.
APPLICANT: Stemmer, William P.C.
APPLICANT: Gates, Christian M.
TITLE OF INVENTION: Peptide Library and Screening Method
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/548,540
FILING DATE: 26-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/290,641
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,321
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,423
REFERENCE/DOCKET NUMBER: 165283-001240US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-548-540-147

Query Match 36.48: Score 4: DB 1: Length 12:
Best Local Similarity 100.0%: Pred. No. 1.9e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 ERQR 7
DB 8 ERQR 11

RESULT 9
US-08-461-384B-7
```

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: Sequence 7, Application US/0846:384b
: Patent No. 6025473
: GENERAL INFORMATION:
: APPLICANT: Cole, Susan P.C.
: APPLICANT: Cole, Roger G.
: TITLE OF INVENTION: MULTIDRUG RESISTANCE PROTEINS
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
: STREET: Queen's University at Kingston
: CITY: Kingston
: STATE: Ontario
: COUNTRY: CANADA
: ZIP: K7L 3N6
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/461,484B
: FILING DATE: 05-JUN-95
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/966,923
: FILING DATE: 27-OCT-1992
: APPLICATION NUMBER: 08/029,440
: FILING DATE: 8-MAR-1993
: APPLICATION NUMBER: 08/141,893
: FILING DATE: 26-OCT-1993
: APPLICATION NUMBER: 08/407,207
: FILING DATE: 20-MAR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Steeg, Carol Meinick
: REGISTRATION NUMBER: 39,539
: REFERENCE/DOCKET NUMBER: Q1547
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (613) 545-2342
: TELEFAX: (613) 545-6853
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 12 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-461-384B-7

Query Match 36.4% Score 4: DB 3: Length 12:
Best Local Similarity 100.0%: Pred. No. 1.9e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY : AKKE 4
ID : 8 AKKE 11

RESULT 1:
US 08-407 207A 4
: Sequence 4, Application US/08407207A
: Patent No. 6061621
: GENERAL INFORMATION:
: APPLICANT: Deeley, Roger G.
: APPLICANT: Cole, Susan P.C.
: TITLE OF INVENTION: ANTIBODIES TO A MULTIDRUG RESISTANCE PROTEIN
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: PARTEQ RESEARCH & DEVELOPMENT INNOVATIONS
: STREET: Queen's University at Kingston
: CITY: Kingston
: STATE: Ontario
: COUNTRY: CANADA
: ZIP: K7L 3N6
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

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: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/407,207A
: FILING DATE: 20-MAR-1995
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/966,923
: FILING DATE: 27-OCT-1992
: APPLICATION NUMBER: 08/029,440
: FILING DATE: 8-MAR-1993
: APPLICATION NUMBER: 08/141,893
: FILING DATE: 26-OCT-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Steeg, Carol Meinick
: REGISTRATION NUMBER: 39,539
: REFERENCE/DOCKET NUMBER: Q1512
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (613) 545-2342
: TELEFAX: (613) 545-6853
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 12 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-407-207A-4

Query Match 36.4% Score 4: DB 3: Length 12:
Best Local Similarity 100.0%: Pred. No. 1.9e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY : 1 AKKE 4
ID : 8 AKKE 11

RESULT 1:
US-09-035-249A-18
: Sequence 18, Application US/09035249A
: Patent No. 6184203
: GENERAL INFORMATION:
: APPLICANT: Bokoch, Gary M.
: APPLICANT: Curdutt, John T.
: TITLE OF INVENTION: REGULATION OF OXIDATIVE BURST USING
: TITLE OF INVENTION: LMWG-DERIVED PEPTIDES AND ANALOGS
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: The Scripps Research Institute, Office of
: ADDRESSEE: Patent Counsel
: STREET: 10666 No. 6184203th Torrey Pines Road, TPC 8
: CITY: La Jolla
: STATE: CA
: COUNTRY: USA
: ZIP: 92037
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/035,249A
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/18/156,552
: FILING DATE: 15-NOV-1993
: APPLICATION NUMBER: US 08/102,944
: FILING DATE: 02-AUG-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Logan, April C.
: REGISTRATION NUMBER: 33,950

```

REFERENCE/DOCKET NUMBER: SCORE 281.1
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-035-249A-18

Query Match 36.4% Score 4: DB 0: Length 12
Best Local Similarity 100.0% Pred. No. 1.9e+02
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 RKDT 10
DB 9 RKDT 12

RESULT 12
PCT-US96-09809-147
Sequence 147, Application PC/TUS36G9809
GENERAL INFORMATION:
APPLICANT: Schatz, Peter A.
APPLICANT: Cull, Millard G.
APPLICANT: Miller, Jeff F.
APPLICANT: Stemmer, William P.
APPLICANT: Gates, Christian M.
TITLE OF INVENTION: Peptide Library and Screening Method
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.26
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09809
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,541
FILING DATE: 26-OCT-1995
APPLICATION NUMBER: US 08/290,641
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,321
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 165282-001240015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 147:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-09809-147

Query Match 36.4% Score 4: DB 0: Length 12

Best Local Similarity 100.0% Pred. No. 1.9e+02
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY 4 ERQR 7
DB 8 ERQR 11
RESULT 13
US-08-796-598-15
Sequence 15, Application US/08796598
Patent No. 5827659
GENERAL INFORMATION:
APPLICANT: PATTERSON, DALE H.
APPLICANT: TARR, GEORGE E.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
TITLE OF INVENTION: POLYMERS USING MASS SPECTROMETRY.
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Administrator - Testa, Hurwitz &
ADDRESSEE: Thibeault
STREET: High Street Tower, 125 High Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/796,598
FILING DATE: 07-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,055
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FLYNN ESQ., Kerry A.
REGISTRATION NUMBER: 33,693
REFERENCE/DOCKET NUMBER: SYP-115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-796-598-15

Query Match 36.4% Score 4: DB 2: Length 13
Best Local Similarity 100.0% Pred. No. 2e+02
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 6 QRKD 9
DB 3 QRKD 6

RESULT 14
US-08-447-175A-15
Sequence 15, Application US/08447175A
Patent No. 5869240
GENERAL INFORMATION:
APPLICANT: PATTERSON, DALE H.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SEQUENCING
TITLE OF INVENTION: POLYMERS WITH A STATISTICAL CERTAINTY USING MASS
SPECTROMETRY.
NUMBER OF SEQUENCES: 23

1 CORRESPONDENCE ADDRESS:
 2 ADDRESSEE: Patent Administrator - Testa, Hurwitz &
 3 ADDRESSEE: Thibault, LLP
 4 STREET: High Street Tower, 125 High Street
 5 CITY: Boston
 6 STATE: MA
 7 COUNTRY: USA
 8 ZIP: 02110
 9 COMPUTER READABLE FORM:
 10 MEDIUM TYPE: Floppy disk
 11 COMPUTER: IBM PC compatible
 12 OPERATING SYSTEM: PC-DOS/MS-DOS
 13 SOFTWARE: Patent Release #1.0, Version #1.0
 14 CURRENT APPLICATION DATA:
 15 APPLICATION NUMBER: US/08/447,175A
 16 FILING DATE: 19-MAY-1995
 17 CLASSIFICATION: 422
 18 ATTORNEY/AGENT INFORMATION:
 19 NAME: RAUSCHENBACH, KAT
 20 REGISTRATION NUMBER: 43,147
 21 REFERENCE/DOCKET NUMBER: SYP-114
 22 TELECOMMUNICATION INFORMATION:
 23 TELEPHONE: (617) 248-7000
 24 TELEFAX: (617) 248-7100
 25 INFORMATION FOR SEQ ID NO: 15:
 26 SEQUENCE CHARACTERISTICS:
 27 LENGTH: 13 amino acids
 28 TYPE: amino acid
 29 STRANDEDNESS: single
 30 TOPOLOGY: linear
 31 MOLECULE TYPE: peptide
 32 US-08-447,175A 15
 33
 34 Query Match: 36.4%, Score 4; DB 2; Length 13;
 35 Best Local Similarity: 100.0%; Pred. No. 2e+02;
 36 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 37
 38 QY 6 QKRD 9
 39 DB 1 IIII 6
 40
 41 RESULT 16
 42 US-09-747-137 77
 43 Sequence 77; Application US/08/447,175A
 44 Patent No. 5945043
 45 GENERAL INFORMATION:
 46 APPLICANT: YEN, Richard C.K.
 47 TITLE OF INVENTION: NON-CROSS-LINKED PEPTIDE COMPOUNDS FOR P
 48 TITLE OF INVENTION: THERAPEUTIC AND DIAGNOSTIC USE
 49 NUMBER OF SEQUENCES: 184
 50 CORRESPONDENCE ADDRESS:
 51 ADDRESSEE: Townsend and Townsend and Clerkin LLP
 52 STREET: Two Embarcadero Center, Suite 2000
 53 CITY: San Francisco
 54 STATE: CA
 55 COUNTRY: USA
 56 ZIP: 94111
 57 COMPUTER READABLE FORM:
 58 MEDIUM TYPE: Floppy disk
 59 COMPUTER: IBM PC compatible
 60 OPERATING SYSTEM: PC-DOS/MS-DOS
 61 SOFTWARE: Patent Release #1.0, Version #1.0
 62 CURRENT APPLICATION DATA:
 63 APPLICATION NUMBER: US/08/747,137
 64 FILING DATE: 12-NOV-1996
 65 CLASSIFICATION: 424
 66 PRIOR APPLICATION DATA:
 67 APPLICATION NUMBER: US 08/212,545
 68 FILING DATE: 14-MAR-1994
 69 PRIOR APPLICATION DATA:
 70 APPLICATION NUMBER: US 08/069,843
 71 FILING DATE: 01-JUN-1993

1 PRIOR APPLICATION DATA:
 2 APPLICATION NUMBER: US 07/959,560
 3 FILING DATE: 13-OCT-1992
 4 PRIOR APPLICATION DATA:
 5 APPLICATION NUMBER: US 07/941,720
 6 FILING DATE: 15-JAN-1991
 7 ATTORNEY/AGENT INFORMATION:
 8 NAME: Apple, Raulolph T.
 9 REGISTRATION NUMBER: 36,429
 10 REFERENCE/DOCKET NUMBER: 016147-0008400US
 11 TELECOMMUNICATION INFORMATION:
 12 TELEPHONE: 415 576-0200
 13 INFORMATION FOR SEQ ID NO: 77:
 14 SEQUENCE CHARACTERISTICS:
 15 LENGTH: 13 amino acids
 16 TYPE: amino acid
 17 STRANDEDNESS: not relevant
 18 TOPOLOGY: not relevant
 19 US-08-747-137-77
 20
 21 Query Match: 36.4%, Score 4; DB 2; Length 13;
 22 Best Local Similarity: 100.0%; Pred. No. 2e+02;
 23 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 24
 25 QY 6 QKRD 9
 26 DB 3 IIII 6
 27
 28 RESULT 16
 29 US-09-400-564 6
 30 Sequence 6; Application US/09400564
 31 Patent No. 6350574
 32 GENERAL INFORMATION:
 33 APPLICANT: Montclair, Ronald C.
 34 APPLICANT: Tencza, Sarah B.
 35 APPLICANT: Jolley, Michael S.
 36 APPLICANT: Nasir, Mohammad S.
 37 TITLE OF INVENTION: A Fluorescence Polarization-Based Diagnostic Assay
 38 TITLE OF INVENTION: FOR Equine Infectious Anemia Virus
 39 FILE REFERENCE: Case No. 6350574 99,579
 40 CURRENT APPLICATION NUMBER: US/09/400,564
 41 CURRENT FILING DATE: 1999-09-21
 42 EARLIER APPLICATION NUMBER: US 60/101,553
 43 NUMBER OF SEQ ID NOS: 21
 44 SEQ ID NO 6
 45 LENGTH: 13
 46 TYPE: PEPT
 47 ORGANISM: Equine infectious anemia virus
 48 US-09-400-564 6
 49
 50 Query Match: 36.4%, Score 4; DB 4; Length 13;
 51 Best Local Similarity: 100.0%; Pred. No. 2e+02;
 52 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 53
 54 QY 3 KERQ 6
 55 DB 1 KERQ 4
 56
 57 RESULT 17
 58 US-09-325-601-44
 59 Sequence 44; Application US/09325601
 60 Patent No. 6573045
 61 GENERAL INFORMATION:
 62 APPLICANT: Kato
 63 APPLICANT: Prescott
 64 TITLE OF INVENTION: Methods and Kits for Discovery of RNA-Binding Compounds
 65 FILE REFERENCE: 3950/81245
 66 CURRENT APPLICATION NUMBER: US/09/325,601
 67 CURRENT FILING DATE: 1999-06-03
 68 NUMBER OF SEQ ID NOS: 63
 69 SOFTWARE: Patent In Ver 2.1

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1 SEQ ID NO 44
2 LENGTH: 13
3 TYPE: PRT
4 ORGANISM: Artificial Sequence
5 FEATURE:
6 OTHER INFORMATION: Description of Artificial Sequence: peptide from X.
7 OTHER INFORMATION: Q, R-peptideptide library
8 US-09-425-601-44

Query Match
Best Local Similarity 100.0% Score 4.0 DB 3: Length 14
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 5 ERQR 8
BB 4 ERQR 7

RESULT 16
US-08-484-905-55
1 Sequence 55, Application US/06444905
2 Patent No. 5976551
3 GENERAL INFORMATION:
4 APPLICANT: Motiez, Estelle
5 APPLICANT: Abastado, Jean-Pierre
6 APPLICANT: Kourilsky, Philippe
7 TITLE OF INVENTION: An Altered Major Histocompatibility
8 TITLE OF INVENTION: Complex(MHC) Determinant and Methods for Using the
9 NUMBER OF SEQUENCES: 127
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
12 ADDRESSEE: Dunner
13 STREET: 1400 I Street, N.W., Suite 700
14 CITY: Washington
15 STATE: D.C.
16 ZIP: 20005-4315
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC DOS/MS-DOS
21 SOFTWARE: Patent in Release #1.0, Version #1.25
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/484,905
24 FILING DATE: 07-JUNE-1995
25 CLASSIFICATION: 530
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 07/792,473
28 FILING DATE: 15-NOV-1991
29 CLASSIFICATION: 530
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Potter, Jane E. R.
32 REGISTRATION NUMBER: 33,432
33 REFERENCE/DOCKET NUMBER: 03495.0106-0400
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: 202-408-4000
36 TELEFAX: 202-408-4400
37 INFORMATION FOR SEQ ID NO: 55:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 14 amino acids
40 TYPE: amino acid
41 TOPOLOGY: linear
42 MOLECULE TYPE: peptide
43 US-08-484-905-55

Query Match
Best Local Similarity 100.0% Score 4.0 DB 3: Length 14
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0
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```
QY 4 ERQR 7
BB 11 ERQR 14

RESULT 19
US-08-481-985B-55
1 Sequence 55, Application US/08481985B
2 Patent No. 6011142
3 GENERAL INFORMATION:
4 APPLICANT: Motiez, Estelle
5 APPLICANT: Abastado, Jean-Pierre
6 APPLICANT: Kourilsky, Philippe
7 TITLE OF INVENTION: Altered Major Histocompatibility Complex
8 TITLE OF INVENTION:
9 NUMBER OF SEQUENCES: 148
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
12 ADDRESSEE: Dunner
13 STREET: 1400 I Street, N.W., Suite 700
14 CITY: Washington
15 STATE: D.C.
16 ZIP: 20005-4315
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC DOS/MS-DOS
21 SOFTWARE: Patent in Release #1.0, Version #1.25
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/481,985B
24 FILING DATE: 07-JUNE-1995
25 CLASSIFICATION: 435
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: US 07/801,818
28 FILING DATE: 05-DEC-1991
29 CLASSIFICATION: 435
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Meyers, Kenneth J.
32 REGISTRATION NUMBER: 25,146
33 REFERENCE/DOCKET NUMBER: 03495.0106-04000
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: 202-408-4000
36 TELEFAX: 202-408-4400
37 INFORMATION FOR SEQ ID NO: 55:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 14 amino acids
40 TYPE: amino acid
41 TOPOLOGY: linear
42 MOLECULE TYPE: peptide
43 US-08-481-985B-55

Query Match
Best Local Similarity 100.0% Score 4.0 DB 3: Length 14
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 4 ERQR 7
BB 11 ERQR 14

RESULT 20
US-08-370-476-55
1 Sequence 55, Application US/08370476
2 Patent No. 615408
3 GENERAL INFORMATION:
4 APPLICANT: Motiez, Estelle
5 APPLICANT: Abastado, Jean-Pierre
6 APPLICANT: Kourilsky, Philippe
7 APPLICANT: Lone, Yu-Chan
```

1 APPLICANT: Ojcius, David
2 APPLICANT: Casrouge, Amanda
3 TITLE OF INVENTION: Altered Major Histocompatibility Complex
4 TITLE OF INVENTION:
5 NUMBER OF SEQUENCES: 127
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: Finnegan, Henderson, Farrel W. Jantell &
8 STREET: 1300 I Street, N.W., Suite 700
9 CITY: Washington
10 STATE: D.C.
11 ZIP: 20005-4335
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 OPERATING SYSTEM: IBM PC compatible
15 SOFTWARE: Patent Release #1.0, Version #1.25
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/08/476-405A
18 FILING DATE:
19 CLASSIFICATION: 445
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US 08/417,595
22 FILING DATE: 07-SEP-1994
23 APPLICATION NUMBER: US 08/572,787
24 FILING DATE: 06-JUN-1994
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 07/611,817
27 FILING DATE: 05-DEC-1991
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 07/794,478
30 FILING DATE: 15-NOV-1991
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Meyers, Kenneth J.
33 REGISTRATION NUMBER: 25,146
34 REFERENCE/DOCKET NUMBER: 5241, 001 of 0600
35 TELEPHONE: 202-408-4000
36 TELEFAX: 202-408-4400
37 INFORMATION FOR SEQ ID NO: 55:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 14 amino acids
40 TYPE: amino acid
41 TOPOLOGY: Linear
42 Molecule type: peptide
43 US-08-476-476-55
44
45 Query Match: 46.5% Score 4: 1P 4: Length 14:
46 Best Local Similarity 100.0% Pred. No. 2.1e+02:
47 Matches 4: Conservative 0: Mismatches 0: Gaps 0:
48
49 4 ERROR 7
50 11
51 ERROR 14
52
53 RESULT 21
54 US-08-476-477-45
55 Sequence 35: Application US/084942877
56 Patent No. 640461
57 GENERAL INFORMATION:
58 APPLICANT: Torman, David S
59 TITLE OF INVENTION: SUPERANTIGEN BASED METHOD AND COMPOSITIONS FOR
60 TREATMENT OF INFECTIOUS DISEASE
61 FILE REFERENCE: superantigen
62 CURRENT APPLICATION NUMBER: US/08/992,877
63 CURRENT FILING DATE: 1997-12-17
64 PRIOR APPLICATION NUMBER: 60/044,074
65 PRIOR FILING DATE: 1997-04-17
66 NUMBER OF SEQ ID NOS: 78
67 SOFTWARE: PatentIn Ver. 2.1
68 SEQ ID NO 35
69 LENGTH: 14

1 TYPE: PRT
2 ORGANISM: Artificial Sequence
3 FEATURE:
4 OTHER INFORMATION: Description of Artificial Sequence: antigen
5 US-08-992-877-45
6
7 Query Match: 66.4% Score 4: DR 4: Length 14:
8 Best Local Similarity 100.0% Pred. No. 2.1e+02:
9 Matches 4: Conservative 0: Mismatches 0: Gaps 0:
10
11 4 ERROR 7
12 11
13 ERROR 14
14
15 RESULT 22
16 US-08-476-405A-24
17 Sequence 23: Application US/08476405A
18 Patent No. 5776459
19 GENERAL INFORMATION:
20 APPLICANT: Vandenbark, Arthur A.
21 TITLE OF INVENTION: Method of Treatment Using TCR VBeta5 Peptides
22 NUMBER OF SEQUENCES: 27
23 CORRESPONDENCE ADDRESS:
24 ADDRESSEE: Connective Therapeutics, Inc.
25 STREET: 3400 West Bayshore Road
26 CITY: Palo Alto
27 STATE: California
28 COUNTRY: USA
29 ZIP: 94303
30 COMPUTER READABLE FORM:
31 MEDIUM TYPE: Floppy disk
32 COMPUTER: IBM PC compatible
33 OPERATING SYSTEM: PC-DOS/MS DOS
34 SOFTWARE: Patent Release #1.0, Version #1.25
35 CURRENT APPLICATION DATA:
36 APPLICATION NUMBER: US/08/476,405A
37 FILING DATE:
38 CLASSIFICATION: 424
39 PRIOR APPLICATION DATA:
40 APPLICATION NUMBER: US 08/059,020
41 FILING DATE: 16-MAR-1993
42 PRIOR APPLICATION DATA:
43 APPLICATION NUMBER: US 07/735,612
44 FILING DATE: 16-JUL-1991
45 PRIOR APPLICATION DATA:
46 APPLICATION NUMBER: US 07/708,022
47 FILING DATE: 31-MAY-1992
48 PRIOR APPLICATION DATA:
49 APPLICATION NUMBER: US 07/554,529
50 FILING DATE: 19-JUL-1990
51 PRIOR APPLICATION DATA:
52 APPLICATION NUMBER: US 07/467,577
53 FILING DATE: 19-JAN-1990
54 PRIOR APPLICATION DATA:
55 APPLICATION NUMBER: US 07/382,804
56 FILING DATE: 19-JUL-1989
57 ATTORNEY/AGENT INFORMATION:
58 NAME: Lowin, David A.
59 REGISTRATION NUMBER: 29,326
60 REFERENCE/DOCKET NUMBER: 886 #15
61 TELECOMMUNICATION INFORMATION:
62 TELEPHONE: 415-843-2800
63 TELEFAX: 415-843-2899
64 INFORMATION FOR SEQ ID NO: 23:
65 SEQUENCE CHARACTERISTICS:
66 LENGTH: 15 amino acids
67 TYPE: amino acid
68 STRANDEDNESS: Single
69 TOPOLOGY: Linear
70 Molecule type: peptide
71 US-08-476-405A-24

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Query Match 36.4% Score 4: DB 1: Length 15:
Best Local Similarity 100.0% Pred. No. 2.2e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 ERQR 7
DB 9 ERQR 12

RESULT 23
US-08-466-860-12
: Sequence 12: Application US/08466860
: Patent No. 5985552
: GENERAL INFORMATION:
: APPLICANT: HOWELL, MARK D.
: APPLICANT: BROSTOFF, STEVEN W.
: APPLICANT: CARLO, DENNIS J.
: TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
: TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
: TITLE OF INVENTION: POPULATIONS
: NUMBER OF SEQUENCES: 75
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CAMPBELL AND FLORES
: STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
: CITY: SAN DIEGO
: STATE: CALIFORNIA
: COUNTRY: UNITED STATES
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/466-860
: FILING DATE:
: CLASSIFICATION: 424
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/915,567
: FILING DATE: 24-DEC-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: CAMPBELL, CATHRYN
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P 1M 9107
: TELEPHONE: 619-535-8949
: TELEFAX: 619-535-9001
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: N-terminal
US-08-466-860-12

Query Match 36.4% Score 4: DB 1: Length 15:
Best Local Similarity 100.0% Pred. No. 2.2e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 KKER 5
DB 9 KKER 12

RESULT 24
US-08-559-397A-13
: Sequence 33: Application US/08559397A
: Patent No. 6083713
: GENERAL INFORMATION:
: APPLICANT: Madly, Susan P.
: APPLICANT: Kozlowski, Michael R.
```

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APPLICANT: Neve, Rachael L.
TITLE OF INVENTION: CLONING AND EXPRESSION OF
: TITLE OF INVENTION: BETA APP-C100 RECEPTOR (C100-R)
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: NY
: COUNTRY: USA
: ZIP: 10036/2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/559,397A
: FILING DATE: 15-NOV-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Coruzzi, Laura A
: REGISTRATION NUMBER: 30,742
: REFERENCE/DOCKET NUMBER: 6013-135
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-790-9090
: TELEFAX: 212-869-8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 33:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: unknown
: MOLECULE TYPE: peptide
US-08-559-397A-33

Query Match 36.4% Score 4: DB 3: Length 15:
Best Local Similarity 100.0% Pred. No. 2.2e+02:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 RGRK 8
DB 4 RGRK 7

RESULT 25
US-08-472-040A-12
: Sequence 12: Application US/08472040A
: Patent No. 6093387
: GENERAL INFORMATION:
: APPLICANT: HOWELL, MARK D.
: APPLICANT: BROSTOFF, STEVEN W.
: APPLICANT: CARLO, DENNIS J.
: TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
: TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
: NUMBER OF SEQUENCES: 77
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CAMPBELL & FLORES LLP
: STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
: CITY: SAN DIEGO
: STATE: CALIFORNIA
: COUNTRY: UNITED STATES
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/472,040A
: FILING DATE: 05-JUN-1995
```



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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHRYN
REGISTRATION NUMBER: 31,815
REFERENCE/Docket NUMBER: P-1M 9107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-472-040A-12

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Prod. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 KKER 5
DB 9 KKER 12

RESULT 25
US-08-276-776-12
: Sequence 12, Application US/08276776
: Patent No. 6207645
: GENERAL INFORMATION:
: APPLICANT: HOWELL, MARK D.
: APPLICANT: BROSTOFF, STEVEN W.
: APPLICANT: CARLO, DENNIS J.
: TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
: TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
: NUMBER OF SEQUENCES: 75
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CAMPBELL AND FLORES
: STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
: CITY: SAN DIEGO
: STATE: CALIFORNIA
: COUNTRY: UNITED STATES
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/276,776
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/813,867
: FILING DATE: 24-DEC-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: CAMPBELL, CATHRYN
: REGISTRATION NUMBER: 31,815
: REFERENCE/Docket NUMBER: P-1M 9107
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-535-9001
: TELEFAX: 619-535-8949
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: N-terminal
US-08-276-776-12

```

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Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Prod. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 KKER 5
DB 9 KKER 12

RESULT 27
US-08-471-209-12
: Sequence 12, Application US/08471209
: Patent No. 6221952
: GENERAL INFORMATION:
: APPLICANT: HOWELL, MARK D.
: APPLICANT: BROSTOFF, STEVEN W.
: APPLICANT: CARLO, DENNIS J.
: TITLE OF INVENTION: VACCINATION AND METHODS AGAINST DISEASES
: TITLE OF INVENTION: RESULTING FROM PATHOGENIC RESPONSES BY SPECIFIC T CELL
: NUMBER OF SEQUENCES: 75
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: CAMPBELL AND FLORES
: STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
: CITY: SAN DIEGO
: STATE: CALIFORNIA
: COUNTRY: UNITED STATES
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/471,209
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/07/813,867
: FILING DATE: 24-DEC-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: CAMPBELL, CATHRYN
: REGISTRATION NUMBER: 31,815
: REFERENCE/Docket NUMBER: P-1M 9107
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-535-9001
: TELEFAX: 619-535-8949
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: N-terminal
US-08-471-209-12

```

```

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Prod. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 2 KKER 5
DB 9 KKER 12

RESULT 28
US-09-308-935-14
: Sequence 14, Application US/09308935
: Patent No. 6268334
: GENERAL INFORMATION:
: APPLICANT: La Thaque, Nicholas H
: APPLICANT: Randara, Lashantha R
: TITLE OF INVENTION: Peptide antagonists of DP transcription factors

```

FILE REFERENCE: 620-67
CURRENT APPLICATION NUMBER: US/99/308,965
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: PCI/3997/03505
EARLIER FILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: GB 9626589.7
EARLIER FILING DATE: 1996-12-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US 09-308-935-14

Query Match 36.4% Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ERROR 7
DB 3 ERROR 6

RESULT 29
US-09-009-953-240
Sequence 240, Application US/09/009953;
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Settle, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Free LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/009,953
FILING DATE: 21-JAN-1998
CLASSIFICATION: <unknown>
PUBLICATION DATA:
APPLICATION NUMBER: US 60/345,333
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/907,452
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Laurel
REGISTRATION NUMBER: 32,752
REFERENCE/DOCKET NUMBER: 018623 0112 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 240:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 240:
US-09-009-953-240

Query Match 36.4% Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ERROR 8
DB 6 ERROR 9

RESULT 30
US-09-311-784A-319
Sequence 319, Application US/09/311784A
Patent No. 6534482
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Settle, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-20022.01
CURRENT APPLICATION NUMBER: US/99/311,784A
CURRENT FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/385,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 319
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HIV VPU 31 (peptide 35.0135)
US-09-311-784A-319

Query Match 36.4% Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ERROR 8
DB 6 ERROR 9

RESULT 31
US-08-103-490A-6
Sequence 6, Application US/08103490A
Patent No. 5422341
GENERAL INFORMATION:
APPLICANT: Macielag, Mark J.
TITLE OF INVENTION: Motilin-like Polypeptides With
Gastrointestinal Motor Stimulating Activity
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: The BOC Group, Inc.
STREET: 100 Mountain Avenue
CITY: Murray Hill
STATE: New Jersey
COUNTRY: USA
ZIP: 07974
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/103,490A
FILING DATE: 06-AUG-1993
CLASSIFICATION: 514

1 ALTERNATE/AGENT INFORMATION:
 2 NAME: SWOPE, R. Bain
 3 REGISTRATION NUMBER: 24,864
 4 REFERENCE/DOCKET NUMBER: 94H817
 5 TELECOMMUNICATION INFORMATION:
 6 TELEPHONE: 908-771-6292
 7 TELEFAX: 908-771-6159
 8 INFORMATION FOR SEQ ID NO: 6:
 9 SEQUENCE CHARACTERISTICS:
 10 LENGTH: 8 amino acids
 11 TYPE: amino acid
 12 STRANDEDNESS: unknown
 13 TOPOLOGY: unknown
 14 MODIFIER TYPE: peptide
 15 US 08 103 496A 6

Query Match: 27.3% Score 5: 10 1: Length 8:
 Best Local Similarity: 100.0%, Prod. No. 2 5000:
 Matches: 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

17 5 KER 5
 18 5 KER 7

19 RESULT 42
 20 US 08 246 246 5
 21 Sequence 3: Application US/08246246
 22 Patent No. 6446124
 23 GENERAL INFORMATION:
 24 APPLICANT: Kahn, Michael
 25 TITLE OF INVENTION: Alpha-helix motifs and methods
 26 NUMBER OF SEQUENCES: 9
 27 CORRESPONDENCE ADDRESS:
 28 ADDRESSEE: Seed and Berry
 29 STREET: 640 Columbia Center, 701 Fifth Avenue
 30 CITY: Seattle
 31 STATE: Washington
 32 COUNTRY: USA
 33 ZIP: 98104
 34 COMPUTER READABLE FORM:
 35 MEDIUM TYPE: Floppy disk
 36 OPERATING SYSTEM: IBM PC compatible
 37 SOFTWARE: Patent In Release #1.0, Version #1.25
 38 CURRENT APPLICATION DATA:
 39 APPLICATION NUMBER: US/08/246,246
 40 FILING DATE: 18 JUN 1993
 41 CLASSIFICATION: 514
 42 NAME: Hermans, Karl R.
 43 REGISTRATION NUMBER: 33,507
 44 REFERENCE/DOCKET NUMBER: 6486443
 45 TELECOMMUNICATION INFORMATION:
 46 TELEPHONE: (206) 622-4900
 47 TELEFAX: (206) 682-6031
 48 INFORMATION FOR SEQ ID NO: 4:
 49 SEQUENCE CHARACTERISTICS:
 50 LENGTH: 8 amino acids
 51 TYPE: amino acid
 52 TOPOLOGY: linear
 53 MODIFIER TYPE: peptide
 54 US 08 246 246 5

Query Match: 27.3% Score 5: 10 1: Length 8:
 Best Local Similarity: 100.0%, Prod. No. 2 5000:
 Matches: 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

17 5 KER 7
 18 5 KER 7
 19 RESULT 43
 20 US 08 103 489A 6
 21 Sequence 6: Application US/08103489A
 22 Patent No. 6476830
 23 GENERAL INFORMATION:
 24 APPLICANT: Maciejda, Mark J.
 25 TITLE OF INVENTION: Multichain-like polypeptides that inhibit gastrointestinal motility
 26 NUMBER OF SEQUENCES: 154
 27 CORRESPONDENCE ADDRESS:
 28 ADDRESSEE: The BOC Group, Inc.
 29 STREET: 100 Mountain Avenue
 30 CITY: Murray Hill
 31 STATE: New Jersey
 32 COUNTRY: USA
 33 ZIP: 07974
 34 COMPUTER READABLE FORM:
 35 MEDIUM TYPE: Floppy disk
 36 OPERATING SYSTEM: IBM PC compatible
 37 SOFTWARE: Patent In Release #1.0, Version #1.25
 38 CURRENT APPLICATION DATA:
 39 APPLICATION NUMBER: US/08/103,489A
 40 FILING DATE: 06 AUG 1993
 41 CLASSIFICATION: 514
 42 NAME: Swope, R. Bain
 43 REGISTRATION NUMBER: 24,864
 44 REFERENCE/DOCKET NUMBER: 94H872
 45 TELECOMMUNICATION INFORMATION:
 46 TELEPHONE: 908-771-6292
 47 TELEFAX: 908-771-6159
 48 INFORMATION FOR SEQ ID NO: 6:
 49 SEQUENCE CHARACTERISTICS:
 50 LENGTH: 8 amino acids
 51 TYPE: amino acid
 52 STRANDEDNESS: unknown
 53 TOPOLOGY: unknown
 54 MODIFIER TYPE: peptide
 55 US 08 103 489A 6

Query Match: 27.3% Score 5: 10 1: Length 8:
 Best Local Similarity: 100.0%, Prod. No. 2 5000:
 Matches: 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

17 5 KER 5
 18 5 KER 7

19 RESULT 44
 20 US 08 103 489A 6
 21 Sequence 5: Application US/08064395A
 22 Patent No. 649719
 23 GENERAL INFORMATION:
 24 APPLICANT: YAMADA, YUKIO
 25 APPLICANT: ASAMI, OSAMU
 26 APPLICANT: SUGIYAMA, HIROSHI
 27 APPLICANT: IZUKAWA, CHIE
 28 APPLICANT: HOSHINO, FUMIHIKO
 29 APPLICANT: HIRAI, MASANA
 30 APPLICANT: KALIN, ISIDORE
 31 APPLICANT: CHADA, JAGAT
 32 APPLICANT: SARAL, KIRAN
 33 TITLE OF INVENTION: POLYPEPTIDES POSSESSING PROTEIN DISULFIDE
 34 TITLE OF INVENTION: ISOMERACTIVITY GENE ENCODING THE SAME AND PROCESS FOR
 35 NUMBER OF SEQUENCES: 1
 36 MODIFIER TYPE: peptide
 37 US 08 103 489A 6

Query Match: 27.3% Score 5: 10 1: Length 8:
 Best Local Similarity: 100.0%, Prod. No. 2 5000:
 Matches: 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

17 5 KER 5
 18 5 KER 7

19 RESULT 45
 20 US 08 103 489A 6
 21 Sequence 5: Application US/08064395A
 22 Patent No. 649719
 23 GENERAL INFORMATION:
 24 APPLICANT: YAMADA, YUKIO
 25 APPLICANT: ASAMI, OSAMU
 26 APPLICANT: SUGIYAMA, HIROSHI
 27 APPLICANT: IZUKAWA, CHIE
 28 APPLICANT: HOSHINO, FUMIHIKO
 29 APPLICANT: HIRAI, MASANA
 30 APPLICANT: KALIN, ISIDORE
 31 APPLICANT: CHADA, JAGAT
 32 APPLICANT: SARAL, KIRAN
 33 TITLE OF INVENTION: POLYPEPTIDES POSSESSING PROTEIN DISULFIDE
 34 TITLE OF INVENTION: ISOMERACTIVITY GENE ENCODING THE SAME AND PROCESS FOR
 35 NUMBER OF SEQUENCES: 1
 36 MODIFIER TYPE: peptide
 37 US 08 103 489A 6

ADDRESSEE: OHLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,555A
FILING DATE: 19930527
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 4-135254
FILING DATE: 27-MAY 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5-44013
FILING DATE: 04-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 5 44014
FILING DATE: 04-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: OHION, NO. 5496719nd F.
REGISTRATION NUMBER: 24,619
REFERENCE/DOCKET NUMBER: 19-228-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-1000
TELEFAX: (703) 413-2220
TELEX: 249855 GPAT UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US 08-068-195A-5

Query Match 27.3%, Score 3, DB 1, Length 8;
Best Local Similarity 100.0%, Pred. No. 2.5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KER 10
DE 1 KER 3

RESULT 16
US-08-014-426-21
Sequence 23, Application US/08014426
Patent No. 5512435
GENERAL INFORMATION:
APPLICANT: Renschler, Markus F.
APPLICANT: Levy, Ronald
APPLICANT: Bhattacharya, Ramesh
APPLICANT: Dower, William
TITLE OF INVENTION: RECEPTOR-BINDING ANTIPROLIFERATIVE
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kleinfelder and Chow
STREET: 375 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/014,426
FILING DATE: 05-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 5490A-204
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-014-426-23

Query Match 27.3%, Score 3, DB 1, Length 8;
Best Local Similarity 100.0%, Pred. No. 2.5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KER 5
DE 4 KER 6

RESULT 16
US-08-036-555R-15
Sequence 15, Application US/08036555R
Patent No. 5530109
GENERAL INFORMATION:
APPLICANT: Goodeall, Andrew; Stroobant, Paul;
APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchionni, Mark;
APPLICANT: Chen, Mao Su; Hiles, Ian
TITLE OF INVENTION: Glial Mitogenic Factors, Their
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felte & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/036,555B
FILING DATE: 24-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,173
FILING DATE: 23-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/940,389
FILING DATE: 03-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/907,138
FILING DATE: 30-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/864,703
FILING DATE: 03-APRIL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08,91 07566,3
FILING DATE: 10-APRIL-1991

ATTORNEY/AGENT INFORMATION:
 NAME: Tsai, Christine H
 REGISTRATION NUMBER: 34,266
 REFERENCE/DOCKET NUMBER: LUD 5250.4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 818-3884
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 FEATURE: CHARACTERISTICS:
 OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

US-08-046 555b 15

Query Match 27.3% Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AKK 3
 DE 111
 6 AKK 8

RESULT 47
 US-08-201-046A 27
 Sequence 27, Application US/0426103A
 Patent No. 5945719
 GENERAL INFORMATION:
 APPLICANT: Shasqua, Victor E
 TITLE OF INVENTION: NERVE GROWTH RECEPTORS AND USES THEREOF
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: WOLL, Greenfield & SARKIS, P.C.
 STREET: 600 Atlantic Ave.
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02210

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #100, Version #1.2
 CURRENT APPLICATION DATA:
 FILING DATE: 24-FEB-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Plumer, Elizabeth R.
 REGISTRATION NUMBER: 36,647
 REFERENCE/DOCKET NUMBER: N2260/2014
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 517-720-3500
 TELEFAX: 517-720-2441
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 FEATURE: CHARACTERISTICS:
 FRAGMENT TYPE: internal

US-08-201-046A-27

Query Match 27.3% Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
 DE 111
 3 KKE 3

RESULT 38
 US-08-469-569-15
 Sequence 15, Application US/08469509
 Patent No. 5506032
 GENERAL INFORMATION:
 APPLICANT: Goodheart, Andrew; Stroubant, Paul;
 APPLICANT: Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark;
 APPLICANT: Chen, Mao Su; Miles, Ian
 TITLE OF INVENTION: Glial Mitogenic Factors, Their
 NUMBER OF SEQUENCES: 184
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Felice & Lyset
 STREET: 805 Third Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10022

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage

COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,569
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/046,555
 FILING DATE: 24-MAR-1994
 APPLICATION NUMBER: 07/965,173
 FILING DATE: 23-OCT-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/940,389
 FILING DATE: 03-SEP-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/907,138
 FILING DATE: 30-JUN-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/864,703
 FILING DATE: 03-APRIL-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/046,555
 FILING DATE: 10-APRIL-1991

ATTORNEY/AGENT INFORMATION:
 NAME: Tsai, Christine H.
 REGISTRATION NUMBER: 34,266
 REFERENCE/DOCKET NUMBER: LUD 5250.4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200
 TELEFAX: (212) 818-3884

INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear

FEATURE:
 OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

US-08-469-569-15

Query Match 27.3% Score 3; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AKK 3
 DE 111
 6 AKK 8

RESULT 39

```

US-08-472-952-3
: Sequence 3, Application US/08372952
: Patent No. 5645837
: GENERAL INFORMATION:
: APPLICANT: Jamason, Bradford A.
: APPLICANT: Choksi, Swati
: APPLICANT: Kordgold, Robert
: TITLE OF INVENTION: CD8 Antagonists
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Markiewicz &
: STREET: One Liberty Place, 40th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/372,952
: FILING DATE:
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Deluca, Mark
: REGISTRATION NUMBER: 34,229
: REFERENCE/DOCKET NUMBER: TJU-1440
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-568-3100
: TELEFAX: 215-568-3439
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-472-952-3

Query Match 27.3% Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 DTQ 11
Db 1 1
5 DTQ 7

RESULT 40
US-08-475-6450-9
: Sequence 9, Application US/084556450
: Patent No. 5650487
: GENERAL INFORMATION:
: APPLICANT: Chang, Y-H.
: APPLICANT: Abraham, E.
: TITLE OF INVENTION: Serum Immunoregulatory Polypeptide and
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pons, Smith, Lande & Rose
: STREET: 2029 Century Park East, Suite 400
: CITY: Los Angeles
: STATE: CA
: COUNTRY: USA
: ZIP: 90067
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

```

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: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/455,645D
: FILING DATE: May 31, 1995
: CLASSIFICATION: 436
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/204,486
: FILING DATE: March 2, 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Oldenkamp, David J.
: REGISTRATION NUMBER: 29,421
: REFERENCE/DOCKET NUMBER: 109-175
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (310) 788-5000
: TELEFAX: (310) 277-1297
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY:
: LOCATION:
: IDENTIFICATION METHOD:
: US-08-455-645D-9

Query Match 27.3% Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RKD 9
Db 4 RKD 6

RESULT 41
US-08-249-387-2
: Sequence 2, Application US/08249387
: Patent No. 5681700
: GENERAL INFORMATION:
: APPLICANT: Reichlin, Morris
: APPLICANT: Koren, Eugen
: TITLE OF INVENTION: Assay for Pathogenicity of Anti-DNA
: TITLE OF INVENTION: Antibodies
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Patrice L. Pabst
: STREET: 1100 Peachtree Street, Suite 2800
: CITY: Atlanta
: STATE: Georgia
: COUNTRY: USA
: ZIP: 30309-4530
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/249,387
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Pabst, Patrice L.
: REGISTRATION NUMBER: 31,284
: REFERENCE/DOCKET NUMBER: OMR#145
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (404) 815-6508
: TELEFAX: (404) 815-6555
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:

```

: LENGTH: 8 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: peptide
 : HYPOTHETICAL: NO
 : ANTI SENSE: NO
 : FRAGMENT TYPE: Internal
 : US-08-249-387-2

Query Match 27.3% Score 3: DB 1: Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3: Conservative 0: Mismatches 0: Gaps 0:

QY 1 AKK 4
 ID 6 AKK 8

RESULT 42
 : US 08 464 365-5
 : Sequence 5: Application US/08464365
 : Patent No. 5700659

: GENERAL INFORMATION:
 : APPLICANT: YAMADA, YUKIO
 : APPLICANT: ASAMI, OSAMU
 : APPLICANT: SUGIYAMA, HIDEHIKO
 : APPLICANT: IDEKUBA, CHIE
 : APPLICANT: HOSHINO, FUMHIKO
 : APPLICANT: HIRAI, MASANA
 : APPLICANT: KAJINO, TSUTOMU
 : APPLICANT: IMAEDA, TAKAO
 : APPLICANT: SARAI, KIYOKO
 : TITLE OF INVENTION: POLYPEPTIDE PROCESSING PROTEIN D-SERLEUF
 : TITLE OF INVENTION: ISOMERASE ACTIVITY GENE ENCODING THE SAME AND PROCESS FOR
 : TITLE OF INVENTION: PRODUCING THE SAME
 : NUMBER OF SEQUENCES: 10
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATHER & NEUSTADT
 : ADDRESS: P.C.
 : STREET: 1755 S. Jefferson Davis Highway, Suite 400
 : CITY: Arlington
 : STATE: Virginia
 : COUNTRY: U.S.A.
 : ZIP: 22202

: COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #10, Version #1.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/464,365
 : FILING DATE:

: CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: JP 4 135254
 : FILING DATE: 27-MAY-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: JP 5-44-113
 : FILING DATE: 04-MAR-1993
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: JP 5-44-014
 : FILING DATE: 04-MAR-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Oblon, No. 5700659man P.
 : REGISTRATION NUMBER: 24,618
 : REFERENCE/DOCKET NUMBER: 68-226-C
 : TELEPHONE: (703) 413-3000
 : TELEFAX: (703) 413-2220
 : TELEX: 248855 OPAT UR
 : INFORMATION FOR SEQ ID NO: 5:
 : SEQUENCE CHARACTERISTICS:

: LENGTH: 8 amino acids
 : TYPE: amino acid
 : TOPOLOGY: linear
 : MOLECULE TYPE: peptide
 : US-08-464-365-5

Query Match 27.3% Score 3: DB 1: Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 3: Conservative 0: Mismatches 0: Gaps 0:

QY 8 KDT 16
 ID 111
 ID 1 KDT 4

RESULT 43
 : US-08-249-322A-15
 : Sequence 15: Application US/08249322A
 : Patent No. 5716930

: GENERAL INFORMATION:
 : APPLICANT: Goodheart, Andrew; Stroobant, Paul;
 : APPLICANT: Minnetti, Luisa; Waterfield, Michael; Marchioni, Mark;
 : APPLICANT: Chen, Maio Su; Hiles, Ian
 : TITLE OF INVENTION: Glial Mitogenic Factors, Their
 : TITLE OF INVENTION: Preparation and Use
 : NUMBER OF SEQUENCES: 184
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Pelfe & Lynch
 : STREET: 805 Third Avenue
 : CITY: New York City
 : STATE: New York
 : COUNTRY: USA
 : ZIP: 10022

: COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 : COMPUTER: IBM
 : OPERATING SYSTEM: PC-DOS
 : SOFTWARE: Wordperfect
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/249,322A
 : FILING DATE: 26-MAY-1994

: CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 08/036,555
 : FILING DATE: 24-MAR-1993
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/965,173
 : FILING DATE: 23-OCT-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/940,389
 : FILING DATE: 03-SEP-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/907,138
 : FILING DATE: 30-JUN-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/863,703
 : FILING DATE: 03-APRIL-1992
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: U.K. 91 07566.3
 : FILING DATE: 10-APRIL-1991
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Tsai, Christine H.
 : REGISTRATION NUMBER: 34,266
 : REFERENCE/DOCKET NUMBER: LMD 250.4
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (212) 688-9200
 : TELEFAX: (212) 838-3884
 : INFORMATION FOR SEQ ID NO: 15:
 : SEQUENCE CHARACTERISTICS:

: LENGTH: 8
 : TYPE: amino acid
 : STRANDEDNESS:
 : TOPOLOGY: linear

1 FEATURE:
2 OTHER INFORMATION: Xaa at position 1 is Cysteine or Arginine.
3 US:GB 249-322A-15

Query Match: 27.4%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
1-1
DB 6 AKK 8

RESULT 44
US-08-461-597-8
Sequence 8, Application US/08461597
Patent No. 5759834
GENERAL INFORMATION:
APPLICANT: ALASSI, M. Zohair
TITLE OF INVENTION: Synthetic Sterically Constrained Catalysts
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas D. Paul
STREET: 1401 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77010-4095
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461-597
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/603,644
FILING DATE: 18-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 42,717
REFERENCE/DRAWET NUMBER: 1-536
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5345
TELEFAX: 713/651-4246
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYDROPHILIC: NO
AMBI SENSE: NO
FRAGMENT TYPE: not applicable

Query Match: 27.3%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
1-1
DB 6 AKK 8

RESULT 45
US-08-461-597-8
Sequence 8, Application US/08461597
Patent No. 5759834
GENERAL INFORMATION:
APPLICANT: ALASSI, M. Zohair
TITLE OF INVENTION: Synthetic Sterically Constrained Catalysts
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas D. Paul
STREET: 1401 McKinney, Suite 5100
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77010-4095
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461-597
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/603,644
FILING DATE: 18-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Paul, Thomas D.
REGISTRATION NUMBER: 42,717
REFERENCE/DRAWET NUMBER: 1-536
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/651-5345
TELEFAX: 713/651-4246
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYDROPHILIC: NO
AMBI SENSE: NO
FRAGMENT TYPE: not applicable

QY 1 AKK 3
1-1
DB 6 AKK 8

GENERAL INFORMATION:
APPLICANT: KIMACHI, Kazuhiko
APPLICANT: MAEDA, Hiroaki
APPLICANT: NISHIYAMA, Kiyoto
APPLICANT: TOKIYOSHI, Sachio
APPLICANT: TOHYA, Yukihiro
APPLICANT: MIKAMI, Takeshi
TITLE OF INVENTION: ANTI-PELINE CALCIVIRUS RECOMBINANT
TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT ENCODING THE SAME
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: WEGNER, CANTOR, MUELLER & PLAYER
STREET: 1235 20th Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20036-8218
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/024-253
FILING DATE: 19930301
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 79189/1992
FILING DATE: 28-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: CANTOR, Herbert J.
REGISTRATION NUMBER: 24,192
REFERENCE/DRAWET NUMBER: P-500-23744
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0400
TELEFAX: (202) 845-0995
TELEX: 440706 WEGUR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US:08-024-253-13

Query Match: 27.4%; Score 3; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KDI 10
1-1
DB 6 KDI 5

RESULT 46
US-08-461-526A-15
Sequence 15, Application US/08461526A
Patent No. 5792849
GENERAL INFORMATION:
APPLICANT: Gossard, L. Andrew
APPLICANT: Stroobant, Paul
APPLICANT: Minghetti, Luisa
APPLICANT: Waterfield, Michael
APPLICANT: Marchionni, Mark
APPLICANT: Chen, Moto S.
APPLICANT: BLOS, Jan
TITLE OF INVENTION: GLOBAL MITOGENIC FACTORS, THEIR PREPARATION AND USE
NUMBER OF SEQUENCES: 187
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Bedford LLP
STREET: 770, Federal Street
CITY: Boston


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1 STATE: MA
2 COUNTRY: USA
3 ZIP: 02110
4 COMPUTER READABLE FORM:
5 MEDIUM TYPE: Diskette
6 COMPUTER: IBM Compatible
7 OPERATING SYSTEM: DOS
8 SOFTWARE: FASTSEQ for Windows Version 1.5
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10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/08/429,527A
12 FILING DATE: 06 June 1995
13 CLASSIFICATION: 445
14
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: 08/036,555
17 FILING DATE: 24-MAR-1993
18 APPLICATION NUMBER: 07/905,173
19 FILING DATE: 23-OCT-1992
20 APPLICATION NUMBER: 07/940,349
21 FILING DATE: 03-SEP-1992
22 APPLICATION NUMBER: 07/907,138
23 FILING DATE: 03-JUN-1992
24 APPLICATION NUMBER: 07/963,793
25 FILING DATE: 03-APR-1992
26 APPLICATION NUMBER: 01-K-91-07566-3
27 FILING DATE: 10-APR-1991
28
29 ATTORNEY/AGENT INFORMATION:
30 NAME: Broker Brady, Kristina
31 REGISTRATION NUMBER: 39,109
32 REFERENCE/DOCKET NUMBER: 045065/0209A
33 TELECOMMUNICATION INFORMATION:
34 TELEPHONE: 617-428-0200
35 TELEFAX: 617-428-7045
36
37 INFORMATION FOR SEQ ID NO: 15:
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 8
40 TYPE: amino acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43 FEATURE:
44 OTHER INFORMATION: Xaa is position 15 in sequence
45
46 US 09 469 526A-15
47
48 Query Match 27.3%, Score 3, DB 15, Length 8
49 Best local Similarity 100.0%, Pred. No. 2.5e+05
50 Matches 3, Conservative 0, Mismatches 0, Gaps 0
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: APPLICATION NUMBER: 07/907,118
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: APPLICATION NUMBER: UK 91 07566,3
: FILING DATE: 10-APR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Bleker-Brady, Kristina
: REGISTRATION NUMBER: 39,709
: REFERENCE/DOCKET NUMBER: 04585/00200P
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 428-0200
: TELEFAX: (617) 428-7045
: TELEX:
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: FEATURE:
: OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
US 08-734-591A-15

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Query Match: 27.3%, Score 3, DB 2: Length 8;
Best Local Similarity: 100.0%, Pred. No. 2.5e+05;
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QY 1 AKK 3
IU 6 AKK 8

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: Sequence 15, Application US/08/545298
: Patent No. 5861477
: GENERAL INFORMATION:
: APPLICANT: Atassi, Zouhair
: TITLE OF INVENTION: Synthetic Stereoregular Polystyrenes
: NUMBER OF SEQUENCES: 13
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: C. Steven McDaniel
: STREET: 600 Travis Street, Suite 1400
: CITY: Houston
: STATE: Texas
: COUNTRY: USA
: ZIP: 77002-2912
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Microsoft Word 97 (running under MS Windows 95)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/545,298
: FILING DATE: 19-JUNE-1996
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: C. Steven McDaniel
: REGISTRATION NUMBER: 33,962
: REFERENCE/DOCKET NUMBER: 1515-0310A
: TELECOMMUNICATION INFORMATION:

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: TELEPHONE: 714/248-8000
: TELEFAX: 714/238-8008
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: not applicable
US-08 545-298-10

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Query Match: 27.3%, Score 3; DB 2: Length 8;
Best Local Similarity: 100.0%, Pred. No. 2.5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AKK 3
DB 1 AKK 3

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RESULT 50
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: Patent No. 5876973
: GENERAL INFORMATION:
: APPLICANT: Gwynne, David I.; Marchionni, Mark;
: APPLICANT: McBurney, Robert N.
: TITLE OF INVENTION: INHIBITORS OF CELL PROLIFERATION,
: TITLE OF INVENTION: THEIR PREPARATION AND USE
: NUMBER OF SEQUENCES: 184
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: Massachusetts
: ZIP: 02111-2804
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
: COMPUTER: IBM
: OPERATING SYSTEM: PC DOS
: SOFTWARE: Wordperfect
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/469,660
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/011,196
: FILING DATE: 29-JAN-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/984,085
: FILING DATE: 01-OCT-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/951,747
: FILING DATE: 25-SEP-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/927,337
: FILING DATE: 10-AUG-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Clark, Paul T.
: REGISTRATION NUMBER: 30,162
: REFERENCE/DOCKET NUMBER: 04585/017004
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 542-5070
: TELEFAX: 200154
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear

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: FEATURE:
: OTHER INFORMATION: Xaa in position 1 is Lysine or
: OTHER INFORMATION: Arginine.
US-08-469-660 15
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Best Local Similarity 100.0%; Pred. Neg. 2.5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AKK 3
Db 6 AKK 8
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Job time : 16.9167 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2003, 10:10:03 : Search time 21.5 Seconds
(without alignments)
77.413 Million cell updates/sec

Title: US-09-787-443-2

Perfect score: 11

Sequence: 1 AKKERQKDIQ 11

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Gapop 60.0 , Gapext 60.0

Searched: 566894 seqs, 151307093 residues

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Pred. No. is the number of results predicted by change to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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116	3	27.3	9	10	US-09-872-1856-15	Sequence 15, Appl	189	3	27.3	9	12	US-10-172-425B-22	Sequence 22, App
117	3	27.3	9	10	US-09-792-480-8	Sequence 8, Appl	190	3	27.3	9	12	US-10-172-425B-22	Sequence 22, App
118	3	27.3	9	10	US-09-792-480-14	Sequence 14, Appl	191	3	27.3	9	12	US-10-190-082-270	Sequence 270, App
119	3	27.3	9	10	US-09-792-480-14	Sequence 14, Appl	192	3	27.3	9	12	US-10-201-389A-18	Sequence 18, Appl
120	3	27.3	9	10	US-09-792-480-15	Sequence 15, Appl	193	3	27.3	9	12	US-10-169-223-6	Sequence 6, Appl
121	3	27.3	9	10	US-09-792-480-15	Sequence 15, Appl	194	3	27.3	9	12	US-09-793-451-522	Sequence 522, App
122	3	27.3	9	10	US-09-792-480-20	Sequence 20, Appl	195	3	27.3	9	12	US-09-793-451-643	Sequence 643, App
123	3	27.3	9	10	US-09-792-480-20	Sequence 20, Appl	196	3	27.3	9	12	US-10-308-967-22	Sequence 22, Appl
124	3	27.3	9	10	US-09-792-480-22	Sequence 22, Appl	197	3	27.3	9	12	US-10-308-967-22	Sequence 22, Appl
125	3	27.3	9	10	US-09-792-480-26	Sequence 26, Appl	198	3	27.3	9	12	US-10-338-348-1	Sequence 1, Appl
126	3	27.3	9	10	US-09-731-558-8	Sequence 8, Appl	199	3	27.3	9	12	US-10-022-066-21	Sequence 21, Appl
127	3	27.3	9	10	US-09-779-308-182	Sequence 182, App	200	3	27.3	9	12	US-10-022-066-158	Sequence 158, App
128	3	27.3	9	10	US-09-779-308-196	Sequence 196, App	201	3	27.3	9	12	US-10-077-106-13	Sequence 13, Appl
129	3	27.3	9	10	US-09-779-308-407	Sequence 407, App	202	3	27.3	9	12	US-10-077-106-15	Sequence 15, Appl
130	3	27.3	9	10	US-09-779-308-481	Sequence 481, App	203	3	27.3	9	12	US-10-262-435-4	Sequence 4, Appl
131	3	27.3	9	10	US-09-984-057-10	Sequence 10, Appl	204	3	27.3	9	12	US-09-942-052-15	Sequence 15, Appl
132	3	27.3	9	10	US-09-942-087A-13	Sequence 10, Appl	205	3	27.3	9	12	US-09-942-052-115	Sequence 115, App
133	3	27.3	9	10	US-09-942-090-13	Sequence 10, Appl	206	3	27.3	9	12	US-09-942-052-220	Sequence 220, App
134	3	27.3	9	10	US-09-966-561A-14	Sequence 66, App	207	3	27.3	9	12	US-09-942-052-224	Sequence 224, App
135	3	27.3	9	10	US-09-966-561A-14	Sequence 66, App	208	3	27.3	9	12	US-09-942-052-528	Sequence 528, App
136	3	27.3	9	10	US-09-968-561A-14	Sequence 162, App	209	3	27.3	9	12	US-09-942-052-617	Sequence 617, App
137	3	27.3	9	10	US-09-968-561A-262	Sequence 282, App	210	3	27.3	9	12	US-10-280-137-237	Sequence 237, App
138	3	27.3	9	10	US-09-968-561A-262	Sequence 282, App	211	3	27.3	9	12	US-10-304-443-112	Sequence 112, App
139	3	27.3	9	10	US-09-978-611-23	Sequence 23, Appl	212	3	27.3	9	12	US-10-239-313A-692	Sequence 692, App
140	3	27.3	9	10	US-09-779-102A-22	Sequence 22, Appl	213	3	27.3	9	12	US-10-353-929-13	Sequence 13, Appl
141	3	27.3	9	10	US-09-779-102A-22	Sequence 22, Appl	214	3	27.3	9	12	US-10-353-929-13	Sequence 13, Appl
142	3	27.3	9	11	US-09-864-291-17	Sequence 67, Appl	215	3	27.3	9	12	US-10-412-105-33	Sequence 33, Appl
143	3	27.3	9	11	US-09-846-034H-214	Sequence 214, App	216	3	27.3	9	14	US-10-011-321-4	Sequence 1, Appl
144	3	27.3	9	11	US-09-925-179-11	Sequence 11, Appl	217	3	27.3	9	15	US-10-211-207-13	Sequence 13, Appl
145	3	27.3	9	11	US-09-925-179-28	Sequence 28, Appl	218	3	27.3	9	15	US-10-211-207-14	Sequence 14, Appl
146	3	27.3	9	11	US-09-990-186-6	Sequence 5, Appl	219	3	27.3	9	15	US-10-211-207-15	Sequence 15, Appl
147	3	27.3	9	11	US-09-936-864-46	Sequence 46, App	220	3	27.3	9	15	US-10-006-069A-214	Sequence 214, App
148	3	27.3	9	11	US-09-936-864-80	Sequence 80, Appl	221	3	27.3	9	15	US-10-125-635A-128	Sequence 128, App
149	3	27.3	9	11	US-09-938-864-124	Sequence 128, App	222	3	27.3	9	15	US-10-125-635A-163	Sequence 163, App
150	3	27.3	9	11	US-09-938-864-164	Sequence 163, App	223	3	27.3	9	15	US-10-125-635A-219	Sequence 219, App
151	3	27.3	9	11	US-09-938-864-172	Sequence 172, App	224	3	27.3	9	15	US-10-125-635A-300	Sequence 300, App
152	3	27.3	9	11	US-09-938-864-219	Sequence 219, App	225	3	27.3	9	15		
153	3	27.3	9	11	US-09-938-864-460	Sequence 300, App	226	3	27.3	9	15		
154	3	27.3	9	11	US-09-876-904A-272	Sequence 272, App	227	3	27.3	9	15		
155	3	27.3	9	11	US-09-876-904A-466	Sequence 276, App	228	3	27.3	9	15		
156	3	27.3	9	11	US-09-876-904A-466	Sequence 466, App	229	3	27.3	9	15		
157	3	27.3	9	11	US-09-876-904A-586	Sequence 586, App	230	3	27.3	9	15		
158	3	27.3	9	11	US-09-876-904A-596	Sequence 596, App	231	3	27.3	9	15		
159	3	27.3	9	11	US-09-791-477-46	Sequence 46, Appl	232	3	27.3	9	15		
160	3	27.3	9	11	US-09-791-477-80	Sequence 80, Appl	233	3	27.3	9	15		
161	3	27.3	9	11	US-09-791-477-164	Sequence 164, App	234	3	27.3	9	15		

235	1	27.3	9	15	US-10-039-831-16	Sequence 16, Appl	308	3	27.3	9	15	US-10-001-459-1966	Sequence 1566, Ap
236	3	27.3	9	15	US-10-055-713-8	Sequence 8, Appl	309	3	27.3	9	15	US-10-001-459-2007	Sequence 2007, Ap
237	3	27.3	9	15	US-10-239-804-1	Sequence 1, Appl	310	3	27.3	9	15	US-10-001-469-2008	Sequence 2008, Ap
238	3	27.3	9	15	US-10-084-813-987	Sequence 987, App	311	3	27.3	9	15	US-10-001-469-2013	Sequence 2013, Ap
239	3	27.3	9	15	US-10-084-813-988	Sequence 988, App	312	3	27.3	9	15	US-10-001-469-2062	Sequence 2062, Ap
240	3	27.3	9	15	US-10-084-813-989	Sequence 989, App	313	3	27.3	9	15	US-10-001-469-2063	Sequence 2063, Ap
241	3	27.3	9	15	US-10-084-813-990	Sequence 990, App	314	3	27.3	9	15	US-10-001-469-2132	Sequence 2132, Ap
242	3	27.3	9	15	US-10-084-813-991	Sequence 991, App	315	3	27.3	9	15	US-10-103-901-29	Sequence 29, Appl
243	3	27.3	9	15	US-10-084-813-992	Sequence 992, App	316	3	27.3	9	15	US-10-023-282-832	Sequence 832, App
244	3	27.3	9	15	US-10-084-813-993	Sequence 993, App	317	3	27.3	9	15	US-10-002-603-46	Sequence 46, Appl
245	3	27.3	9	15	US-10-040-013-4	Sequence 4, Appl	318	3	27.3	9	15	US-10-002-603-80	Sequence 80, Appl
246	3	27.3	9	15	US-10-059-261-239	Sequence 239, App	319	3	27.3	9	15	US-10-002-603-128	Sequence 128, App
247	3	27.3	9	15	US-10-059-261-325	Sequence 325, App	320	3	27.3	9	15	US-10-002-603-163	Sequence 163, App
248	3	27.3	9	15	US-10-059-261-322	Sequence 322, App	321	3	27.3	9	15	US-10-002-603-172	Sequence 172, App
249	3	27.3	9	15	US-10-059-261-325	Sequence 325, App	322	3	27.3	9	15	US-10-002-603-219	Sequence 219, App
250	3	27.3	9	15	US-10-006-869-531	Sequence 531, App	323	3	27.3	9	15	US-10-002-603-300	Sequence 300, App
251	3	27.3	9	15	US-10-006-869-545	Sequence 545, App	324	3	27.3	9	15	US-10-133-210-58	Sequence 58, Appl
252	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	325	3	27.3	9	15	US-10-133-210-193	Sequence 193, App
253	3	27.3	9	15	US-10-006-869-536	Sequence 3194, App	326	3	27.3	9	15	US-10-211-088-203	Sequence 203, App
254	3	27.3	9	15	US-10-006-869-536	Sequence 3194, App	327	3	27.3	9	15	US-10-211-088-271	Sequence 271, App
255	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	328	3	27.3	9	15	US-10-091-724-49	Sequence 49, Appl
256	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	329	3	27.3	9	15	US-10-113-424-5	Sequence 5, Appl
257	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	330	3	27.3	9	15	US-10-165-250A-9	Sequence 9, Appl
258	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	331	3	27.3	9	15	US-10-165-250A-10	Sequence 10, Appl
259	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	332	3	27.3	9	15	US-10-055-711-8	Sequence 8, Appl
260	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	333	3	27.3	9	15	US-10-136-738-46	Sequence 46, Appl
261	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	334	3	27.3	9	15	US-10-109-171-40	Sequence 40, Appl
262	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	335	3	27.3	9	15	US-10-109-171-122	Sequence 122, App
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266	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	339	3	27.3	9	15	US-10-301-644-16	Sequence 16, Appl
267	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	340	3	27.3	9	15	US-10-301-644-17	Sequence 17, Appl
268	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	341	3	27.3	9	15	US-10-012-806A-43	Sequence 43, Appl
269	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	342	3	27.3	9	15	US-10-201-394A-18	Sequence 18, Appl
270	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	343	3	27.3	10	8	US-08-927-939-27	Sequence 27, Appl
271	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	344	3	27.3	10	8	US-08-873-601-5	Sequence 5, Appl
272	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	345	3	27.3	10	9	US-09-157-748-12	Sequence 12, Appl
273	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	346	3	27.3	10	9	US-09-010-714-4	Sequence 4, Appl
274	3	27.3	9	15	US-10-006-869-534	Sequence 3194, App	347	3	27.3	10	9	US-09-834-765-487	Sequence 487, App
275	3	27.3	9	15	US-10-209-421-11	Sequence 11, Appl	348	3	27.3	10	9	US-09-834-765-606	Sequence 606, App
276	3	27.3	9	15	US-10-209-421-28	Sequence 28, Appl	349	3	27.3	10	9	US-09-834-765-672	Sequence 672, App
277	3	27.3	9	15	US-10-229-915-26	Sequence 26, Appl	350	3	27.3	10	9	US-09-802-109-10	Sequence 10, Appl
278	3	27.3	9	15	US-10-229-915-31	Sequence 31, Appl	351	3	27.3	10	10	US-09-950-692-4	Sequence 4, Appl
279	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	352	3	27.3	10	10	US-09-972-016-2	Sequence 2, Appl
280	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	353	3	27.3	10	10	US-09-972-016-3	Sequence 3, Appl
281	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	354	3	27.3	10	10	US-09-977-831-36	Sequence 36, Appl
282	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	355	3	27.3	10	10	US-09-984-056-91	Sequence 91, Appl
283	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	356	3	27.3	10	10	US-09-963-206B-14	Sequence 14, Appl
284	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	357	3	27.3	10	10	US-09-916-940-9	Sequence 9, Appl
285	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	358	3	27.3	10	10	US-09-970-515-7	Sequence 7, Appl
286	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	359	3	27.3	10	10	US-09-824-588-5	Sequence 5, Appl
287	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	360	3	27.3	10	10	US-09-779-308-150	Sequence 150, App
288	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	361	3	27.3	10	10	US-09-779-308-356	Sequence 356, App
289	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	362	3	27.3	10	10	US-09-922-364A-18	Sequence 18, Appl
290	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	363	3	27.3	10	10	US-09-254-590-18	Sequence 18, Appl
291	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	364	3	27.3	10	10	US-09-792-630-58	Sequence 58, Appl
292	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	365	3	27.3	10	10	US-09-966-976A-14	Sequence 14, Appl
293	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	366	3	27.3	10	10	US-09-910-552-55	Sequence 55, Appl
294	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	367	3	27.3	10	11	US-09-978-178-1	Sequence 1, Appl
295	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	368	3	27.3	10	11	US-09-959-845-8	Sequence 8, Appl
296	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	369	3	27.3	10	11	US-09-882-774-12	Sequence 12, Appl
297	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	370	3	27.3	10	11	US-09-782-672-47	Sequence 47, Appl
298	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	371	3	27.3	10	11	US-09-994-595-26	Sequence 26, Appl
299	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	372	3	27.3	10	11	US-09-994-595-63	Sequence 63, Appl
300	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	373	3	27.3	10	11	US-09-994-595-67	Sequence 67, Appl
301	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	374	3	27.3	10	11	US-09-994-595-83	Sequence 83, Appl
302	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	375	3	27.3	10	11	US-09-866-512A-15	Sequence 15, Appl
303	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	376	3	27.3	10	11	US-09-876-904A-41	Sequence 41, Appl
304	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	377	3	27.3	10	11	US-09-876-904A-87	Sequence 87, Appl
305	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	378	3	27.3	10	11	US-09-876-904A-90	Sequence 90, Appl
306	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	379	3	27.3	10	11	US-09-876-904A-257	Sequence 257, App
307	3	27.3	9	15	US-10-001-469-94	Sequence 94, Appl	380	3	27.3	10	11	US-09-876-904A-440	Sequence 440, App

381	3	27.3	10	11	US-09-876-904A-463	Sequence 463, App	454	3	27.3	10	12	US-10-022-066-398	Sequence 398, App
382	3	27.3	10	11	US-09-876-904A-572	Sequence 572, App	455	3	27.3	10	12	US-10-167-831-38	Sequence 38, App
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385	3	27.3	10	11	US-09-572-404B-250	Sequence 250, App	458	3	27.3	10	12	US-10-262-435-29	Sequence 29, App
386	3	27.3	10	11	US-09-572-404B-252	Sequence 252, App	459	3	27.3	10	12	US-10-262-435-52	Sequence 52, App
387	3	27.3	10	11	US-09-572-404B-820	Sequence 820, App	460	3	27.3	10	12	US-10-262-435-53	Sequence 53, App
388	3	27.3	10	11	US-09-572-404B-971	Sequence 971, App	461	3	27.3	10	12	US-10-262-435-59	Sequence 59, App
389	3	27.3	10	11	US-09-572-404B-1067	Sequence 1067, App	462	3	27.3	10	12	US-10-262-435-60	Sequence 60, App
390	3	27.3	10	11	US-09-572-404B-1183	Sequence 1183, App	463	3	27.3	10	12	US-10-262-435-61	Sequence 61, App
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392	3	27.3	10	11	US-09-572-404B-1594	Sequence 1594, App	465	3	27.3	10	12	US-10-262-435-63	Sequence 63, App
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396	3	27.3	10	11	US-09-572-404B-1747	Sequence 1747, App	469	3	27.3	10	12	US-10-262-435-82	Sequence 82, App
397	3	27.3	10	11	US-09-572-404B-1842	Sequence 1842, App	470	3	27.3	10	12	US-10-262-435-83	Sequence 83, App
398	3	27.3	10	11	US-09-572-404B-1942	Sequence 1942, App	471	3	27.3	10	12	US-10-262-435-107	Sequence 0, App
399	3	27.3	10	11	US-09-572-404B-1947	Sequence 1947, App	472	3	27.3	10	12	US-09-942-052-52	Sequence 52, App
400	3	27.3	10	11	US-09-572-404B-1947	Sequence 1949, App	473	3	27.3	10	12	US-09-942-052-167	Sequence 167, App
401	3	27.3	10	11	US-09-572-404B-2141	Sequence 2141, App	474	3	27.3	10	12	US-09-942-052-180	Sequence 180, App
402	3	27.3	10	11	US-09-572-404B-2152	Sequence 2152, App	475	3	27.3	10	12	US-09-942-052-200	Sequence 200, App
403	3	27.3	10	11	US-09-572-404B-2171	Sequence 2171, App	476	3	27.3	10	12	US-09-942-052-253	Sequence 253, App
404	3	27.3	10	11	US-09-572-404B-2176	Sequence 2178, App	477	3	27.3	10	12	US-09-942-052-298	Sequence 298, App
405	3	27.3	10	11	US-09-572-404B-2183	Sequence 2183, App	478	3	27.3	10	12	US-09-942-052-354	Sequence 354, App
406	3	27.3	10	11	US-09-572-404B-2520	Sequence 2520, App	479	3	27.3	10	12	US-09-942-052-376	Sequence 376, App
407	3	27.3	10	11	US-09-572-404B-2522	Sequence 2522, App	480	3	27.3	10	12	US-09-942-052-587	Sequence 587, App
408	3	27.3	10	11	US-09-572-404B-4116	Sequence 2616, App	481	3	27.3	10	12	US-09-942-052-661	Sequence 661, App
409	3	27.3	10	11	US-09-820-553A-37	Sequence 37, App	482	3	27.3	10	12	US-10-036-550-9	Sequence 9, App
410	3	27.3	10	11	US-09-820-553A-13	Sequence 38, App	483	3	27.3	10	12	US-10-280-137-114	Sequence 114, App
411	3	27.3	10	11	US-09-820-553A-13	Sequence 39, App	484	3	27.3	10	12	US-10-155-693-26	Sequence 26, App
412	3	27.3	10	11	US-09-820-553A-14	Sequence 143, App	485	3	27.3	10	12	US-10-239-313A-458	Sequence 458, App
413	3	27.3	10	11	US-09-952-056A-54	Sequence 54, App	486	3	27.3	10	12	US-10-315-920-11	Sequence 11, App
414	3	27.3	10	12	US-09-532-155-549	Sequence 539, App	487	3	27.3	10	14	US-10-007-761-9	Sequence 9, App
415	3	27.3	10	12	US-09-532-155-549	Sequence 26, App	488	3	27.3	10	14	US-10-117-476-6	Sequence 6, App
416	3	27.3	10	12	US-10-177-725-158	Sequence 138, App	489	3	27.3	10	14	US-10-080-376-58	Sequence 58, App
417	3	27.3	10	12	US-10-426-877A-34	Sequence 14, App	490	3	27.3	10	14	US-10-006-557-13	Sequence 13, App
418	3	27.3	10	12	US-10-348-584-102	Sequence 102, App	491	3	27.3	10	14	US-10-061-395-6	Sequence 6, App
419	3	27.3	10	12	US-09-572-270A-49	Sequence 49, App	492	3	27.3	10	14	US-10-115-695-18	Sequence 18, App
420	3	27.3	10	12	US-09-572-270A-41	Sequence 41, App	493	3	27.3	10	15	US-10-096-339-5	Sequence 5, App
421	3	27.3	10	12	US-09-572-270A-52	Sequence 52, App	494	3	27.3	10	15	US-10-165-015-16	Sequence 16, App
422	3	27.3	10	12	US-09-572-270A-52	Sequence 56, App	495	3	27.3	10	15	US-10-108-795-13	Sequence 13, App
423	3	27.3	10	12	US-09-572-270A-55	Sequence 60, App	496	3	27.3	10	15	US-10-116-661-18	Sequence 18, App
424	3	27.3	10	12	US-09-572-270A-54	Sequence 64, App	497	3	27.3	10	15	US-10-012-542-405	Sequence 405, App
425	3	27.3	10	12	US-09-572-270A-54	Sequence 68, App	498	3	27.3	10	15	US-10-115-671-18	Sequence 18, App
426	3	27.3	10	12	US-09-572-270A-72	Sequence 72, App	499	3	27.3	10	15	US-10-194-155-3	Sequence 3, App
427	3	27.3	10	12	US-09-572-270A-72	Sequence 89, App	500	3	27.3	10	15	US-10-043-487-495	Sequence 495, App
428	3	27.3	10	12	US-09-572-270A-73	Sequence 97, App							
429	3	27.3	10	12	US-09-572-270A-73	Sequence 99, App							
430	3	27.3	10	12	US-09-572-270A-74	Sequence 318, App							
431	3	27.3	10	12	US-09-572-270A-74	Sequence 420, App							
432	3	27.3	10	12	US-09-572-270A-74	Sequence 428, App							
433	3	27.3	10	12	US-09-572-270A-74	Sequence 438, App							
434	3	27.3	10	12	US-09-572-270A-74	Sequence 441, App							
435	3	27.3	10	12	US-09-572-270A-74	Sequence 443, App							
436	3	27.3	10	12	US-09-572-270A-74	Sequence 445, App							
437	3	27.3	10	12	US-09-572-270A-74	Sequence 447, App							
438	3	27.3	10	12	US-09-572-270A-74	Sequence 449, App							
439	3	27.3	10	12	US-09-572-270A-74	Sequence 451, App							
440	3	27.3	10	12	US-09-572-270A-74	Sequence 453, App							
441	3	27.3	10	12	US-09-572-270A-74	Sequence 455, App							
442	3	27.3	10	12	US-10-133-973-33	Sequence 33, App							
443	3	27.3	10	12	US-10-133-973-33	Sequence 494, App							
444	3	27.3	10	12	US-10-169-423-24	Sequence 24, App							
445	3	27.3	10	12	US-10-295-731-1	Sequence 2, App							
446	3	27.3	10	12	US-09-793-111-154	Sequence 573, App							
447	3	27.3	10	12	US-09-793-111-154	Sequence 575, App							
448	3	27.3	10	12	US-09-793-111-154	Sequence 577, App							
449	3	27.3	10	12	US-09-793-111-154	Sequence 579, App							
450	3	27.3	10	12	US-09-793-111-154	Sequence 581, App							
451	3	27.3	10	12	US-09-793-111-154	Sequence 583, App							
452	3	27.3	10	12	US-09-793-111-154	Sequence 585, App							
453	3	27.3	10	12	US-09-793-111-154	Sequence 587, App							
454	3	27.3	10	12	US-09-793-111-154	Sequence 589, App							
455	3	27.3	10	12	US-09-793-111-154	Sequence 591, App							
456	3	27.3	10	12	US-09-793-111-154	Sequence 593, App							
457	3	27.3	10	12	US-09-793-111-154	Sequence 595, App							

ALIGNMENTS

RESULT: 1

US-09-876-904A-215

1 Sequence 215, Application: US/09876904A

2 Publication No. US20030072794A1

3 GENERAL INFORMATION:

4 APPLICANT: BELLKAS, INC.

5 TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

6 AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/LIPOGENIC PEPTIDE

7 TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSONE COMPLEXES

8 FILE REFERENCE: IB-2002.00

9 CURRENT APPLICATION NUMBER: US/09/876,904A

10 CURRENT FILING DATE: 2001 06 28

11 PRIOR APPLICATION NUMBER: US 60/210,925

12 PRIOR FILING DATE: 2000 06 09

13 NUMBER OF SEQ ID NOS: 629

14 SOFTWARE: Patent In. Ver. 2.1

15 SEQ ID NO: 215

16 LENGTH: 14

17 TYPE: CDS

18 ORGANISM: Homo sapiens

19 US 09-876-904A-215

```

Query Match          45.5%; Score 5; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RORKE 9
DB 9 RORKE 13

RESULT 2
US-09-876-904A-426
; Sequence 426; Application US/09/876-904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002-00
; CURRENT APPLICATION NUMBER: US/09/876-904A
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/210,925
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 426
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TFE3 binds to both enhancers.
US-09-876-904A-426

Query Match          36.4%; Score 4; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KKKK 6
DB 2 KKKQ 5

RESULT 3
US-09-876-904A-428
; Sequence 428; Application US/09/876-904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; FILE REFERENCE: TB-2002-00
; CURRENT APPLICATION NUMBER: US/09/876-904A
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 60/210,925
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 428
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Human TFE3 (536 aa).
US-09-876-904A-428

Query Match          36.4%; Score 4; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKKQ 6
DB 11

RESULT 4
US-09-876-904A-439
; Sequence 439; Application US/09/876-904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
; FILE REFERENCE: TB-2002-00
; CURRENT APPLICATION NUMBER: US/09/876-904A
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/210,925
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 439
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; OTHER INFORMATION: Yeast NES1 transcription protein factor (1359 aa)
US-09-876-904A-439

Query Match          36.4%; Score 4; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKKK 4
DB 4 KKKK 7

RESULT 5
US-09-922-226-84
; Sequence 84; Application US/09/922-226
; Publication No. US20030077664A1
; GENERAL INFORMATION:
; APPLICANT: Zhao, YJ
; APPLICANT: Thatcher, Scott M.
; APPLICANT: Xiao, Jia-Bao
; APPLICANT: Kusari, Jyotirmoy
; APPLICANT: Chandraharan, Roshantha A.
; TITLE OF INVENTION: Methods of Screening For Compounds That
; TITLE OF INVENTION: Modulate Hormone Receptor Activity
; FILE REFERENCE: P-RAR 4681
; CURRENT APPLICATION NUMBER: US/09/922-226
; CURRENT FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/284,797
; PRIOR FILING DATE: 2001-04-18
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 10
; TYPE: PRI
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-922-226-84

Query Match          36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KKKK 10
DB 4 KKKK 7

```



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RESULT 5
US-09-879-946-10
: Sequence 10, Application US/09879936
: Patent No. US20020045564A1
: GENERAL INFORMATION:
: TITLE OF INVENTION: METHODS OF MODULATING MUSCLE CONTRACTION
: APPLICANT: Van Eyk, Jennifer E.
: APPLICANT: Mak, Alan S.
: APPLICANT: Cote, Graham P.
: TITLE OF INVENTION: Methods of Modulating Muscle Contraction
: FILE REFERENCE: 1997-021-030S
: CURRENT APPLICATION NUMBER: US/09/879,946
: PRIOR FILING DATE: 2001-06-14
: PRIOR APPLICATION NUMBER: 60/050,478
: PRIOR FILING DATE: 1997-06-25
: PRIOR APPLICATION NUMBER: 60/089,505
: PRIOR FILING DATE: 1998-06-16
: NUMBER OF SEQ ID NOS: 26
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 10
: LENGTH: 11
: TYPE: PRT
: ORGANISM: Unknown
: FEATURE:
: NAME/KEY: PEPTIDE
: LOCATION: (1)..(11)
: OTHER INFORMATION: Residues 423 to 433 of chickenizzard caldesmon.
: NAME/KEY: PEPTIDE
: LOCATION: (11)
: OTHER INFORMATION: Targeted Ser phospho-amino acid
US-09-879-946-10

Query Match          36.4%; Score 4; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKKE 4
DB      1111
       7 AKKE 10

RESULT 7
US-10-304-443-118
: Sequence 118, Application US/10304443
: Publication No. US20030170229A1
: GENERAL INFORMATION:
: APPLICANT: Smithkline Beecham Pharmaceuticals S.A.
: APPLICANT: Peptide Therapeutics Ltd.
: TITLE OF INVENTION: Vaccine
: FILE REFERENCE: B45173CIP
: CURRENT APPLICATION NUMBER: US/10/304,443
: CURRENT FILING DATE: 2002-11-25
: PRIOR APPLICATION NUMBER: US/09/698,946A
: PRIOR FILING DATE: 2001-02-20
: NUMBER OF SEQ ID NOS: 121
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 118
: LENGTH: 11
: TYPE: PRT
: ORGANISM: Human peptide sequence
US-10-304-443-118

Query Match          36.4%; Score 4; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 EKQR 7
DB      1111
       2 EKQR 5

RESULT 8
US-09-876-904A-285
: Sequence 285, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOsome COMPLEXES
: FILE REFERENCE: FR 2402-00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR APPLICATION NUMBER: US 60/210,925
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 285
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Saccharomyces cerevisiae
US-09-876-904A-285

Query Match          36.4%; Score 4; DB 11; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KQKK 8
DB      1111
       1 KQKK 4

RESULT 9
US-09-746-170-33
: Sequence 33, Application US/09746170
: Patent No. US20020127543A1
: GENERAL INFORMATION:
: APPLICANT: Karo, Jonathan
: APPLICANT: Walker, Stephen
: TITLE OF INVENTION: Methods and Compositions Utilizing Hepatitis C Virus Molecular
: FILE REFERENCE: 22623/1280
: CURRENT APPLICATION NUMBER: US/09/746,170
: CURRENT FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/171,804
: PRIOR FILING DATE: 1999-12-22
: NUMBER OF SEQ ID NOS: 48
: SOFTWARE: Patent In version 3.0
: SEQ ID NO 33
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Hepatitis C virus
US-09-746-170-33

Query Match          36.4%; Score 4; DB 10; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 KQKK 6
DB      1111
       4 KQKK 7

RESULT 10
US-09-820-053A-88
: Sequence 88, Application US/09820053A
: Publication No. US20030083243A1
: GENERAL INFORMATION:
: APPLICANT: Owen, Donald R.
: TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
: FILE REFERENCE: HELX027
: CURRENT APPLICATION NUMBER: US/09/820,053A
: CURRENT FILING DATE: 2001-03-28
: NUMBER OF SEQ ID NOS: 165
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 88
: LENGTH: 13
: TYPE: PRT

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: ORGANISM: ARTIFICIAL SEQUENCE
: FEATURE:
: OTHER INFORMATION: SYNTHETIC SEQUENCE
: NAME/KEY: MOD_RES
: LOCATION: (13)
: OTHER INFORMATION: AMIDATION
US 09-820-053A-88

Query Match      36.4%; Score 4; DB 13; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKKE 4
DB      9 AKKE 12

RESULT 11
US-10-304-443-113
: Sequence 113, Application US/12304443
: Publication No. US20030170229A1
: GENERAL INFORMATION:
: APPLICANT: SmithKline Beecham Biologicals S.A.
: TITLE OF INVENTION: Vaccine
: FILE REFERENCE: R45173C1P
: CURRENT APPLICATION NUMBER: US/10/304,443
: PRIOR FILING DATE: 2002-11-26
: PRIOR APPLICATION NUMBER: US/95/698,906A
: PRIOR FILING DATE: 2001-02-20
: NUMBER OF SEQ ID NOS: 121
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 113
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Human peptide sequence
US-10-304-443-113

Query Match      36.4%; Score 4; DB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 ERQR 7
DB      3 ERQR 6

RESULT 12
US-10-109-171-88
: Sequence 68, Application US/10109171
: Publication No. US20030109452A1
: GENERAL INFORMATION:
: APPLICANT: Owen, Donald R.
: TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
: FILE REFERENCE: HELX028
: CURRENT APPLICATION NUMBER: US/10/109,171
: CURRENT FILING DATE: 2002-03-28
: NUMBER OF SEQ ID NOS: 165
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 88
: LENGTH: 13
: TYPE: PRT
: ORGANISM: ARTIFICIAL SEQUENCE
: FEATURE:
: OTHER INFORMATION: SYNTHETIC SEQUENCE
: NAME/KEY: MOD_RES
: LOCATION: (13)
: OTHER INFORMATION: AMIDATION
US 10-109-171-88

Query Match      36.4%; Score 4; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 ERQR 7
DB      3 ERQR 6

RESULT 13
US-10-109-171-88
: Sequence 68, Application US/10109171
: Publication No. US20030109452A1
: GENERAL INFORMATION:
: APPLICANT: Owen, Donald R.
: TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
: FILE REFERENCE: HELX028
: CURRENT APPLICATION NUMBER: US/10/109,171
: CURRENT FILING DATE: 2002-03-28
: NUMBER OF SEQ ID NOS: 165
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 88
: LENGTH: 13
: TYPE: PRT
: ORGANISM: ARTIFICIAL SEQUENCE
: FEATURE:
: OTHER INFORMATION: SYNTHETIC SEQUENCE
: NAME/KEY: MOD_RES
: LOCATION: (13)
: OTHER INFORMATION: AMIDATION
US 10-109-171-88

Query Match      36.4%; Score 4; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 ERQR 7
DB      3 ERQR 6

RESULT 14
US-09-900-147-14
: Sequence 14, Application US/09900147
: Patent No. US20020103121A1
: GENERAL INFORMATION:
: APPLICANT: La Thangue, Nicholas B
: APPLICANT: Bandaru, Laxantha R
: TITLE OF INVENTION: Peptide antagonists of DP transcription factors
: FILE REFERENCE: 620-67
: CURRENT APPLICATION NUMBER: US/09/900,147
: CURRENT FILING DATE: 2001-07-09
: PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-05-27
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-05-27
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: GB 9626589.7
: PRIOR FILING DATE: EARLIER FILING DATE: 1996-12-20
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 14
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-900-147-14

Query Match      36.4%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 ERQR 7
DB      3 ERQR 6

RESULT 14
US-09-894-018-203
: Sequence 203, Application US/09894018
: Patent No. US20020119127A1
: GENERAL INFORMATION:
: APPLICANT: EPIMMUNE, Inc.
: APPLICANT: Settle, Alessandro
: APPLICANT: Chestnut, Robert
: APPLICANT: Livingston, Brian
: APPLICANT: Baker, Dennis
: APPLICANT: Newman, Mark
: APPLICANT: Brown, David
: TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
: TITLE OF INVENTION: MINIGENES AND PEPTIDES THEREBY
: FILE REFERENCE: 39963-20033.00
: CURRENT APPLICATION NUMBER: US/09/894,018
: CURRENT FILING DATE: 2001-06-27
: PRIOR APPLICATION NUMBER: PCT/US00/35568
: PRIOR FILING DATE: 2000-12-28
: PRIOR APPLICATION NUMBER: US 60/173,390
: PRIOR FILING DATE: 1999-12-28
: PRIOR APPLICATION NUMBER: US 60/284,221
: PRIOR FILING DATE: 2001-04-16
: NUMBER OF SEQ ID NOS: 368
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 203
: LENGTH: 15
: TYPE: PRT
: ORGANISM: Transgenic mouse
US-09-894-018-203

Query Match      36.4%; Score 4; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 ERQR 7
DB      3 ERQR 6
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Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 RQR 8

DB 5 RQR 9

RESULT 15

US-08-831-310-14
 : Sequence 15, Application US/0941310
 : Publication No. US2002026635A1
 : GENERAL INFORMATION:
 : APPLICANT: Kleantous, Harold et al
 : TITLE OF INVENTION: Helicobacter GABA_A receptors
 : TITLE OF INVENTION: GABA_A 750 Polypeptides and Corresponding Polynucleotides
 : NUMBER OF SEQUENCES: 18
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Clark & Elbing LLP
 : STREET: 176 Federal Street
 : CITY: Boston
 : STATE: MA
 : COUNTRY: USA
 : ZIP: 02110
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Diskette
 : COMPUTER: IBM Compatible
 : OPERATING SYSTEM: DOS
 : SOFTWARE: FASTSEQ for Windows Version 2.0
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/831,310
 : FILING DATE: 01-APR-1997
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Clark, Paul T.
 : REGISTRATION NUMBER: 30,175
 : REFERENCE/DOCKET NUMBER: 6612/667001
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 617-428-0200
 : TELEFAX: 617-428-7045
 : TELEX:
 : INFORMATION FOR SEQ ID NO: 15:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 8 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : MOLECULE TYPE: Peptide
 : US-08-831-310-14

Query Match 27.4% Score 3: DB 9: Length 8:

Best Local Similarity 100.0%: Pred. No. 5e-05:
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AKK 3

DB 3 AKK 5

RESULT 16

US-09-813-653-5
 : Sequence 5, Application US/0941653
 : Patent No. US20020064770A1
 : GENERAL INFORMATION:
 : APPLICANT: Nestor, John
 : APPLICANT: Wilson, Carol
 : APPLICANT: See, Raymond
 : APPLICANT: Ian Hehir, Christina
 : TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compounds
 : FILE REFERENCE: CNS-005
 : CURRENT APPLICATION NUMBER: US/09/813,653
 : CURRENT FILING DATE: 2001-03-20
 : PRIOR APPLICATION NUMBER: US 60/190,946
 : PRIOR FILING DATE: 2000-03-21

: PRIOR APPLICATION NUMBER: US 60/190,996
 : PRIOR FILING DATE: 2000-03-21
 : PRIOR APPLICATION NUMBER: US 60/191,299
 : PRIOR FILING DATE: 2000-03-21
 : NUMBER OF SEQ ID NOS: 44
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 5
 : LENGTH: 8
 : TYPE: PRT
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: Preferred peptide for pdz binding domain
 : US-09-813-653-5

Query Match 27.4% Score 3: DB 9: Length 8:
 Best Local Similarity 100.0%: Pred. No. 5e-05:
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 KKE 4

DB 3 KKE 5

RESULT 17

US-09-875-519A-34
 : Sequence 34, Application US/09875519A
 : Patent No. US20020068059A1
 : GENERAL INFORMATION:
 : APPLICANT: Parries, Timothy C.
 : TITLE OF INVENTION: Down-Regulation Resistant C3 Convertase
 : FILE REFERENCE: 4-30443/A/IMU/PC1
 : CURRENT APPLICATION NUMBER: US/09/875,519A
 : CURRENT FILING DATE: 2001-06-06
 : PRIOR APPLICATION NUMBER: PC1/GB97/00603
 : PRIOR FILING DATE: 1997-03-04
 : NUMBER OF SEQ ID NOS: 35
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 34
 : LENGTH: 8
 : TYPE: PRT
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: Description of Artificial Sequence: replacement
 : OTHER INFORMATION: sequence
 : US-09-875-519A-34

Query Match 27.4% Score 3: DB 9: Length 8:
 Best Local Similarity 100.0%: Pred. No. 5e-05:
 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 RQR 7

DB 4 RQR 6

RESULT 18

US-09-792-480-9
 : Sequence 9, Application US/09792480
 : Patent No. US20020127198A1
 : GENERAL INFORMATION:
 : APPLICANT: Rothbard, Jonathan B.
 : APPLICANT: Wender, Paul A.
 : APPLICANT: McGrane, P. Leo
 : APPLICANT: Sista, Lalitha V.S.
 : APPLICANT: Kirschberg, Thorsten A.
 : APPLICANT: CellGate, Inc.
 : TITLE OF INVENTION: Compositions and Methods for Enhancing Drug Delivery
 : FILE REFERENCE: 019801-0002300S
 : CURRENT APPLICATION NUMBER: US/09/792,480
 : CURRENT FILING DATE: 2001-02-23
 : PRIOR APPLICATION NUMBER: US 09/648,400

1 PRIOR FILING DATE: 2000-08-24
2 PRIOR APPLICATION NUMBER: US 60/150,510
3 PRIOR FILING DATE: 1999-08-24
4 NUMBER OF SEQ ID NOS: 57
5 SOFTWARE: PatentIn Ver. 2.1
6 SEQ ID NO 9
7 LENGTH: 8
8 TYPE: PRT
9 ORGANISM: Artificial Sequence
10 FEATURE:
11 OTHER INFORMATION: Description of Artificial Sequence: region 49-56
12 OTHER INFORMATION: truncated analog of HIV-1 tat protein basic region
13 OTHER INFORMATION: Tat-49-57
14 NAME/KEY: MOD_RES
15 LOCATION: (1)
16 OTHER INFORMATION: Xaa = fluorosulfon linked to amino group of
17 OTHER INFORMATION: aminohexanoic acid (H1 aux) attached to the
18 OTHER INFORMATION: N-terminal amino group of Arg
19 US-09-792-480-9

Query Match 27.4% Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RGR 7
111
10 5 RGR 7

RESULT 19
US-09-792-480-11
1 Sequence 11, Application US/09792480
2 Patent No. US20020127198A1
3 GENERAL INFORMATION:
4 APPLICANT: Rothbard, Jonathan B.
5 APPLICANT: Wendel, Paul A.
6 APPLICANT: McGrane, P. Leo
7 APPLICANT: Sista, Lalitha V.S.
8 APPLICANT: Kirschberg, Thorsten A.
9 APPLICANT: Celigate, Inc.
10 TITLE OF INVENTION: Compositions and Methods for Enhancing Gene Delivery
11 FILE REFERENCE: 019801-000230US
12 CURRENT APPLICATION NUMBER: US/09/792-480
13 CURRENT FILING DATE: 2001-02-23
14 PRIOR APPLICATION NUMBER: US 09/248,430
15 PRIOR FILING DATE: 2000-08-24
16 PRIOR APPLICATION NUMBER: US 60/150,510
17 PRIOR FILING DATE: 1999-08-24
18 NUMBER OF SEQ ID NOS: 57
19 SOFTWARE: PatentIn Ver. 2.1
20 SEQ ID NO 11
21 LENGTH: 8
22 TYPE: PRT
23 ORGANISM: Artificial Sequence
24 FEATURE:
25 OTHER INFORMATION: Description of Artificial Sequence: region 49-57
26 OTHER INFORMATION: truncated analog of HIV-1 tat protein basic region
27 OTHER INFORMATION: Tat-49-57
28 NAME/KEY: MOD_RES
29 LOCATION: (1)
30 OTHER INFORMATION: Xaa = fluorosulfon linked to amino group of
31 OTHER INFORMATION: aminohexanoic acid (H1 aux) attached to the
32 OTHER INFORMATION: N-terminal amino group of Lys
33 US-09-792-480-11

Query Match 27.4% Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RGR 7
111
10 4 RGR 6

RESULT 20
US-09-813-448-2
1 Sequence 2, Application US/09813448
2 Patent No. US20020142346A1
3 GENERAL INFORMATION:
4 APPLICANT: Nestor, John
5 APPLICANT: Wilson, Carol
6 TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compoun
7 FILE REFERENCE: CNS-006
8 CURRENT APPLICATION NUMBER: US/09/813,448
9 CURRENT FILING DATE: 2001-03-20
10 PRIOR APPLICATION NUMBER: US 60/190,946
11 PRIOR FILING DATE: 2000-03-21
12 PRIOR APPLICATION NUMBER: US 60/190,996
13 PRIOR FILING DATE: 2000-03-21
14 PRIOR APPLICATION NUMBER: US 60/191,299
15 PRIOR FILING DATE: 2000-03-21
16 NUMBER OF SEQ ID NOS: 8
17 SOFTWARE: PatentIn version 3.0
18 SEQ ID NO 2
19 LENGTH: 8
20 TYPE: PRT
21 ORGANISM: Artificial Sequence
22 FEATURE:
23 OTHER INFORMATION: preferred amino acids for PDZ binding domain
24 US-09-813-448-2

Query Match 27.4% Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
111
10 3 KKE 5

RESULT 21
US-09-943-123-19
1 Sequence 19, Application US/09943123
2 Publication No. US20020182701A1
3 GENERAL INFORMATION:
4 APPLICANT: CHANG, Y-H
5 APPLICANT: MICKA, W.S.
6 TITLE OF INVENTION: Dominant Negative Variants of Methionine Aminopeptidase
7 FILE REFERENCE: 16153-8007
8 CURRENT APPLICATION NUMBER: US/09/943,123
9 CURRENT FILING DATE: 2001-08-30
10 NUMBER OF SEQ ID NOS: 26
11 SOFTWARE: PatentIn Ver. 2.0
12 SEQ ID NO 19
13 LENGTH: 8
14 TYPE: PRT
15 ORGANISM: Artificial Sequence
16 FEATURE:
17 OTHER INFORMATION: Description of Artificial Sequence: synthetic
18 OTHER INFORMATION: transit peptide
19 US-09-943-123-19

Query Match 27.4% Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RGR 7
111
10 5 RGR 8

RESULT 22
US-09-729-476-9

Sequence 67, Application: US/9726470A
 Publication No. US20030036628A1
 GENERAL INFORMATION:
 APPLICANT: Zheleva, Daniela J
 APPLICANT: Fischer, Peter M
 APPLICANT: McInnes, Campbell
 APPLICANT: Andrews, Martin J1
 APPLICANT: Chan, Wong C
 APPLICANT: Atkinson, Gail E
 TITLE OF INVENTION: p21 Peptides
 FILE REFERENCE: CCI-014
 CURRENT APPLICATION NUMBER: US/9726470A
 CURRENT FILING DATE: 2000-11-29
 PRIOR APPLICATION NUMBER: GB 96283236
 PRIOR FILING DATE: 1999-11-30
 NUMBER OF SEQ ID NOS: 275
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 67
 LENGTH: 8
 TYPE: PPT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: pat derived
 FEATURE:
 OTHER INFORMATION: Synthesised with free amino terminus and as the
 OTHER INFORMATION: C-terminal carboxamide
 US-09-726-470A-67

Query Match 27.4%, Score 31, DB 11, Length 8;
 Best Local Similarity 100.0%, Pred. No. 5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 AKK 4
 II
 DB 2 AKK 4

RESULT 24
 US-09-765-655-17

Sequence 60, Application: US/976155
 Publication No. US20030037459A1
 GENERAL INFORMATION:
 APPLICANT: The Scripps Research Institute
 TITLE OF INVENTION: Methods and compositions to modulate
 TITLE OF INVENTION: expression in plants
 FILE REFERENCE: 2780-250014-46
 CURRENT APPLICATION NUMBER: US/976155
 CURRENT FILING DATE: 2002-05-24
 PRIOR APPLICATION NUMBER: US 09/620,499
 PRIOR FILING DATE: 2000-01-21
 PRIOR APPLICATION NUMBER: US 62/377,438
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 75
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO: 60
 LENGTH: 8
 TYPE: PPT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: ZFP domain
 US-09-765-655-60

Query Match 27.4%, Score 31, DB 11, Length 8;
 Best Local Similarity 100.0%, Pred. No. 5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 7 RKO 9
 II
 DB 2 RKO 4

RESULT 24

US-09-880-748-2779
 Sequence 2779, Application: US/9880748
 Publication No. US2003005997A1
 GENERAL INFORMATION:
 APPLICANT: Rubin et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PFS25
 CURRENT APPLICATION NUMBER: US/09/880,748
 CURRENT FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/212,210
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: 60/430,816
 PRIOR FILING DATE: 2000-10-17
 PRIOR APPLICATION NUMBER: 60/226,248
 PRIOR FILING DATE: 2000-03-16
 PRIOR APPLICATION NUMBER: 60/211,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/493,499
 PRIOR FILING DATE: 2001-05-25
 NUMBER OF SEQ ID NOS: 3239
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 2779
 LENGTH: 8
 TYPE: PPT
 ORGANISM: Homo sapiens
 US-09-880-748-2779

Query Match 27.4%, Score 31, DB 11, Length 8;
 Best Local Similarity 100.0%, Pred. No. 5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 6 RKO 8
 II
 DB 2 RKO 4

RESULT 25

US-09-876-904A-317
 Sequence 317, Application: US/0876904A
 Publication No. US2003022794A1
 GENERAL INFORMATION:
 APPLICANT: KODOLIKAS, TONY
 TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES IM) AND THERAPEUTIC
 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/LIPOGENIC PEPTIDE
 TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOsome COMPLEXES
 FILE REFERENCE: TB 2002-09
 CURRENT APPLICATION NUMBER: US/09/876,904A
 CURRENT FILING DATE: 2001-06-08
 PRIOR APPLICATION NUMBER: US 60/210,925
 PRIOR FILING DATE: 2000-06-09
 NUMBER OF SEQ ID NOS: 629
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 317
 LENGTH: 6
 TYPE: PPT
 ORGANISM: Saccharomyces cerevisiae
 FEATURE:
 OTHER INFORMATION: Recombination repair protein
 US-09-876-904A-317

Query Match 27.4%, Score 31, DB 11, Length 8;
 Best Local Similarity 100.0%, Pred. No. 5e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 7 RKO 9
 II
 DB 6 RKO 8

RESULT 24

US-09-876-904A-352
 Sequence 352, Application: US/0876904A
 Publication No. US2003022794A1

GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 352
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Human ATF-1, its basic region/leucine zipper.
US-09-876-904A-352

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
DB 6 KKE 8

RESULT 27
US-09-876-904A-393
Sequence 393, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 393
LENGTH: 8
TYPE: PRT
ORGANISM: Drosophila sp.
FEATURE:
OTHER INFORMATION: Drosophila BDF-2 (related to DREF/ATF)
US-09-876-904A-393

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
DB 6 KKE 8

RESULT 28
US-09-876-904A-394
Sequence 394, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A

CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 394
LENGTH: 8
TYPE: PRT
ORGANISM: Xenopus sp.
FEATURE:
OTHER INFORMATION: Xenopus KAR (retinoic acid receptor)
US-09-876-904A-394

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KKE 4
DB 6 KKE 8

RESULT 29
US-09-876-904A-493
Sequence 493, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 493
LENGTH: 8
TYPE: PRT
ORGANISM: Rattus sp.
FEATURE:
OTHER INFORMATION: Rat ORP a protein factor that binds to the D site
US-09-876-904A-493

Query Match 27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KKE 5
DB 4 KKE 6

RESULT 30
US-09-876-904A-502
Sequence 502, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: TB-2002.00
CURRENT APPLICATION NUMBER: US/09/876,904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/210,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 502

```
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Mus sp.
: FEATURE:
: OTHER INFORMATION: Mouse ACP/EBP.
US-09-876-904A-502

Query Match      27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
   III
Db 5 AKK 7

RESULT 41
US-09-876-904A-505
: Sequence 505, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 505
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Rattus sp.
: FEATURE:
: OTHER INFORMATION: Rat LAP, a 32-KD liver-enriched transcriptional
: OTHER INFORMATION: activator, also present in lung, with 71% sequence
: OTHER INFORMATION: similarity to C/EBP.
US-09-876-904A-505

Query Match      27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
   III
Db 5 AKK 7

RESULT 42
US-09-876-904A-515
: Sequence 515, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 515
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Rattus sp.
: FEATURE:
: OTHER INFORMATION: Rat IL-60BP interacting with interleukin-6
: OTHER INFORMATION:
US-09-876-904A-515

Query Match      27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
   III
Db 5 AKK 7

RESULT 43
US-09-876-904A-516
: Sequence 516, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 516
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Mus sp.
: FEATURE:
: OTHER INFORMATION: Mouse H 2RBP.
US-09-876-904A-516

Query Match      27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RQR 7
   III
Db 3 RQR 5

RESULT 34
US-09-876-904A-517
: Sequence 517, Application US/09876904A
: Publication No. US20030072794A1
: GENERAL INFORMATION:
: APPLICANT: BOULIKAS, TENI
: TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
: TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
: TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
: FILE REFERENCE: TB-2002.00
: CURRENT APPLICATION NUMBER: US/09/876,904A
: CURRENT FILING DATE: 2001-06-08
: PRIOR FILING DATE: 2000-06-09
: NUMBER OF SEQ ID NOS: 629
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 517
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Gallus sp.
: FEATURE:
: OTHER INFORMATION: Chicken RXR.
US-09-876-904A-517

Query Match      27.3% Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 5 QQR 7
III
DB 3 QQR 5

RESULT 35

US-09-876-904A-518
; Sequence 518, Application US/09876904A
; Publication No. US20030072794A1

GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 518

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Human NF-116 (345 aa)

US-09-876-904A-518

Query Match 27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
III
DB 5 AKK 7

RESULT 36

US-09-876-904A-537
; Sequence 537, Application US/09876904A
; Publication No. US20030072794A1

GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 537

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Xenopus laevis

; FEATURE:

; OTHER INFORMATION: Xenopus laevis 11 ribosomal protein (homologous to

; OTHER INFORMATION: yeast I2).

US-09-876-904A-537

Query Match 27.3%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
III
DB 5 AKK 7

RESULT 37

US-09-876-904A-599

; Sequence 599, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 599

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Parachinus angulosus

; FEATURE:

; OTHER INFORMATION: Sea urchin Parachinus angulosus sperm H1 (248 aa).

US-09-876-904A-599

Query Match 27.3%; Score 3; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3

III

DB 3 AKK 5

US-09-876-904A-599

; Sequence 599, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 595

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Parachinus angulosus

; FEATURE:

; OTHER INFORMATION: Sea urchin Parachinus angulosus sperm H1 (248 aa).

US-09-876-904A-595

Query Match 27.3%; Score 3; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3

III

DB 3 AKK 5

US-09-876-904A-599

; Sequence 599, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 549

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae

; FEATURE:

; OTHER INFORMATION: Yeast S10 ribosomal protein (homologous to human

; OTHER INFORMATION: S6).

US-09-876-904A-549

Query Match 27.4%; Score 3; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 QQR 8

III

DB 4 QQR 6

US-09-876-904A-549

; Sequence 549, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 549

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Parachinus angulosus

; FEATURE:

; OTHER INFORMATION: Sea urchin Parachinus angulosus sperm H1 (248 aa).

US-09-876-904A-595

Query Match 27.3%; Score 3; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3

III

DB 3 AKK 5

US-09-876-904A-599

; Sequence 599, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 595

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Parachinus angulosus

; FEATURE:

; OTHER INFORMATION: Sea urchin Parachinus angulosus sperm H1 (248 aa).

US-09-876-904A-595

Query Match 27.3%; Score 3; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3

III

DB 3 AKK 5

US-09-876-904A-599

; Sequence 599, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 595

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Parachinus angulosus

; FEATURE:

; OTHER INFORMATION: Sea urchin Parachinus angulosus sperm H1 (248 aa).

US-09-876-904A-595

Query Match 27.3%; Score 3; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3

III

DB 5 AKK 7

US-09-876-904A-537

; Sequence 537, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 537

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Xenopus laevis

; FEATURE:

; OTHER INFORMATION: Xenopus laevis 11 ribosomal protein (homologous to

; OTHER INFORMATION: yeast I2).

US-09-876-904A-537

Query Match 27.3%; Score 3; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3

III

DB 5 AKK 7

US-09-876-904A-537

; Sequence 537, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:

; APPLICANT: BOULIKAS, TENI

; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC

; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE

; TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES

; FILE REFERENCE: TB-2002.00

; CURRENT APPLICATION NUMBER: US/09/876,904A

; PRIOR FILING DATE: 2001-06-08

; PRIOR APPLICATION NUMBER: US 60/210,925

; NUMBER OF SEQ ID NOS: 629

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 537

; LENGTH: 8

; TYPE: PRT

; ORGANISM: Xenopus laevis

; FEATURE:

; OTHER INFORMATION: Xenopus laevis 11 ribosomal protein (homologous to

; OTHER INFORMATION: yeast I2).

US-09-876-904A-537

Query Match 27.3%; Score 3; DB 11; Length 8;

Best Local Similarity 100.0%; Pred. No. 5e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3

III

DB 5 AKK 7

US-09-876-904A-537

; Sequence 537, Application US/09876904A

; Publication No. US20030072794A1

; GENERAL INFORMATION:


```

1 TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
2 TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPID-SOME COMPLEXES
3 FILE REFERENCE: TB-2002.00
4 CURRENT APPLICATION NUMBER: US/09/876,904A
5 PRIOR FILING DATE: 2001-05-08
6 PRIOR APPLICATION NUMBER: US 66/210,925
7 NUMBER OF SEQ ID NOS: 629
8 SOFTWARE: Patented Ver. 2.1
9 SEQ ID NO 599
10 LENGTH: 8
11 TYPE: PPT
12 ORGANISM: Parachinus angulosus
13 FEATURE:
14 OTHER INFORMATION: Sea urchin Parachinus ananulosus spm HI (248 aa)
15 US-09-876-904A-599

Query Match 27.3% Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 5 AKK 7

RESULT 40
US-10-039-183A-13
1 Sequence 13, Application US/10039183A
2 Publication NO. US2003013242A1
3 GENERAL INFORMATION:
4 APPLICANT: Kleanthous, Harold
5 APPLICANT: Iassolo, Ling
6 APPLICANT: Tomb, Jean-Francois
7 APPLICANT: Miller, Charles
8 APPLICANT: Al-Gardwi, Amal
9 TITLE OF INVENTION: Helicobacter GHPs 100 and GHPs 750
10 TITLE OF INVENTION: Polypeptides and corresponding polypeptide molecules
11 FILE REFERENCE: 061327037002
12 CURRENT APPLICATION NUMBER: US/10/039,183A
13 CURRENT FILING DATE: 2002-12-13
14 PRIOR APPLICATION NUMBER: US-08/941,410
15 PRIOR FILING DATE: 1997-04-01
16 NUMBER OF SEQ ID NOS: 18
17 SOFTWARE: FastSeq for Windows Version 2.0
18 SEQ ID NO 13
19 LENGTH: 8
20 TYPE: PPT
21 ORGANISM: Helicobacter pylori
22 US-10-039-183A-13

Query Match 27.3% Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 4
DB 4 AKK 5

RESULT 41
US-10-048-504-78
1 Sequence 79, Application US/1048504
2 Publication NO. US20030138914A1
3 GENERAL INFORMATION:
4 APPLICANT: Himmelspach, Michael
5 APPLICANT: Pfeleiderer, Michael
6 APPLICANT: Falkner, Falko-Guenther
7 APPLICANT: Eibl, Johann
8 APPLICANT: Dörner, Friedrich
9 APPLICANT: Schlokat, Uwe
10 TITLE OF INVENTION: Factor X Deficient Mutants
11 and Analogues Thereof

```

```

1 NUMBER OF SEQUENCES: 145
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: Townsend and Townsend and Crew LLP
4 STREET: Two Embarcadero Center, Eighth Floor
5 CITY: San Francisco
6 STATE: CA
7 COUNTRY: USA
8 ZIP: 94111-8834
9 COMPUTER READABLE FORM:
10 MEDIUM TYPE: Diskette
11 COMPUTER: IBM Compatible
12 OPERATING SYSTEM: Dos
13 SOFTWARE: FastSeq for Windows Version 2.0
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/10/348,504
16 FILING DATE: 29-Jan-2003
17 CLASSIFICATION: <Unknown>
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US/09/367,777
20 FILING DATE: 10-No. US/0030138914A1-1999
21 APPLICATION NUMBER: AT A 336/97
22 FILING DATE: 27-FEB-1997
23 APPLICATION NUMBER: WO PCT/AT98/00046
24 FILING DATE: 27-FEB-1998
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Auschelus, Scott L.
27 REGISTRATION NUMBER: 42,271
28 REFERENCE/DOCKET NUMBER: 20695D-0009000US
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 415-576-0200
31 TELEFAX: 415-576-0400
32 TELEX: <Unknown>
33 INFORMATION FOR SEQ ID NO: 78:
34 LENGTH: 8 amino acids
35 TYPE: amino acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38 MOLECULE TYPE: peptide
39 SEQUENCE DESCRIPTION: SEQ ID NO: 78:
40 US-10-348-504-78

Query Match 27.3% Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 KER 5
DB 2 KER 4

RESULT 42
US-10-014-322A-62
1 Sequence 62, Application US/10014322A
2 Publication NO. US20030167129A1
3 GENERAL INFORMATION:
4 APPLICANT: Nestor, Jr., John
5 APPLICANT: Wilson, Carol
6 APPLICANT: Ian Hehir, Christina
7 APPLICANT: Kates, Steven
8 APPLICANT: Krstenansky, John
9 TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compou
10 FILE REFERENCE: CNS-008
11 CURRENT APPLICATION NUMBER: US/10/014,322A
12 CURRENT FILING DATE: 2002-07-08
13 PRIOR APPLICATION NUMBER: US 60/243,587
14 PRIOR FILING DATE: 2000-10-27
15 PRIOR APPLICATION NUMBER: US 09/813,651
16 PRIOR FILING DATE: 2001-03-20
17 PRIOR APPLICATION NUMBER: US 09/813,653
18 PRIOR FILING DATE: 2001-03-20
19 PRIOR APPLICATION NUMBER: US 09/813,448
20 PRIOR FILING DATE: 2001-03-20

```

```
1 NUMBER OF SEQ ID NOS: 126
2 SOFTWARE: PatentIn version 3.0
3 SEQ ID NO 62
4 LENGTH: 8
5 TYPE: PRI
6 ORGANISM: Artificial sequence
7 FEATURE:
8 OTHER INFORMATION: Preferred pep'ide for HIV binding domain
US-10-014-322A-62

Query Match      27.3%  Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KKE 4
DB      1
        3 KKE 5

RESULT 43
US 10-293-580-4;
1 Sequence 41, Application US/10293580
2 Publication No. US20030170767A1
3 GENERAL INFORMATION:
4 APPLICANT: Aurora Biosciences Corporation
5 APPLICANT: Cubitt, Andrew B.
6 TITLE OF INVENTION: Fluorescent protein sensors of post-translational modifications
7 FILE REFERENCE: AURO1270 (08306/031301)
8 CURRENT APPLICATION NUMBER: US/10/293,580
9 PRIOR FILING DATE: 2002-11-12
10 PRIOR APPLICATION NUMBER: US/09/129,112
11 PRIOR FILING DATE: 1998-07-24
12 NUMBER OF SEQ ID NOS: 74
13 SOFTWARE: PatentIn version 3.0
14 SEQ ID NO 41
15 LENGTH: 8
16 TYPE: PRI
17 ORGANISM: Artificial sequence
18 FEATURE:
19 OTHER INFORMATION: Adenovirus endopapillase
US-10-293-580-41

Query Match      27.3%  Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKK 3
DB      1
        5 AKK 7

RESULT 44
US 10-024-945-19
1 Sequence 19, Application US/10024445
2 Publication No. US20020142965A2
3 GENERAL INFORMATION:
4 APPLICANT: Kenneth Walter Bail
5 APPLICANT: Ningnan Pan Chen
6 APPLICANT: Timothy Michael Ramsey
7 APPLICANT: Michael Lloyd Sabio
8 APPLICANT: Sushill Kumar Sharma
9 TITLE OF INVENTION: Inhibitors of 12-O-tetradecanoylphorbol-13-acetate
10 FILE REFERENCE: 4-31664PI/Prov
11 CURRENT APPLICATION NUMBER: US/10/024,945
12 CURRENT FILING DATE: 2001-12-19
13 NUMBER OF SEQ ID NOS: 19
14 SOFTWARE: FastSeq for Windows version 4.0
15 SEQ ID NO 19
16 LENGTH: 8
17 TYPE: PRI
18 ORGANISM: Artificial sequence
19 FEATURE:
```

```
1 OTHER INFORMATION: Synthetic protein
US-10-024-945-19

Query Match      27.3%  Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AKK 4
DB      1
        2 AKK 4

RESULT 45
US-10-040-572-8
1 Sequence 8, Application US/10040572
2 Publication No. US20020155183A1
3 GENERAL INFORMATION:
4 APPLICANT: Sky High, LLC
5 APPLICANT: Bathurst, Ian G.
6 APPLICANT: Foster, Matthew
7 TITLE OF INVENTION: AQUEOUS ANTI-APOPTOTIC COMPOSITIONS
8 FILE REFERENCE: 4147-23-1
9 CURRENT APPLICATION NUMBER: US/10/040,572
10 CURRENT FILING DATE: 2002-03-12
11 NUMBER OF SEQ ID NOS: 13
12 SOFTWARE: PatentIn version 3.1
13 SEQ ID NO 8
14 LENGTH: 8
15 TYPE: PRI
16 ORGANISM: Glycine max
17 OTHER INFORMATION:
US-10-040-572-8

Query Match      27.3%  Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 KKE 4
DB      1
        4 KKE 5

RESULT 46
US-10-057-505-7
1 Sequence 7, Application US/10057505
2 Publication No. US20020164674A1
3 GENERAL INFORMATION:
4 APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
5 APPLICANT: AUREA BIOSCIENCES CORPORATION
6 APPLICANT: ISEN, Roger
7 APPLICANT: HEZM, Roger
8 APPLICANT: CURTIS, Andrew
9 TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
10 FILE REFERENCE: PEGEN1260-3
11 CURRENT APPLICATION NUMBER: US/10/057,505
12 CURRENT FILING DATE: 2002-01-25
13 PRIOR APPLICATION NUMBER: US 08/792,553
14 PRIOR FILING DATE: 1997-01-31
15 PRIOR APPLICATION NUMBER: US 09/196,003
16 PRIOR FILING DATE: 1999-09-13
17 NUMBER OF SEQ ID NOS: 31
18 SOFTWARE: PatentIn version 3.1
19 SEQ ID NO 7
20 LENGTH: 8
21 TYPE: PRI
22 ORGANISM: Artificial sequence
23 FEATURE:
24 OTHER INFORMATION: Linker moiety
US-10-057-505-7

Query Match      27.3%  Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 1 AKK 3
DB 5 AKK 7

RESULT 47

US-10-060-100-9
Sequence 49, Application US/10060100
Publication No. US20020165356A1
GENERAL INFORMATION:
APPLICANT: Paribas, Carlos
TITLE OF INVENTION: Zinc Finger Binding Domains
FILE REFERENCE: TSRI 760.0
CURRENT APPLICATION NUMBER: US/10/060-100
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US/09/791-106
NUMBER OF SEQ ID NOS: 113
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthesized
US-10-060-100-5

Query Match 27.3%; Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KER 5
DB 3 KER 5

RESULT 48

US-10-061-395-65
Sequence 49, Application US/10061395
Publication No. US20020165356A1
GENERAL INFORMATION:
APPLICANT: Paribas, Carlos
TITLE OF INVENTION: Zinc Finger Binding Domains
FILE REFERENCE: TSRI 760.0
CURRENT APPLICATION NUMBER: US/10/061-395
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: US/09/791-106
NUMBER OF SEQ ID NOS: 113
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthesized
US-10-061-395-65

Query Match 27.3%; Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 RKD 9
DB 2 RKD 4

RESULT 49

US-10-014-485A-48

Sequence 48, Application US/1001485A
Publication No. US20020166844A1
GENERAL INFORMATION:
APPLICANT: Cell Signaling Technology, Inc.
APPLICANT: ZHANG, Hui
APPLICANT: ZHANG, Yi
TITLE OF INVENTION: PRODUCTION OF MOTIF-SPECIFIC AND CONTEXT-INDEPENDENT ANTIBODIES
FILE REFERENCE: CSH-132 CIPZ
CURRENT APPLICATION NUMBER: US/10/014-485A
PRIOR FILING DATE: 2002-03-16
PRIOR APPLICATION NUMBER: US 09/148,712
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: US 09/545,364
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 145
SOFTWARE: Patent In version 4.1
SEQ ID NO 48
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (6)...(6)
OTHER INFORMATION: PHOSPHORYLATION: serine at position 6 is phosphorylated
US-10-014-485A-48

Query Match 27.3%; Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RQR 7
DB 1 RQR 3

RESULT 50

US-10-061-395-65
Sequence 65, Application US/10061395
Publication No. US20020166758A1
GENERAL INFORMATION:
APPLICANT: Zardner, Maurice
APPLICANT: Smith, Ernest S.
TITLE OF INVENTION: Methods of Identifying Regulator Molecules
FILE REFERENCE: 1821.008003
CURRENT APPLICATION NUMBER: US/10/061-395
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/271,423
PRIOR FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: 65/265,480
PRIOR FILING DATE: 2001-02-05
PRIOR APPLICATION NUMBER: 65/265,589
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patent In version 4.1
SEQ ID NO 65
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Myristoylation signal sequence from cAMP-dependent kinase
US-10-061-395-65

Query Match 27.3%; Score 3; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKK 3
DB 5 AKK 8

Search completed: September 30, 2003, 10:32:51
Job time : 25.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw mode.

Run on: September 30, 2003, 10:07:04 : Search time: 41.0844 Seconds
(without alignment)
42.499 Million cell updates/sec

Title: US-09-787-443-2

Perfect score: 11

Sequence: AKKERQRKDTQ 11

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 1107863 seqs, 15672613 residues

Word size: 0

Total number of hits satisfying chosen parameters: 274822

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database: A_Geneseq_19Jun03:

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Proj. No. is the number of results produced by change to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
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2	11	100.0	11	21	AA188561			NCAM Igl binding p
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129	5	45.5	10	24	ABP45675	HLA protein 121P2A	202	4	36.4	8	22	ABP16592	HIV A24 super moti
130	5	45.5	10	24	ABP45675	HLA protein 121P2A	203	4	36.4	8	22	ABP17494	HIV B27 super moti
131	5	45.5	10	24	ABP45675	HLA protein 121P2A	204	4	36.4	8	22	ABP19685	HIV B62 super moti
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137	5	45.5	10	24	ABP45675	HLA protein 121P2A	210	4	36.4	9	22	ARP16400	HIV A24 super moti
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140	5	45.5	10	24	ABP45675	HLA protein 121P2A	213	4	36.4	9	22	ABP19687	HIV B62 super moti
141	5	45.5	10	24	ABP45675	HLA protein 121P2A	214	4	36.4	9	22	ABK22276	HIV A03 motif vpu
142	5	45.5	10	24	ABP45675	HLA protein 121P2A	215	4	36.4	9	22	ABK24033	HIV A11 motif vpu
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144	5	45.5	10	24	ABP45675	HLA protein 121P2A	217	4	36.4	9	24	ABK20464	Human cancer-relat
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231	4	36.4	9	24	ABP84348	H-A protein 121P2A	304	4	36.4	11	22	ABP17507	HIV B27 super moti
232	4	36.4	9	24	ABP84349	H-A protein 121P2A	305	4	36.4	11	22	ABP19679	HIV B62 super moti
233	4	36.4	9	24	ABP84350	H-A protein 121P2A	306	4	36.4	11	22	ABP24378	HIV A24 motif vpu
234	4	36.4	9	24	ABP84351	H-A protein 121P2A	307	4	36.4	11	23	ABG69345	Human neural cell
235	4	36.4	9	24	ABP84352	H-A protein 121P2A	308	4	36.4	11	23	AAO18039	Human immunoglobul
236	4	36.4	9	24	ABP84353	H-A protein 121P2A	309	4	36.4	12	24	AAO18039	Sequence of peptid
237	4	36.4	9	24	ABP84354	H-A protein 121P2A	310	4	36.4	12	24	AAO18039	Multi-drug resista
238	4	36.4	9	24	ABP84355	H-A protein 121P2A	311	4	36.4	12	17	AAW96957	Peptide clone Laci
239	4	36.4	9	24	ABP84356	H-A protein 121P2A	312	4	36.4	12	18	AAW25309	Multi-drug resista
240	4	36.4	9	24	ABP84357	H-A protein 121P2A	313	4	36.4	12	21	AAH03584	Multidrug resistan
241	4	36.4	9	24	ABP84358	H-A protein 121P2A	314	4	36.4	12	21	AAH03584	Immunogenic peptid
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243	4	36.4	9	24	ABP84360	H-A protein 121P2A	316	4	36.4	12	23	ABO42999	DNA repair protein
244	4	36.4	9	24	ABP84361	H-A protein 121P2A	317	4	36.4	13	14	AAH30447	Synthetic sequence
245	4	36.4	9	24	ABP84362	H-A protein 121P2A	318	4	36.4	13	18	AAW04620	Thymopoietin II 29
246	4	36.4	9	24	ABP84363	H-A protein 121P2A	319	4	36.4	13	20	AAW31028	Non-crosslinked pr
247	4	36.4	9	24	ABP84364	H-A protein 121P2A	320	4	36.4	13	21	AAH79338	Equine infectious
248	4	36.4	9	24	ABP84365	H-A protein 121P2A	321	4	36.4	13	21	AAH79338	RNA binding peptid
249	4	36.4	9	24	ABP84366	H-A protein 121P2A	322	4	36.4	13	22	AAU06104	RNA binding peptid
250	4	36.4	9	24	ABP84367	H-A protein 121P2A	323	4	36.4	13	22	AAH91755	Thymic peptide SEQ
251	4	36.4	9	24	ABP84368	H-A protein 121P2A	324	4	36.4	13	23	AAE27460	Human keratinocyte
252	4	36.4	9	24	ABP84369	H-A protein 121P2A	325	4	36.4	13	23	ABG79737	Human keratinocyte
253	4	36.4	9	24	ABP84370	H-A protein 121P2A	326	4	36.4	13	23	ABG79737	Human keratinocyte
254	4	36.4	9	24	ABP84371	H-A protein 121P2A	327	4	36.4	13	23	ABG79737	Human keratinocyte
255	4	36.4	9	24	ABP84372	H-A protein 121P2A	328	4	36.4	13	23	AAO18034	Human immunoglobul
256	4	36.4	9	24	ABP84373	H-A protein 121P2A	329	4	36.4	13	24	ABJ00535	Human IgE cyclic i
257	4	36.4	9	24	ABP84374	H-A protein 121P2A	330	4	36.4	14	12	AAH15705	Bioactive syntheti
258	4	36.4	10	22	ABP14254	HIV A02 super moti	331	4	36.4	14	14	AAH30462	Synthetic sequence
259	4	36.4	10	22	ABP14255	HIV A03 super moti	332	4	36.4	14	14	AAH30441	Synthetic sequence
260	4	36.4	10	22	ABP16609	HIV A24 super moti	333	4	36.4	14	14	AAH31169	Synthetic sequence
261	4	36.4	10	22	ABP17504	HIV B27 super moti	334	4	36.4	14	14	AAH31169	Human glycoalbumin
262	4	36.4	10	22	ABP17505	HIV B27 super moti	335	4	36.4	14	19	AAW68346	MHC binding peptid
263	4	36.4	10	22	ABP17506	HIV B27 super moti	336	4	36.4	14	19	AAW68346	Human immunodefici
264	4	36.4	10	22	ABP22277	HIV A03 motif vpu	337	4	36.4	14	21	AAH58223	Altered MHC determ
265	4	36.4	10	22	ABP22278	HIV A11 motif vpu	338	4	36.4	14	21	AAH58223	Altered MHC determ
266	4	36.4	10	22	ABP22279	Saccharomycete cere	339	4	36.4	14	22	ABH56784	Human SNP related
267	4	36.4	10	23	ABH11534	Immunogenic HIV pe	340	4	36.4	14	22	ABH56784	Human peptide #150
268	4	36.4	10	24	ABH69842	Human immunodefici	341	4	36.4	14	22	AAH56875	Human peptide #151
269	4	36.4	10	24	ABH69843	Human immunodefici	342	4	36.4	14	22	AAH56875	Human peptide #151
270	4	36.4	10	24	ABH70008	Human immunodefici	343	4	36.4	14	22	AAH56875	Human peptide #151
271	4	36.4	10	24	ABH70009	Human immunodefici	344	4	36.4	14	22	AAH56875	Human peptide #151
272	4	36.4	10	24	ABH70010	Human immunodefici	345	4	36.4	14	22	AAH56875	Human peptide #151
273	4	36.4	10	24	ABH70011	Human immunodefici	346	4	36.4	14	22	AAH56875	Human peptide #151
274	4	36.4	10	24	ABH70012	Human immunodefici	347	4	36.4	14	22	AAH56875	Human peptide #151
275	4	36.4	10	24	ABH70013	Human immunodefici	348	4	36.4	14	22	AAH56875	Human peptide #151
276	4	36.4	10	24	ABH70014	Human immunodefici	349	4	36.4	14	22	AAH56875	Human peptide #151
277	4	36.4	10	24	ABH70015	Human immunodefici	350	4	36.4	14	22	AAH56875	Human peptide #151
278	4	36.4	10	24	ABH70016	Human immunodefici	351	4	36.4	14	22	AAH56875	Human peptide #151
279	4	36.4	10	24	ABH70017	Human immunodefici	352	4	36.4	14	22	AAH56875	Human peptide #151
280	4	36.4	10	24	ABH70018	Human immunodefici	353	4	36.4	14	22	AAH56875	Human peptide #151
281	4	36.4	10	24	ABH70019	Human immunodefici	354	4	36.4	14	22	AAH56875	Human peptide #151
282	4	36.4	10	24	ABH70020	Human immunodefici	355	4	36.4	14	22	AAH56875	Human peptide #151
283	4	36.4	10	24	ABH70021	Human immunodefici	356	4	36.4	14	22	AAH56875	Human peptide #151
284	4	36.4	10	24	ABH70022	Human immunodefici	357	4	36.4	14	22	AAH56875	Human peptide #151
285	4	36.4	10	24	ABH70023	Human immunodefici	358	4	36.4	14	22	AAH56875	Human peptide #151
286	4	36.4	10	24	ABH70024	Human immunodefici	359	4	36.4	14	22	AAH56875	Human peptide #151
287	4	36.4	10	24	ABH70025	Human immunodefici	360	4	36.4	14	22	AAH56875	Human peptide #151
288	4	36.4	10	24	ABH70026	Human immunodefici	361	4	36.4	14	22	AAH56875	Human peptide #151
289	4	36.4	10	24	ABH70027	Human immunodefici	362	4	36.4	14	22	AAH56875	Human peptide #151
290	4	36.4	10	24	ABH70028	Human immunodefici	363	4	36.4	14	22	AAH56875	Human peptide #151
291	4	36.4	10	24	ABH70029	Human immunodefici	364	4	36.4	14	22	AAH56875	Human peptide #151
292	4	36.4	10	24	ABH70030	Human immunodefici	365	4	36.4	14	22	AAH56875	Human peptide #151
293	4	36.4	11	17	AAH96841	Human immunodefici	366	4	36.4	14	22	AAH96841	Human immunodefici
294	4	36.4	11	18	AAH11749	Human immunodefici	367	4	36.4	14	22	AAH11749	Human immunodefici
295	4	36.4	11	18	AAH11750	Human immunodefici	368	4	36.4	14	22	AAH11750	Human immunodefici
296	4	36.4	11	18	AAH11751	Human immunodefici	369	4	36.4	14	22	AAH11751	Human immunodefici
297	4	36.4	11	20	AAH09654	Human immunodefici	370	4	36.4	14	22	AAH09654	Human immunodefici
298	4	36.4	11	20	AAH09655	Human immunodefici	371	4	36.4	14	22	AAH09655	Human immunodefici
299	4	36.4	11	20	AAH09656	Human immunodefici	372	4	36.4	14	22	AAH09656	Human immunodefici
300	4	36.4	11	22	ABH14259	HIV A32 super moti	373	4	36.4	14	22	ABH14259	HIV A32 super moti
301	4	36.4	11	22	ABH14260	HIV A32 super moti	374	4	36.4	14	22	ABH14260	HIV A32 super moti

475	4	36.4	15	24	ABR36319	Human cancer relat	448	3	27.3	8	21	AA808328	Epitope derived fr
476	4	36.4	15	24	ABR36319	Human cancer relat	449	3	27.3	8	21	AA93161	Peptide motif #2 a
477	4	36.4	15	24	ABR36340	Human cancer relat	450	3	27.3	8	21	AA959137	Human PAK65 kinase
478	4	36.4	15	24	ABR36444	Human cancer relat	451	3	27.3	8	21	AA966392	HLA-B8-binding HIV
479	4	36.4	15	24	ABR36445	Human cancer relat	452	3	27.3	8	21	AA963610	Desmoglein cell ad
480	4	36.4	15	24	ABR36670	Human cancer relat	453	3	27.3	8	21	AA963612	Desmoglein cell ad
481	4	36.4	15	24	ABR36671	Human cancer relat	454	3	27.3	8	21	AA963649	Desmoglein cell ad
482	4	36.4	15	24	ABR37211	Human cancer relat	455	3	27.3	8	21	AA963651	Desmoglein cell ad
483	4	36.4	15	24	ABR37237	Human cancer relat	456	3	27.3	8	21	AA963694	Desmoglein cell ad
484	4	36.4	15	24	ABR37340	Human cancer relat	457	3	27.3	8	21	AA963696	Desmoglein cell ad
485	4	36.4	15	24	ABR37432	Human cancer relat	458	3	27.3	8	21	AA963739	Desmoglein cell ad
486	4	36.4	15	24	ABR37433	Human cancer relat	459	3	27.3	8	21	AA963741	Desmoglein cell ad
487	4	36.4	15	24	ABR37647	Human cancer relat	460	3	27.3	8	21	AA963784	Desmoglein cell ad
488	4	36.4	15	24	ABR37648	Human cancer relat	461	3	27.3	8	21	AA963786	Desmoglein cell ad
489	4	36.4	15	24	ABR94146	HLA protein 121P2A	462	3	27.3	8	21	AA963829	Desmoglein cell ad
490	4	36.4	15	24	ABR94141	HLA protein 121P2A	463	3	27.3	8	21	AA963831	Desmoglein cell ad
491	4	36.4	15	24	ABR94543	HLA protein 121P2A	464	3	27.3	8	21	AA963871	Desmoglein cell ad
492	4	36.4	15	24	ABR94551	HLA protein 121P2A	465	3	27.3	8	21	AA963873	Desmoglein cell ad
493	4	36.4	15	24	ABR95144	HLA protein 121P2A	466	3	27.3	8	21	AA963885	Desmoglein cell ad
494	4	36.4	15	24	ABR95146	HLA protein 121P2A	467	3	27.3	8	21	AA963887	Desmoglein cell a
495	4	36.4	15	24	ABR95577	HLA protein 121P2A	468	3	27.3	8	21	AA963920	Desmocollin cell a
496	3	27.3	8	11	AA802190	Peptide which bind	469	3	27.3	8	21	AA963922	Desmocollin cell a
497	3	27.3	8	11	AA805924	Low toxicity immun	470	3	27.3	8	21	AA963962	Desmocollin cell a
498	3	27.3	8	11	AA805925	Low toxicity immun	471	3	27.3	8	21	AA963964	Desmocollin cell a
499	3	27.3	8	13	AA829309	Nerve growth stimu	472	3	27.3	8	21	AA964004	Desmocollin cell a
500	3	27.3	8	14	AA84895	YK tryptic peptide	473	3	27.3	8	21	AA964006	Desmocollin cell a
501	3	27.3	8	14	AA843534	Sm b/b' epitope 83	474	3	27.3	8	21	AA964046	Desmocollin cell a
502	3	27.3	8	15	AA852631	Sm b/b' epitope 88	475	3	27.3	8	21	AA964088	Desmocollin cell a
503	3	27.3	8	15	AA852631	Newcastle Disease	476	3	27.3	8	21	AA964090	Desmocollin cell a
504	3	27.3	8	15	AA848277	cAMP-dependent kin	477	3	27.3	8	21	AA964133	Desmocollin cell a
505	3	27.3	8	15	AA860431	Antiproliferative	478	3	27.3	8	21	AA964135	Desmocollin cell a
506	3	27.3	8	16	AAW21399	Plasminogen activa	479	3	27.3	8	21	AA964135	Desmocollin cell a
507	3	27.3	8	16	AA873509	Human TSH receptor	480	3	27.3	8	21	AA964135	Desmocollin cell a
508	3	27.3	8	16	AA873507	Human TSH receptor	481	3	27.3	8	22	ABP11642	HIV A01 super moti
509	3	27.3	8	16	AA873508	Human TSH receptor	482	3	27.3	8	22	ABP11748	HIV A01 super moti
510	3	27.3	8	16	AA873553	Human TSH receptor	483	3	27.3	8	22	ABP12549	HIV A02 super moti
511	3	27.3	8	16	AA873556	Human TSH receptor	484	3	27.3	8	22	ABP12550	HIV A02 super moti
512	3	27.3	8	16	AA873556	Human TSH receptor	485	3	27.3	8	22	ABP12582	HIV A02 super moti
513	3	27.3	8	16	AA873556	Human TSH receptor	486	3	27.3	8	22	ABP12584	HIV A02 super moti
514	3	27.3	8	16	AA891050	Acidic acids 152-15	487	3	27.3	8	22	ABP13244	HIV A02 super moti
515	3	27.3	8	17	AAW01570	Compacting peptide	488	3	27.3	8	22	ABP13244	HIV A02 super moti
516	3	27.3	8	17	AAW08502	CD8 alpha chain re	489	3	27.3	8	22	ABP14466	HIV A03 super moti
517	3	27.3	8	17	AAW05582	Fenoldin peptide	490	3	27.3	8	22	ABP14968	HIV A03 super moti
518	3	27.3	8	17	AAW07405	Streptococcal M pr	491	3	27.3	8	22	ABP15086	HIV A03 super moti
519	3	27.3	8	17	AAW07405	Streptococcal M pr	492	3	27.3	8	22	ABP15109	HIV A03 super moti
520	3	27.3	8	17	AAW02223	Small nuclear ribo	493	3	27.3	8	22	ABP15560	HIV A24 super moti
521	3	27.3	8	17	AAW08684	GF1 tryptic pept	494	3	27.3	8	22	ABP15903	HIV A24 super moti
522	3	27.3	8	18	AAW42247	Peptide repeat mot	495	3	27.3	8	22	ABP17131	HIV B27 super moti
523	3	27.3	8	18	AAW10168	Sodium immunoregula	496	3	27.3	8	22	ABP17132	HIV B27 super moti
524	3	27.3	8	19	AAW21598	Human neuroendocr	497	3	27.3	8	22	ABP17309	HIV B27 super moti
525	3	27.3	8	19	AAW44014	Human CYP19A4 spec	498	3	27.3	8	22	ABP17493	HIV B27 super moti
526	3	27.3	8	19	AAW35011	Endobacteri color	499	3	27.3	8	22	ABP17591	HIV B27 super moti
527	3	27.3	8	19	AAW35011	Endobacteri color	500	3	27.3	8	22	ABP17598	HIV B27 super moti
528	3	27.3	8	19	AAW55306	Peptide motif: fo	501	3	27.3	8	22	ABP18859	HIV B58 super moti
529	3	27.3	8	19	AAW65148	Partial sequence o							
530	3	27.3	8	19	AAW48195	Conantokin peptide							
531	3	27.3	8	19	AAW45977	Conantokin peptide							
532	3	27.3	8	20	AAW67194	DNA binding peptid							
533	3	27.3	8	20	AAW44197	Peptide motif #2 1							
534	3	27.3	8	20	AAW44159	Peptide motif: #2 1							
535	3	27.3	8	20	AAW30644	Dehydrogenase pept							
536	3	27.3	8	20	AAW36558	Fragment of human							
537	3	27.3	8	20	AAW21497	V beta 6 clone for							
538	3	27.3	8	20	AAW21563	V beta 6 clone for							
539	3	27.3	8	20	AAW59425	Thrombophilus therm							
540	3	27.3	8	20	AAW96175	Localisation signa							
541	3	27.3	8	20	AAW93867	Bifidobacterium bi							
542	3	27.3	8	20	AAW50884	Timeless gene prot							
543	3	27.3	8	20	AAW10407	T cell epitope/MHC							
544	3	27.3	8	20	AAW97245	Peptide motif of a							
545	3	27.3	8	21	AAW15700	cAMP-dependent kin							
546	3	27.3	8	21	AAW22855	cAMP-dependent pro							
547	3	27.3	8	21	AAW08118	Peptide modulating							
548	3	27.3	8	21	AAW08145	Peptide modulating							

ALIGNMENTS

RESULT 1

AA98528
 ID AA98528 standard: peptide: 11 AA.

XX AC AA98528:
 XX D: 07-AUG-2000 (first entry)
 XX DE NCAM Igl binding peptide D3.

XX AC AA98528:
 XX D: 07-AUG-2000 (first entry)
 XX DE NCAM Igl binding peptide D3.

KW NCAM; neural cell adhesion molecule; Igl; immunoglobulin domain 1;
 KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
 KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
 KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
 KW treatment; prosthetic nerve guide; treatment; nervous system.


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XX OS Synthetic.
XX AC
XX PN W0200018801-A2.
XX PD 06-APR-2000.
XX PF 23-SEP-1999; 99WO-DK00500.
XX PR 29-SEP-1998; 98DK-0001232.
XX PR 29-APR-1999; 99DK-0000592.
XX PA (RONN/) RONN L C B.
XX PA (ROCK/) ROCK E.
XX PA (HOLM/) HOLM A.
XX PA (OLSE/) OLSEN M.
XX PA (JENSE/) JENSEN P H.
XX PA (POUL/) POULSEN F M.
XX PA (SORO/) SOROKA V.
XX PA (RALE/) RALETS I.
XX PA (BERE/) BEREZIN V.
XX PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
XX PI Poulsen FM, Soroka V, Ralets I, Berezin V;
XX DR WPI: 2000-293111/25.
XX PT Compositions that bind neural cell adhesion molecules useful for
XX PT treating disorders of the nervous system and muscles e.g. Alzheimer's
XX PT and Parkinson's diseases
XX PS Claim 20; Page 82; 119pp; English.
XX CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
XX CC NCAM is found in three forms, two of which are transmembrane forms, while
XX CC the third is attached via a lipid anchor to the cell membrane. All three
XX CC NCAM forms have an extracellular structure consisting of five immunoglobulin
XX CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the
XX CC N-terminal. The present sequence represents a peptide which binds to the
XX CC NCAM-Ig1 domain, and is capable of stimulating or promoting neurite
XX CC outgrowth from NCAM presenting cells, and is also capable of promoting
XX CC the proliferation of NCAM presenting cells. The compound may be used in
XX CC the treatment of normal, degenerated or damaged NCAM presenting cells.
XX CC The compound may in particular be used to treat diseases of the central
XX CC and peripheral nervous systems such as post operative nerve damage,
XX CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
XX CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
XX CC dementia, sclerosis, nerve degeneration associated with diabetes,
XX CC mellitus, disorders affecting the circadian clock or neuro-muscular
XX CC transmission and schizophrenia. Conditions affecting the muscles may also
XX CC be treated with the compound, such as conditions associated with impaired
XX CC function of neuromuscular connections (e.g. genetic or traumatic shock or
XX CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
XX CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
XX CC liver and bowel may also be treated using the compound. The compound is
XX CC used in a prosthetic nerve guide, and also to stimulate the ability to
XX CC learn, and to stimulate the memory of a subject.
XX SQ Sequence 11 AA:
XX Query Match 100.0%; Score 11; DB 21; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-05;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX QY 1 AKKERQKDTQ 11
XX DB 1 AKKERQKDTQ 11
XX RESULT 2
XX AAY88561

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AAY88561 standard; peptide; 11 AA.
 AAY88561:
 07-AUG-2000 (first entry)
 NCAM Ig1 binding peptide D3 used as a control peptide.
 NCAM; neural cell adhesion molecule; Ig1; immunoglobulin domain 1;
 neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
 impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
 Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
 treatment; prosthetic nerve guide; treatment; nervous system.
 Synthetic.
 W0200018801-A2.
 06-APR-2000.
 23-SEP-1999; 99WO-DK00500.
 29-SEP-1998; 98DK-0001232.
 29-APR-1999; 99DK-0000592.
 (RONN/) RONN L C B.
 (ROCK/) ROCK E.
 (HOLM/) HOLM A.
 (OLSE/) OLSEN M.
 (JENSE/) JENSEN P H.
 (POUL/) POULSEN F M.
 (SORO/) SOROKA V.
 (RALE/) RALETS I.
 (BERE/) BEREZIN V.
 Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
 Poulsen FM, Soroka V, Ralets I, Berezin V;
 WPI: 2000-293111/25.
 Compositions that bind neural cell adhesion molecules useful for
 treating disorders of the nervous system and muscles e.g. Alzheimer's
 and Parkinson's diseases
 Claim 20; Page 82; 119pp; English.
 Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
 NCAM is found in three forms, two of which are transmembrane forms, while
 the third is attached via a lipid anchor to the cell membrane. All three
 NCAM forms have an extracellular structure consisting of five immunoglobulin
 domains (Ig domains). The Ig domains are numbered 1 to 5 from the
 N-terminal. The present sequence represents a peptide which binds to the
 NCAM-Ig1 domain, and is capable of stimulating or promoting neurite
 outgrowth from NCAM presenting cells, and is also capable of promoting
 the proliferation of NCAM presenting cells. The compound may be used in
 the treatment of normal, degenerated or damaged NCAM presenting cells.
 The compound may in particular be used to treat diseases of the central
 and peripheral nervous systems such as post operative nerve damage,
 traumatic nerve damage, impaired myelination of nerve fibres, conditions
 resulting from a stroke, Parkinson's disease, Alzheimer's disease,
 dementia, sclerosis, nerve degeneration associated with diabetes,
 mellitus, disorders affecting the circadian clock or neuro-muscular
 transmission and schizophrenia. Conditions affecting the muscles may also
 be treated with the compound, such as conditions associated with impaired
 function of neuromuscular connections (e.g. genetic or traumatic shock or
 traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
 (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
 liver and bowel may also be treated using the compound. The compound is
 used in a prosthetic nerve guide, and also to stimulate the ability to
 learn, and to stimulate the memory of a subject.

CC learn, and to stimulate the memory of a subject.

XX Sequence 11 AA;

Query Match 100.0%; Score 11; DB 21; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKERQKDTQ 11

DB 1 AKKERQKDTQ 11

RESULT 4

ABP83746

ID ABP83746 standard; Peptide: 11 AA;

XX AC

XX ABP83746;

ET 21 OCT-2002 (first entry)

DE Human neural cell adhesion molecule (NCAM) peptide #2.

XX Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;
KW acute myocardial infarction; central nervous system disorder; stroke;
KW peripheral nervous system disorder; postoperative nerve damage;
KW traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;
KW postischaemic damage; multifactorial dementia; multiple sclerosis;
KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW atrophic muscle disorder; gonad degeneration; nephrosis.

XX CS

XX Homo sapiens.

XX PN

XX WO200247719-A2.

XX PD

XX 20 JUN-2002.

XX PF

XX 12-DEC-2001; 2001WO-DK00822.

XX PR

XX 12 DEC-2000; 2000DK-0001863.

XX PA (ENKA) ENKAM PHARM AS.

XX PI Bock E, Berezin V, Kohler LB;

XX D8 WPI: 2002-593473/62.

XX PS

XX Claim 26; Page 39; 57pp; English.

XX CC

XX The invention relates to use of a compound (I) comprising a peptide

XX which comprises at least 5 contiguous amino acid residues of a sequence

XX of the neural cell adhesion molecule (NCAM), its fragment, variant or its

XX mimic, for the preparation of a medicament for preventing death of cells

XX presenting the NCAM or an NCAM ligand (I) is useful in the preparation

XX of a medicament for preventing death of cells presenting the NCAM or an

XX NCAM ligand. The medicament is for the stimulation of the survival of

XX heart muscle cells, such as survival after acute myocardial infarction.

XX The medicament is for the treatment of diseases or conditions of the

XX central and peripheral nervous system, such as postoperative nerve

XX damage, traumatic nerve damage, e.g. resulting from spinal cord injury,

XX impaired myelination of nerve fibres, post-ischaemic damage, e.g.

XX resulting from a stroke, multifactorial dementia, multiple sclerosis,

XX degeneration associated with diabetes mellitus, neuro-muscular

XX degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease

XX and Huntington's disease. The medicament is for the treatment of diseases

XX or conditions of the muscles including conditions with impaired function

XX of neuro-muscular connections, such as genetic or traumatic atrophic

XX

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XX

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XX

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XX

XX

CC muscle disorders, and for the treatment of diseases of conditions of
CC various organs, such as degenerative conditions of the gonads, pancreas
CC (e.g. diabetes mellitus type I and II) and kidney (e.g. nephrosis).
CC ABC69429-ABC69452 represent human NCAM peptides of the invention.

SQ Sequence 11 AA;

Query Match 100.0%; Score 11; DB 23; Length 11;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKKERQKDTQ 11

DB 1 AKKERQKDTQ 11

RESULT 4

ABP83746

ID ABP83746 standard; peptide: 9 AA;

XX AC

XX ABP83746;

XX 28-MAR-2003 (first entry)

XX HLA protein 121P2A3 peptide #101.

XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

XX humoral immune response; cellular immune response;

XX suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX CS

XX Homo sapiens.

XX PN

XX WO200283068-A2.

XX PD

XX 24-OCT-2002.

XX PF

XX 09-APR-2002; 2002WO-US11359.

XX PR

XX 10-APR-2001; 2001US-282739P.

XX PR

XX 25-APR-2001; 2001US-286640P.

XX PR

XX 22 JUN-2001; 2001US-300373P.

XX PA (AGEN-) AGENSYS INC.

XX PI Challita-eid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;

XX AFar DEH, Saifran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

XX WPI: 2003-092956/C8.

XX DR

XX New composition comprising a substance that modulates the status of

XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune

XX responses or in assessing the status of 121P2A3 gene products in normal

XX versus cancerous tissues.

XX PS

XX Claim 13; Page 130; 362pp; English.

XX CC

XX The invention relates to a novel composition comprising a substance that

XX modulates the status of a protein, 121P2A3. The composition of the

XX invention has cytostatic and immunostimulant activity, and is useful as a

XX vaccine. The 121P2A3 proteins and polynucleotides are useful for

XX eliciting humoral or cellular immune response. The polynucleotides are

XX useful for characterising cytogenetic abnormalities of this chromosomal

XX locus, as tools that can be used to delineate cytogenetic abnormalities

XX in the chromosomal region that encodes 121P2A3 that may contribute to

XX malignant phenotype, and in assessing the status of 121P2A3 gene

XX products in normal versus cancerous tissues. The proteins are useful

XX for generating and characterising domain-specific antibodies, for

XX identifying agents or cellular factors that bind to 121P2A3 or a

XX particular structure domain, and in various therapeutic and diagnostic

XX contexts, including cancer vaccines. The antibodies or T cells reactive

XX with the product are useful in passive or active immunisation, and in

XX imaging methodologies for the management of cancer. The sequences shown

XX in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of

XX

XX

XX

XX

XX

XX

XX

XX

```

CC the invention.
XX
SQ Sequence 9 AA;
Query Match 45.5%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KERQR 7
DB 4 KERQR 8
RESULT 5
ABP83747
ID ABP83747 standard; peptide: 9 AA.
XX AC ABP83747;
XX DT 28-MAR-2003 (first entry)
XX DE HLA protein L21P2A3 peptide #102.
XX KW Human; L21P2A3; cytostatic; immunostimulant; vaccine; SSH;
XX KW humoral immune response; cellular immune response;
XX KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX OS Homo sapiens.
XX PN W0200283058-A2.
XX PD 24-OCT-2002.
XX PF 09-APR-2002; 2002MO-US11359.
XX PR 10-APR-2001; 2001US-282739P.
XX PR 25-APR-2001; 2001US-286630P.
XX PR 22-JUN-2001; 2001US-300373P.
XX PA (AGEN) AGENSYS INC.
XX PI Chaitana-eid PM, Raitano AH, Faris M, Hubert RS, Mitchell SC;
XX PI Afar DEH, Saitran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX WPI: 2003-092956/08.
XX
XX New composition comprising a substance that modulates the status of
XX L21P2A3 polypeptides, useful for eliciting humoral or cellular immune
XX responses or in assessing the status of L21P2A3 gene products in normal
XX versus cancerous tissues.
XX
XX Claim 13: Page 130; 362pp; English.
XX
XX The invention relates to a novel composition comprising a substance that
XX modulates the status of a protein, L21P2A3. The composition of the
XX invention has cytostatic and immunostimulant activity, and is useful as a
XX vaccine. The L21P2A3 proteins and polynucleotides are useful for
XX eliciting humoral or cellular immune response. The polynucleotides are
XX useful for characterising cytogenetic abnormalities of this chromosomal
XX locus, as tools that can be used to delineate cytogenetic abnormalities
XX in the chromosomal region that encodes L21P2A3 that may contribute to
XX malignant phenotype, and in assessing the status of L21P2A3 gene
XX products in normal versus cancerous tissues. The proteins are useful
XX for generating and characterising domain-specific antibodies, for
XX identifying agents or cellular factors that bind to L21P2A3 or a
XX particular structure domain, and in various therapeutic and diagnostic
XX contexts, including cancer vaccines. The antibodies or T cells reactive
XX with the product are useful in passive or active immunisation, and in
XX imaging methodologies for the management of cancer. The sequences shown
XX in ABP83646 - ABP95595 represent peptides from the L21P2A3 variants of
XX the invention.
XX
XX Sequence 9 AA;
Query Match 45.5%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KERQR 7
DB 4 KERQR 8
RESULT 5
ABP83747
ID ABP83747 standard; peptide: 9 AA.
XX AC ABP83747;
XX DT 28-MAR-2003 (first entry)
XX DE HLA protein L21P2A3 peptide #102.
XX KW Human; L21P2A3; cytostatic; immunostimulant; vaccine; SSH;
XX KW humoral immune response; cellular immune response;
XX KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX OS Homo sapiens.
XX PN W0200283058-A2.
XX PD 24-OCT-2002.
XX PF 09-APR-2002; 2002MO-US11359.
XX PR 10-APR-2001; 2001US-282739P.
XX PR 25-APR-2001; 2001US-286630P.
XX PR 22-JUN-2001; 2001US-300373P.
XX PA (AGEN) AGENSYS INC.
XX PI Chaitana-eid PM, Raitano AH, Faris M, Hubert RS, Mitchell SC;
XX PI Afar DEH, Saitran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX WPI: 2003-092956/08.
XX
XX New composition comprising a substance that modulates the status of
XX L21P2A3 polypeptides, useful for eliciting humoral or cellular immune
XX responses or in assessing the status of L21P2A3 gene products in normal
XX versus cancerous tissues.
XX
XX Claim 13: Page 130; 362pp; English.
XX
XX The invention relates to a novel composition comprising a substance that
XX modulates the status of a protein, L21P2A3. The composition of the
XX invention has cytostatic and immunostimulant activity, and is useful as a
XX vaccine. The L21P2A3 proteins and polynucleotides are useful for
XX eliciting humoral or cellular immune response. The polynucleotides are
XX useful for characterising cytogenetic abnormalities of this chromosomal
XX locus, as tools that can be used to delineate cytogenetic abnormalities
XX in the chromosomal region that encodes L21P2A3 that may contribute to
XX malignant phenotype, and in assessing the status of L21P2A3 gene
XX products in normal versus cancerous tissues. The proteins are useful
XX for generating and characterising domain-specific antibodies, for
XX identifying agents or cellular factors that bind to L21P2A3 or a
XX particular structure domain, and in various therapeutic and diagnostic
XX contexts, including cancer vaccines. The antibodies or T cells reactive
XX with the product are useful in passive or active immunisation, and in
XX imaging methodologies for the management of cancer. The sequences shown
XX in ABP83646 - ABP95595 represent peptides from the L21P2A3 variants of
XX the invention.
XX
XX Sequence 9 AA;
Query Match 45.5%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 KERQR 7
DB 4 KERQR 8

```


KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 OS WO200283068-A2.
 PN 24 OCT-2002.
 PD 09 APR-2002; 2002WO-US11359.
 PP 10 APR-2001; 2001US-282739P.
 PR 25 APR-2001; 2001US-286630P.
 PR 22 JUN-2001; 2001US-300373P.
 XX (AGEN-) AGENSYS INC.
 PA Chailita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 XX Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 PI WPI; 2003-092956/08.
 DR New composition comprising a substance that modulates the status of
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX Claim 13; Page 136; 362pp; English.
 PS The invention relates to a novel composition comprising a substance that
 XX modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX Sequence 9 AA:
 SQ Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DB 11111
 2 KERQR 6
 RESULT 14
 ABP84340
 ID ABP84340 standard; peptide: 9 AA.
 XX AC ABP84340;
 XX 28-MAR-2003 (first entry)
 DE HLA protein 121P2A3 peptide #695.
 XX Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 OS Homo sapiens.
 PN WO200283068-A2.

OS Homo sapiens.
 XX WO200283068-A2.
 PN 24 OCT-2002.
 PD 09 APR-2002; 2002WO-US11359.
 PP 10 APR-2001; 2001US-282739P.
 PR 25 APR-2001; 2001US-286630P.
 PR 22 JUN-2001; 2001US-300373P.
 XX (AGEN-) AGENSYS INC.
 PA Chailita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 XX Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 PI WPI; 2003-092956/08.
 DR New composition comprising a substance that modulates the status of
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX Claim 13; Page 142; 362pp; English.
 PS The invention relates to a novel composition comprising a substance that
 XX modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX Sequence 9 AA:
 SQ Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DB 11111
 5 KERQR 9
 RESULT 15
 ABP84341
 ID ABP84341 standard; peptide: 9 AA.
 XX AC ABP84341;
 XX 28-MAR-2003 (first entry)
 DE HLA protein 121P2A3 peptide #696.
 XX Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 OS Homo sapiens.
 PN WO200283068-A2.

XX 24-OCT-2002.
 PD 09 APR-2002; 2002W0-US11359.
 XX 10 APR-2001; 2001US-282739P.
 PR 25-APR-2001; 2001US-286630P.
 PR 22-JUN-2001; 2001US-300373P.
 XX (AGEN-) AGENSYS INC.
 PA Chailita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC,
 XX Atar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 PI WPI: 2003-092956/08.
 DR New composition comprising a substance that modulates the status of
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PI responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 PI Claim 13; Page 142; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP84346 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX Sequence 9 AA:
 SQ Query Match: 45.5%; Score 5; DP 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9, 3e-05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KERQR 7
 DB 1 KERQR 5
 RESULT 16
 ABP84343
 ID ABP84343 standard; peptide: 9 AA.
 XX AC ABP84343;
 XX 28-MAR-2003 (first entry)
 CT HLA protein 121P2A3 peptide #598.
 XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 XX humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 OS WO200283068-A2.
 PN 24-OCT-2002.
 XX 09-APR-2002; 2002W0-US11359.
 XX 10 APR-2001; 2001US-282739P.
 PR 25-APR-2001; 2001US-286630P.
 PR 22-JUN-2001; 2001US-300373P.
 XX (AGEN-) AGENSYS INC.
 PA Chailita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC,
 XX Atar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 PI WPI: 2003-092956/08.
 DR New composition comprising a substance that modulates the status of
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PI responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 PI Claim 13; Page 142; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP84346 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX Sequence 9 AA:
 SQ Query Match: 45.5%; Score 5; DP 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9, 3e-05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KERQR 7
 DB 1 KERQR 5

PF 09-APR-2002; 2002W0-US11359.
 XX 10-APR-2001; 2001US-282739P.
 PR 25-APR-2001; 2001US-286630P.
 PR 22-JUN-2001; 2001US-300373P.
 XX (AGEN-) AGENSYS INC.
 PA Chailita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC,
 XX Atar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 PI WPI: 2003-092956/08.
 DR New composition comprising a substance that modulates the status of
 XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PI responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 PI Claim 13; Page 142; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP84346 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX Sequence 9 AA:
 SQ Query Match: 45.5%; Score 5; DP 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9, 3e-05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 KERQR 7
 DB 4 KERQR 8
 RESULT 17
 ABP84346
 ID ABP84346 standard; peptide: 9 AA.
 XX AC ABP84346;
 XX 28-MAR-2003 (first entry)
 CT HLA protein 121P2A3 peptide #761.
 XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 OS WO200283068-A2.
 PN 24-OCT-2002.
 XX 09-APR-2002; 2002W0-US11359.
 XX 10 APR-2001; 2001US-282739P.

PR 25 APR-2001; 2001US-286630P.
 XX 22 JUN-2001; 2001US-300373P.
 PA (AGEN-) AGENSYS INC.
 XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC,
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.
 XX New composition comprising a substance that modulates the status of
 PR 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PI versus cancerous tissues
 XX Claim 14; Page 142; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP84646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX Sequence 9 AA;
 SQ
 Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Prod. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DB 3 KERQR 7
 AC
 ABP8448 standard; peptide; 9 AA.
 XX
 AC
 ABP8448.
 XX
 DT 28-MAR-2003 (first entry)
 DE HLA protein 121P2A3 peptide #763.
 XX
 KW Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 CS
 PN W020283068-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 09-APR-2002; 2002MO-US11359.
 XX
 PR 10-APR-2001; 2001US-282739P.
 PR 25-APR-2001; 2001US-286630P.
 PR 22-JUN-2001; 2001US-300373P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX Challita eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;

PA (AGEN-) AGENSYS INC.
 XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.
 XX New composition comprising a substance that modulates the status of
 PR 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PI versus cancerous tissues
 XX Claim 14; Page 142; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX Sequence 9 AA;
 SQ
 Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Prod. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DB 2 KERQR 5
 AC
 ABP84628 standard; peptide; 9 AA.
 XX
 AC
 ABP84628;
 XX
 DT 28-MAR-2003 (first entry)
 DE HLA protein 121P2A3 peptide #983.
 XX
 KW Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 CS
 PN W0200283068-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 09-APR-2002; 2002MO-US11359.
 XX
 PR 10-APR-2001; 2001US-282739P.
 PR 25-APR-2001; 2001US-286630P.
 PR 22-JUN-2001; 2001US-300373P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX Challita eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;

PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues .
 XX Claim 13; Page 147; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX Sequence 9 AA;
 SQ Query Match 45.5%; Score 5; LH 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 Db 4 KERQR 8
 II III
 III II
 3 KERQR 8
 RESULT 22
 ABP84635
 ID ABP84635 standard; peptide: 9 AA.
 XX AC ABP84635;
 XX 28-MAR-2004 (first entry)
 XX HLA protein 121P2A3 peptide #990.
 DE Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 OS WO200283068-A2.
 PN 24-OCT-2002.
 XX 09-APR-2002; 2002WO-US11359.
 XX 10-APR-2001; 2001US-282739P.
 XX 25-APR-2001; 2001US-286630P.
 XX 22-JUN-2001; 2001US-300373P.
 XX (AGEN-) AGENSYS INC.
 XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 P1 Afar DEH, Safran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.
 XX New composition comprising a substance that modulates the status of:
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues .
 XX Claim 13; Page 147; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that

PS Claim 13; Page 147; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX Sequence 9 AA;
 SQ Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 Db 3 KERQR 7
 II III
 III II
 3 KERQR 7
 RESULT 23
 ABP84636
 ID ABP84636 standard; peptide: 9 AA.
 XX AC ABP84636;
 XX 28-MAR-2003 (first entry)
 XX HLA protein 121P2A3 peptide #991.
 DE Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 OS WO200283068-A2.
 PN 24-OCT-2002.
 XX 09-APR-2002; 2002WO-US11359.
 XX 10-APR-2001; 2001US-282739P.
 XX 25-APR-2001; 2001US-286630P.
 XX 22-JUN-2001; 2001US-300373P.
 XX (AGEN-) AGENSYS INC.
 XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 P1 Afar DEH, Safran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.
 XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues .
 XX Claim 13; Page 147; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that

CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

XX Sequence 9 AA:
 SQ Query Match 45.5%; Score 5; DB 24; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 DI 2 KERQR 6

RESULT 24
 ABP84925
 ID ABP84925 standard; peptide: 9 AA.

XX AC ABP84925;
 XX DT 26-MAR-2003 (first entry)
 XX DE HLA protein 121P2A3 peptide #1280.

XX KW Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX OS Homo sapiens.
 XX PN WO200283068-A2.
 XX PD 24 OCT 2002.

XX PF 09-APR-2002; 2002WO-US11359.
 XX PR 10-APR-2001; 2001US-282739P.
 XX PR 25-APR-2001; 2001US-286630P.
 XX PR 22-JUN-2001; 2001US-300373P.
 XX PA (AGEN-) AGENSYS INC.

XX PI Challita-eld PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.

XX PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.

XX PS Claim 13; Page 153; 362pp; English.

XX CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities

CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

XX Sequence 9 AA:
 SQ Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 DI 4 KERQR 8

RESULT 25
 ABP84926
 ID ABP84926 standard; peptide: 9 AA.

XX AC ABP84926;
 XX DT 28-MAR-2003 (first entry)
 XX DE HLA protein 121P2A3 peptide #1281.

XX KW Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX OS Homo sapiens.
 XX PN WO200283068-A2.
 XX PD 24 OCT 2002.

XX PF 09-APR-2002; 2002WO-US11359.
 XX PR 10-APR-2001; 2001US-282739P.
 XX PR 25-APR-2001; 2001US-286630P.
 XX PR 22-JUN-2001; 2001US-300373P.

XX PA (AGEN-) AGENSYS INC.
 XX PI Challita-eld PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.

XX PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.

XX PS Claim 13; Page 153; 362pp; English.

XX CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities

CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83546 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

XX Sequence 9 AA:
 SQ

Query Match 45.5% Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 Db | | | |
 3 KERQR 7

RESULT: 26
 ABP84929
 ID ABP84929 standard; peptide: 9 AA.
 XX AC ABP84929;
 XX DT 28 MAR-2003 (first entry)
 XX DE HLA protein 121P2A3 peptide #1284.
 XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX OS Homo sapiens.
 XX PN W0200283068-A2.
 XX PD 24 OCT-2002.
 XX PF 09-APR-2002; 2002WO-US11359.
 XX PR 10-APR-2001; 2001US-282739P.
 XX PR 25-APR-2001; 2001US-286630P.
 XX PR 22-JUN-2001; 2001US-300373P.
 XX PA (AGEN) AGENSYS INC.
 XX PI Chailita-oid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Safran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPT: 2003-092956/08.
 XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX Claim 13; Page 153; 362pp; English.

CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic

CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83546 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

XX Sequence 9 AA:
 SQ

Query Match 45.5% Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 Db | | | |
 5 KERQR 9

RESULT 27
 ABP84931
 ID ABP84931 standard; peptide: 9 AA.
 XX AC ABP84931;
 XX DT 28-MAR-2003 (first entry)
 XX DE HLA protein 121P2A3 peptide #1286.
 XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX OS Homo sapiens.
 XX PN W0200283068-A2.
 XX PD 24-OCT-2002.
 XX PF 09-APR-2002; 2002WO-US11459.
 XX PR 10-APR-2001; 2001US-282739P.
 XX PR 25-APR-2001; 2001US-286630P.
 XX PR 22-JUN-2001; 2001US-300373P.
 XX PA (AGEN) AGENSYS INC.
 XX PI Chailita-oid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Safran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPT: 2003-092956/08.
 XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX Claim 13; Page 153; 362pp; English.

CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic

CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP84946 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

XX Sequence 9 AA:
 SQ

Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 IIII
 DL 1 KERQR 5

RESULT 28
 ABP84942
 ID ABP84942 standard; peptide: 9 AA.
 XX AC
 XX ABP84942:
 XX DT 28-MAR-2003 (first entry)
 XX DE HLA protein 121P2A3 peptide #1287.
 XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX OS Homo sapiens.
 XX PN W0200283068-A2.
 XX PD 24-OCT-2002.
 XX PF 09-APR-2002; 2002WO-US11359.
 XX PR 10-APR-2001; 2001US-282739P.
 XX PR 25-APR-2001; 2001US-286630P.
 XX PR 22-JUN-2001; 2001US-300373P.
 XX PA (AGEN-) AGENSYS INC.
 XX PF Chalita-eld PM, Raitano AB, Faris M, Hubert RS, Mitchell SC,
 PF Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.
 XX New composition comprising a substance that modulates the status of
 PI 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PI responses or in assessing the status of 121P2A3 gene products in normal
 PI versus cancerous tissues.

XX Claim 13; Page 153; 362pp; English.

CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP84946 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

CC in ABP84946 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

XX Sequence 9 AA:
 SQ

Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 IIII
 DL 2 KERQR 5

RESULT 29
 ABP85222
 ID ABP85222 standard; peptide: 9 AA.
 XX AC
 XX ABP85222:
 XX DT 28-MAR-2003 (first entry)
 XX DE HLA protein 121P2A3 peptide #1577.
 XX KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX OS Homo sapiens.
 XX PN W0200283068-A2.
 XX PD 24-OCT-2002.
 XX PF 09-APR-2002; 2002WO-US11359.
 XX PR 10-APR-2001; 2001US-282739P.
 XX PR 25-APR-2001; 2001US-286630P.
 XX PR 22-JUN-2001; 2001US-300373P.
 XX PA (AGEN-) AGENSYS INC.
 XX PF Chalita-eld PM, Raitano AB, Faris M, Hubert RS, Mitchell SC,
 PF Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI: 2003-092956/08.
 XX New composition comprising a substance that modulates the status of
 PI 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PI responses or in assessing the status of 121P2A3 gene products in normal
 PI versus cancerous tissues.

XX Claim 13; Page 159; 362pp; English.

CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP84946 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

```

SQ      Sequence      9 AA;
Query Match      45.5%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 KERQR 7
      IIIII
Db      3 KERQR 7

RESULT 31
ABP85227
ID      ABP85227 standard; peptide: 9 AA.
XX
AC      ABP85227;
XX
DI      28-MAR-2003 (first entry)
XX
DE      HLA protein 121P2A3 peptide #1582.
XX
KW      Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
KW      humoral immune response; cellular immune response;
KW      suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX
CS      Homo sapiens.
XX
PN      W0200283066 A2.
XX
PD      24-OCT-2002.
XX
PF      09 APR 2002; 2002WO-US11359.
XX
PR      10-APR-2001; 2001US-282739P.
PR      25-APR-2001; 2001US-286630P.
PR      22-JUN-2001; 2001US-300373P.
XX
PA      (AGEN ) AGENSYS INC.
XX
PI      Challita-eld PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
PI      Afar DER, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX
DR      WPI: 2003-092956/08.
XX
PT      New composition comprising a substance that modulates the status of
PT      121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PT      responses or in assessing the status of 121P2A3 gene products in normal
PT      versus cancerous tissues.
XX
PS      Claim 13; Page 159; 362pp; English.
XX
CC      The invention relates to a novel composition comprising a substance that
CC      modulates the status of a protein, 121P2A3. The composition of the
CC      invention has cytostatic and immunostimulant activity, and is useful as a
CC      vaccine. The 121P2A3 proteins and polynucleotides are useful for
CC      eliciting humoral or cellular immune response. The polynucleotides are
CC      useful for characterising cytogenetic abnormalities of this chromosomal
CC      locus, as tools that can be used to delineate cytogenetic abnormalities
CC      in the chromosomal region that encodes 121P2A3 that may contribute to
CC      malignant phenotype, and in assessing the status of 121P2A3 gene
CC      products in normal versus cancerous tissues. The proteins are useful
CC      for generating and characterising domain-specific antibodies, for
CC      identifying agents or cellular factors that bind to 121P2A3 or a
CC      particular structure domain, and in various therapeutic and diagnostic
CC      contexts, including cancer vaccines. The antibodies or T cells reactive
CC      with the product are useful in passive or active immunisation, and in
CC      imaging methodologies for the management of cancer. The sequences shown
CC      in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
CC      the invention.
XX
SQ      Sequence      9 AA;
Query Match      45.5%; Score 5; DB 24; Length 9;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 KERQR 8
      IIIII
Db      4 KERQR 8

RESULT 30
ABP85223
ID      ABP85223 standard; peptide: 9 AA.
XX
AC      ABP85223;
XX
DI      28-MAR-2003 (first entry)
XX
DE      HLA protein 121P2A3 peptide #1578.
XX
KW      Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
KW      humoral immune response; cellular immune response;
KW      suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX
CS      Homo sapiens.
XX
PN      W0200283068 A2.
XX
PD      24-OCT-2002.
XX
PF      09 APR 2002; 2002WO-US11359.
XX
PR      10-APR-2001; 2001US-282739P.
PR      25-APR-2001; 2001US-286630P.
PR      22-JUN-2001; 2001US-300373P.
XX
PA      (AGEN ) AGENSYS INC.
XX
PI      Challita-eld PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
PI      Afar DER, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX
DR      WPI: 2003-092956/08.
XX
PT      New composition comprising a substance that modulates the status of
PT      121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PT      responses or in assessing the status of 121P2A3 gene products in normal
PT      versus cancerous tissues.
XX
PS      Claim 13; Page 159; 362pp; English.
XX
CC      The invention relates to a novel composition comprising a substance that
CC      modulates the status of a protein, 121P2A3. The composition of the
CC      invention has cytostatic and immunostimulant activity, and is useful as a
CC      vaccine. The 121P2A3 proteins and polynucleotides are useful for
CC      eliciting humoral or cellular immune response. The polynucleotides are
CC      useful for characterising cytogenetic abnormalities of this chromosomal
CC      locus, as tools that can be used to delineate cytogenetic abnormalities
CC      in the chromosomal region that encodes 121P2A3 that may contribute to
CC      malignant phenotype, and in assessing the status of 121P2A3 gene
CC      products in normal versus cancerous tissues. The proteins are useful
CC      for generating and characterising domain-specific antibodies, for
CC      identifying agents or cellular factors that bind to 121P2A3 or a
CC      particular structure domain, and in various therapeutic and diagnostic
CC      contexts, including cancer vaccines. The antibodies or T cells reactive
CC      with the product are useful in passive or active immunisation, and in
CC      imaging methodologies for the management of cancer. The sequences shown
CC      in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
CC      the invention.
XX
SQ      Sequence      9 AA;
Query Match      45.5%; Score 5; DB 24; Length 9;

```

QY 3 KERQR 7
 I I I I I
 DB 5 KERQR 9

RESULT 12

ABP85228
 ID ABP85228 standard: peptide; 9 AA.

XX AC ABP85228;
 XX XX

DT 28 MAR-2003 (first entry)

DE HLA protein 121P2A3 peptide #1584.

XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.
 OS
 XX W0200283068-A2.
 PN
 XX 24-OCT-2002.
 PD
 XX 09-APR-2002; 2002WO-US11359.
 PF
 XX 10-APR-2001; 2001US-282739P.
 PR
 XX 25-APR-2001; 2001US-286630P.
 PK
 XX 22-JUN-2001; 2001US-300373P.
 PR
 XX (AGEN-) AGENSYS INC.
 PA
 XX Chalitta eid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;
 PI Atar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI; 2003-092956/08.
 XX

New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal versus cancerous tissues.

Claim 13; Page 159; 362pp; English.

The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 121P2A3 proteins and polynucleotides are useful for eliciting humoral or cellular immune responses. The polynucleotides are useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 121P2A3 that may contribute to malignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancerous tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The sequences shown in ABP8546 - ABP95595 represent peptides from the 121P2A3 variants of the invention.

QY 3 KERQR 7
 I I I I I
 DB 1 KERQR 5

Query Match 45.5%; Score 6; LB 54; Length 9;
 Best Local Similarity 100.0%; Pref. No. 9.4e-05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 33
 ABP85230
 ID ABP85230 standard: peptide; 9 AA.

XX AC ABP85230;
 XX XX

DT 28-MAR-2003 (first entry)

DE HLA protein 121P2A3 peptide #1585.

XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

XX Homo sapiens.
 OS
 XX W0200283068-A2.
 PN
 XX 24-OCT-2002.
 PD
 XX 09-APR-2002; 2002WO-US11359.
 PF
 XX 10-APR-2001; 2001US-282739P.
 PR
 XX 25-APR-2001; 2001US-286630P.
 PK
 XX 22-JUN-2001; 2001US-300373P.
 PR
 XX (AGEN-) AGENSYS INC.
 PA
 XX Chalitta eid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;
 PI Atar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI; 2003-092956/08.
 XX

New composition comprising a substance that modulates the status of 121P2A3 polypeptides, useful for eliciting humoral or cellular immune responses or in assessing the status of 121P2A3 gene products in normal versus cancerous tissues.

Claim 13; Page 159; 362pp; English.

The invention relates to a novel composition comprising a substance that modulates the status of a protein, 121P2A3. The composition of the invention has cytostatic and immunostimulant activity, and is useful as a vaccine. The 121P2A3 proteins and polynucleotides are useful for eliciting humoral or cellular immune responses. The polynucleotides are useful for characterising cytogenetic abnormalities of this chromosomal locus, as tools that can be used to delineate cytogenetic abnormalities in the chromosomal region that encodes 121P2A3 that may contribute to malignant phenotype, and in assessing the status of 121P2A3 gene products in normal versus cancerous tissues. The proteins are useful for generating and characterising domain-specific antibodies, for identifying agents or cellular factors that bind to 121P2A3 or a particular structure domain, and in various therapeutic and diagnostic contexts, including cancer vaccines. The antibodies or T cells reactive with the product are useful in passive or active immunisation, and in imaging methodologies for the management of cancer. The sequences shown in ABP8546 - ABP95595 represent peptides from the 121P2A3 variants of the invention.

Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pref. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 I I I I I
 DB 2 KERQR 6

RESULT 34


```

XX Homo sapiens.
XX
XX W0200284068-A2.
XX
XX 24-OCT-2002.
XX
XX 09-APR-2002; 2002WO-US11359.
XX
XX 10-APR-2001; 2001US-282739P.
XX
XX 25-APR-2001; 2001US-286630P.
XX
XX 22-JUN-2001; 2001US-300373P.
XX
XX (AGEN ) AGENSYS INC.
XX
XX Challita-eld PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
XX Alar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX
XX WPI: 2003-092956/08.
XX
XX New composition comprising a substance that modulates the status of
XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
XX responses or in assessing the status of 121P2A3 gene products in normal
XX versus cancerous tissues.
XX
XX Claim 13: Page 165; 362pp; English.
XX
XX The invention relates to a novel composition comprising a substance that
XX modulates the status of a protein, 121P2A3. The composition of the
XX vaccine has cytostatic and immunostimulant activity, and is useful as a
XX eliciting humoral or cellular immune response. The polynucleotides are
XX useful for characterising cytogenetic abnormalities of this chromosomal
XX locus, as tools that can be used to delineate cytogenetic abnormalities
XX in the chromosomal region that encodes 121P2A3 that may contribute to
XX malignant phenotype, and in assessing the status of 121P2A3 gene
XX products in normal versus cancerous tissues. The proteins are useful
XX for generating and characterising domain-specific antibodies, for
XX identifying agents or cellular factors that bind to 121P2A3 or a
XX particular structure domain, and in various therapeutic and diagnostic
XX contexts, including cancer vaccines. The antibodies or T cells reactive
XX with the product are useful in passive or active immunisation, and in
XX imaging methodologies for the management of cancer. The sequences shown
XX in ABP84646 - ABP95595 represent peptides from the 121P2A3 variants of
XX the invention.
XX
XX Sequence 9 AA;
XX
XX Query Match: 45.5%; Score 5; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 3 KERQR 7
XX 1111
XX 2 KERQR 6
XX
XX RESULT 49
XX ABP86092
XX ID ABP86092 standard; peptide: 9 AA.
XX
XX AC ABP86092;
XX
XX 28-MAR-2004 (first entry)
XX
XX HLA protein 121P2A3 peptide #2447.
XX
XX Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
XX humoral immune response; cellular immune response;
XX suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX
XX Homo sapiens.
XX
XX W0200284068-A2.
XX
XX 24-OCT-2002.

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XX W0200284068-A2.
XX
XX 24-OCT-2002.
XX
XX 09-APR-2002; 2002WO-US11359.
XX
XX 10-APR-2001; 2001US-282739P.
XX
XX 25-APR-2001; 2001US-286630P.
XX
XX 22-JUN-2001; 2001US-300373P.
XX
XX (AGEN ) AGENSYS INC.
XX
XX Challita-eld PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
XX Alar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
XX
XX WPI: 2003-092956/08.
XX
XX New composition comprising a substance that modulates the status of
XX 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
XX responses or in assessing the status of 121P2A3 gene products in normal
XX versus cancerous tissues.
XX
XX Claim 13: Page 177; 362pp; English.
XX
XX The invention relates to a novel composition comprising a substance that
XX modulates the status of a protein, 121P2A3. The composition of the
XX vaccine has cytostatic and immunostimulant activity, and is useful as a
XX eliciting humoral or cellular immune response. The polynucleotides are
XX useful for characterising cytogenetic abnormalities of this chromosomal
XX locus, as tools that can be used to delineate cytogenetic abnormalities
XX in the chromosomal region that encodes 121P2A3 that may contribute to
XX malignant phenotype, and in assessing the status of 121P2A3 gene
XX products in normal versus cancerous tissues. The proteins are useful
XX for generating and characterising domain-specific antibodies, for
XX identifying agents or cellular factors that bind to 121P2A3 or a
XX particular structure domain, and in various therapeutic and diagnostic
XX contexts, including cancer vaccines. The antibodies or T cells reactive
XX with the product are useful in passive or active immunisation, and in
XX imaging methodologies for the management of cancer. The sequences shown
XX in ABP84646 - ABP95595 represent peptides from the 121P2A3 variants of
XX the invention.
XX
XX Sequence 9 AA;
XX
XX Query Match: 45.5%; Score 5; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 3 KERQR 7
XX 1111
XX 2 KERQR 6
XX
XX RESULT 49
XX ABP86093
XX ID ABP86093 standard; peptide: 9 AA.
XX
XX AC ABP86093;
XX
XX 28-MAR-2004 (first entry)
XX
XX HLA protein 121P2A3 peptide #2448.
XX
XX Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
XX humoral immune response; cellular immune response;
XX suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX
XX Homo sapiens.
XX
XX W0200284068-A2.
XX
XX 24-OCT-2002.

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XX PF 09-APR-2002; 2004WO-US11359.
XX XX
XX PR 10-APR-2001; 2001US-282739P.
XX PR 25-APR-2001; 2001US-286630P.
XX PR 22-JUN-2001; 2001US-300373P.
XX PA (AGEN-) AGENSYS INC.
XX XX
XX PI Chaitalia etd PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
XX PI Afar DEB, Saffran D, Morrison K, Morrison KK, Ge W, Jakobovits A;
XX DR WPI, 2003 092956/06.
XX XX
XX PT New composition comprising a substance that modulates the status of
XX PT L21P2A3 polypeptides, useful for eliciting humoral or cellular immune
XX PT responses or in assessing the status of L21P2A3 gene products in normal
XX PT versus cancerous tissues.
XX PS Claim 13; Page 177; 362pp; English.
XX CC The invention relates to a novel composition comprising a substance that
XX CC modulates the status of a protein, L21P2A3. The composition of the
XX CC invention has cytostatic and immunostimulant activity, and is useful as a
XX CC vaccine. The L21P2A3 proteins and polynucleotides are useful for
XX CC eliciting humoral or cellular immune response. The polynucleotides are
XX CC useful for characterising cytogenetic abnormalities of this chromosomal
XX CC locus, as tools that can be used to delineate cytogenetic abnormalities
XX CC in the chromosomal region that encodes L21P2A3 that may contribute to
XX CC malignant phenotype, and in assessing the status of L21P2A3 gene
XX CC products in normal versus cancerous tissues. The proteins are useful
XX CC for generating and characterising domain-specific antibodies, for
XX CC identifying agents or cellular factors that bind to L21P2A3 or a
XX CC particular structure domain, and in various therapeutic and diagnostic
XX CC contexts, including cancer vaccines. The antibodies or T cells reactive
XX CC with the product are useful in passive or active immunisation, and in
XX CC imaging methodologies for the management of cancer. The sequences shown
XX CC in ABP86044 - ABP95595 represent peptides from the L21P2A3 variants of
XX CC the invention.
XX SQ Sequence 9 AA;
XX
XX Query Match 45.5%; Score 5; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9; gaps 0;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 KERQR 7
XX DB 4 KERQR 8
XX
XX RESULT 4;
XX ABP86044
XX ID ABP86044 standard; peptide: 9 AA.
XX AC ABP86044;
XX XX
XX DT 28-MAR-2003 (first entry)
XX XX
XX DE HLA protein L21P2A3 peptide #2441.
XX KW Human; L21P2A3; cytostatic; immunostimulant; vaccine; SSH;
XX KW humoral immune response; cellular immune response;
XX KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX OS Homo sapiens.
XX XX
XX PN W0200283068-A2.
XX PD 24 OCT-2002.
XX XX
XX PF 09-APR-2002; 2004WO-US11359.
XX XX
XX PR 10-APR-2001; 2001US-282739P.
XX PR 25-APR-2001; 2001US-286630P.
XX PR 22-JUN-2001; 2001US-300373P.
XX XX

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XX PR 10-APR-2001; 2001US-282739P.
XX PR 25-APR-2001; 2001US-286630P.
XX PR 22-JUN-2001; 2001US-300373P.
XX PA (AGEN-) AGENSYS INC.
XX XX
XX PI Chaitalia etd PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
XX PI Afar DEB, Saffran D, Morrison K, Morrison KK, Ge W, Jakobovits A;
XX DR WPI, 2003 092956/06.
XX XX
XX PT New composition comprising a substance that modulates the status of
XX PT L21P2A3 polypeptides, useful for eliciting humoral or cellular immune
XX PT responses or in assessing the status of L21P2A3 gene products in normal
XX PT versus cancerous tissues.
XX PS Claim 13; Page 177; 362pp; English.
XX CC The invention relates to a novel composition comprising a substance that
XX CC modulates the status of a protein, L21P2A3. The composition of the
XX CC invention has cytostatic and immunostimulant activity, and is useful as a
XX CC vaccine. The L21P2A3 proteins and polynucleotides are useful for
XX CC eliciting humoral or cellular immune response. The polynucleotides are
XX CC useful for characterising cytogenetic abnormalities of this chromosomal
XX CC locus, as tools that can be used to delineate cytogenetic abnormalities
XX CC in the chromosomal region that encodes L21P2A3 that may contribute to
XX CC malignant phenotype, and in assessing the status of L21P2A3 gene
XX CC products in normal versus cancerous tissues. The proteins are useful
XX CC for generating and characterising domain-specific antibodies, for
XX CC identifying agents or cellular factors that bind to L21P2A3 or a
XX CC particular structure domain, and in various therapeutic and diagnostic
XX CC contexts, including cancer vaccines. The antibodies or T cells reactive
XX CC with the product are useful in passive or active immunisation, and in
XX CC imaging methodologies for the management of cancer. The sequences shown
XX CC in ABP86044 - ABP95595 represent peptides from the L21P2A3 variants of
XX CC the invention.
XX SQ Sequence 9 AA;
XX
XX Query Match 45.5%; Score 5; DB 24; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9; gaps 0;
XX Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 3 KERQR 7
XX DB 3 KERQR 5
XX
XX RESULT 42
XX ABP86096
XX ID ABP86096 standard; peptide: 9 AA.
XX AC ABP86096;
XX XX
XX DT 28-MAR-2003 (first entry)
XX XX
XX DE HLA protein L21P2A3 peptide #2451.
XX KW Human; L21P2A3; cytostatic; immunostimulant; vaccine; SSH;
XX KW humoral immune response; cellular immune response;
XX KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
XX OS Homo sapiens.
XX XX
XX PN W0200283068-A2.
XX PD 24 OCT-2002.
XX XX
XX PF 09-APR-2002; 2004WO-US11359.
XX XX
XX PR 10-APR-2001; 2001US-282739P.
XX PR 25-APR-2001; 2001US-286630P.
XX PR 22-JUN-2001; 2001US-300373P.
XX XX

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XX (AGEN-) AGENSYS INC.
 XX
 PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX
 DR WP1: 2003-092956/08.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX
 PS Claim 13; Page 177; 362pp; English.
 XX
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP8646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX
 SQ Sequence 9 AA;
 Query Match: 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DE IIIII
 3 KERQR 7
 RESULT 4;
 ID ABP86096
 AC ABP86096 standard; peptide: 9 AA.
 AC ABP86096;
 XX 28-MAR-2004 (first entry)
 DE HLA protein 121P2A3 peptide #2451.
 XX Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 DE humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 OS Wo200283068-A2.
 PN 24-OCT-2002.
 XX 09 APR 2002; 2002WO-US11359.
 XX 10 APR 2001; 2001US-282739P.
 XX 25 APR 2001; 2001US-286630P.
 XX 22 JUN 2001; 2001US-300373P.
 XX (AGEN-) AGENSYS INC.
 XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX

PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX
 DR WP1: 2003-092956/08.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX
 PS Claim 13; Page 177; 362pp; English.
 XX
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP8646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX
 SQ Sequence 9 AA;
 Query Match: 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DE IIIII
 5 KERQR 9
 RESULT 44
 ID ABP86576
 AC ABP86576 standard; peptide: 9 AA.
 AC ABP86576;
 XX 28-MAR-2003 (first entry)
 DE HLA protein 121P2A3 peptide #2931.
 XX Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 OS Wo200283068-A2.
 PN 24-OCT-2002.
 XX 09 APR 2002; 2002WO-US11359.
 XX 10 APR 2001; 2001US-282739P.
 XX 25 APR 2001; 2001US-286630P.
 XX 22 JUN 2001; 2001US-300373P.
 XX (AGEN-) AGENSYS INC.
 XX Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX

DR WP1: 2003-092956/08.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues -
 XX
 XX
 PS Claim 13: Page 181: 362pp; English.
 XX
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX
 SQ Sequence 9 AA:
 Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DB I I I I I
 4 KERQR 8
 RESULT 45
 ABP86577
 ID ABP86577 standard; peptide: 9 AA.
 XX
 AC ABP86577;
 XX
 DI 28-MAR 2003 (first entry)
 XX
 DE HLA protein 121P2A3 peptide #2932.
 XX
 KW Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX
 CS Homo sapiens.
 XX
 PN WO200283068-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 04-APR 2002; 2002WO-US11359.
 XX
 PR 10-APR-2001; 2001US-282739P.
 XX
 PR 25-APR-2001; 2001US-286630P.
 XX
 PR 22-JUN-2001; 2001US-300373P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX
 XX WP1: 2003-092956/08.
 XX
 PT New composition comprising a substance that modulates the status of

PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues -
 XX
 XX
 PS Claim 13: Page 182: 362pp; English.
 XX
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX
 SQ Sequence 9 AA:
 Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KERQR 7
 DB I I I I I
 5 KERQR 9
 RESULT 46
 ABP86580
 ID ABP86580 standard; peptide: 9 AA.
 XX
 AC ABP86580;
 XX
 DI 28-MAR 2003 (first entry)
 XX
 DE HLA protein 121P2A3 peptide #2935.
 XX
 KW Human: 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX
 CS Homo sapiens.
 XX
 PN WO200283068-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 09-APR-2002; 2002WO-US11359.
 XX
 PR 10-APR-2001; 2001US-282739P.
 XX
 PR 25-APR-2001; 2001US-286630P.
 XX
 PR 22-JUN-2001; 2001US-300373P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX
 XX WP1: 2003-092956/08.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues -

XX Claim 13; Page 182; 362pp; English.
 XX The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3, the composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX
 SQ Sequence 9 AA;

Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 DB 3 KERQR 7

RESULT 47
 ABP86581
 ID ABP86581 standard; peptide; 9 AA.
 XX
 AC ABP86581;
 XX
 DT 28-MAR-2003 (first entry)
 XX
 DE HLA protein 121P2A3 peptide #2936.
 XX
 KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX
 OS Homo sapiens.
 XX
 PN WC200283068-A2.
 XX
 PD 24-OCT-2002.
 XX
 PF 09-APR-2002; 2002WO-US11359.
 XX
 PR 10-APR-2001; 2001US-282739P.
 XX
 PR 25-APR-2001; 2001US-286630P.
 XX
 PR 22-JUN-2001; 2001US-300373P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX
 WP1: 2003-092956/08.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues -
 XX
 PS Claim 13; Page 182; 362pp; English.
 XX

CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
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 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP83646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.
 XX
 SQ Sequence 9 AA;

Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 DB 1 KERQR 5

RESULT 48
 ABP86583
 ID ABP86583 standard; peptide; 9 AA.
 XX

AC ABP86583;

DT 28-MAR-2003 (first entry)

DE HLA protein 121P2A3 peptide #2938.

KW Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

OS Homo sapiens.

PN WC200283068-A2.

PD 24-OCT-2002.

PF 09-APR-2002; 2002WO-US11359.

PR 10-APR-2001; 2001US-282739P.

PR 25-APR-2001; 2001US-286630P.

PR 22-JUN-2001; 2001US-300373P.

PA (AGEN-) AGENSYS INC.

PI Challita-eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;

WP1: 2003-092956/08.

PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues -
 XX
 PS Claim 13; Page 182; 362pp; English.

CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a

CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP81646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

XX
 XX
 SQ Sequence 9 AA;

Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pied. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 Db 1111
 5 KERQR 6

RESULT: 49
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 ID ABP87064 standard; peptide: 9 AA.
 AC ABP87064.
 XX
 XX 28 MAR 2004 (first entry)
 DE HLA protein 121P2A3 peptide #3419.
 XX
 XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 OS
 XX WO200283068-A2.
 PN 24 OCT 2002.
 XX
 XX 09 APR 2002; 2002WO-US11359.
 XX
 XX 10 APR 2001; 2001US-282739P.
 XX 25 APR 2001; 2001US-286630P.
 XX 22 JUN 2001; 2001US-300373P.
 XX (AGEN) AGENSYS INC.
 XX
 XX Challita-oid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX
 XX WPI: 2003-092956/08.
 XX
 XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues -
 PS
 XX Claim 13: Page 186; 362pp; English.

CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene

CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene
 CC products in normal versus cancerous tissues. The proteins are useful
 CC for generating and characterising domain-specific antibodies, for
 CC identifying agents or cellular factors that bind to 121P2A3 or a
 CC particular structure domain, and in various therapeutic and diagnostic
 CC contexts, including cancer vaccines. The antibodies or T cells reactive
 CC with the product are useful in passive or active immunisation, and in
 CC imaging methodologies for the management of cancer. The sequences shown
 CC in ABP81646 - ABP95595 represent peptides from the 121P2A3 variants of
 CC the invention.

XX
 XX
 SQ Sequence 9 AA;

Query Match 45.5%; Score 5; DB 24; Length 9;
 Best Local Similarity 100.0%; Pied. No. 9.3e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KERQR 7
 Db 1111
 5 KERQR 4

RESULT: 50
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 ID ABP87065 standard; peptide: 9 AA.
 AC ABP87065;
 XX
 XX 28 MAR 2003 (first entry)
 DE HLA protein 121P2A3 peptide #3420.
 XX
 XX Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
 KW humoral immune response; cellular immune response;
 KW suppression subtractive hybridisation; HLA; human leukocyte antigen.
 XX Homo sapiens.
 OS
 XX WO200283068-A2.
 PN 24 OCT 2002.
 XX
 XX 09 APR 2002; 2002WO-US11359.
 XX
 XX 10 APR 2001; 2001US-282739P.
 XX 25 APR 2001; 2001US-286630P.
 XX 22 JUN 2001; 2001US-300373P.
 XX (AGEN) AGENSYS INC.
 XX
 XX Challita-oid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Afar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX
 XX WPI: 2003-092956/08.
 XX
 XX New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues -
 PS
 XX Claim 13: Page 186; 362pp; English.

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 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytostatic and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
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 CC useful for characterising cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC eliciting humoral or cellular immune response. The polynucleotides are
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 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene

CC products in normal versus cancerous tissues. The proteins are useful
CC for generating and characterising domain specific antibodies, for
CC identifying agents or cellular factors that bind to 121P2A3 or a
CC particular structure domain, and in various therapeutic and diagnostic
CC contexts, including cancer vaccines. The antibodies or T cells reactive
CC with the product are useful in passive or active immunisation, and in
CC imaging methodologies for the management of cancer. The sequences shown
CC in AB983646 - AB995595 represent peptides from the 121P2A3 variants of
XX the invention.

SQ Sequence 4 AA:

Query Match: 45.5%; Score 5; Pos 24; Length 9.

Best local Similarity 100.0%; Pred. No. 9; 3c-nsf

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 KERQR 7

DB 1 KERQR 5

Search Completed: September 30, 2003, 13:24:18
Job Time : 47.1657 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compucon Ltd.

OM protein protein search, using sw model

Run on: September 30, 2003, 10:07:04 ; Search time 41.0833 Seconds
(without alignments)
42.499 Million cell updates/sec

Title: US-09-787-443-3

Perfect score: 11

Sequence: 1 ARALNMGAKPK 11

Scoring table: OLICO

Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 273822

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

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23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	ID	Description
1	11	100.0	11	21	AA188529	NCAM Igl binding p
2	11	100.0	11	21	AA188563	NCAM Igl binding p
3	11	100.0	11	23	ABG69331	Human neural cell
4	4	36.4	8	19	AA175820	Mouse mast cell pr
5	4	36.4	8	22	AAJ01170	Hepatitis C virus
6	4	36.4	8	22	AAJ02158	Hepatitis C virus
7	4	36.4	8	22	AAJ02181	Hepatitis C virus
8	4	36.4	8	22	AAJ02671	Hepatitis C virus
9	4	36.4	8	23	AB884505	Encephalomyocardit

4	36.4	8	23	AAG79508	C. trachomatis epi
10	36.4	8	23	AB454443	Desmoglein-1 CAR p
11	36.4	8	23	AB454443	Desmoglein-1 CAR p
12	36.4	8	23	AB454443	Desmoglein-1 CAR p
13	36.4	8	23	AB454448	Desmoglein-1 CAR p
14	36.4	8	23	AB454448	Desmoglein-1 CAR p
15	36.4	8	23	AB454455	Desmoglein-1 CAR p
16	36.4	8	23	AB454456	Desmoglein-1 CAR p
17	36.4	8	23	AB454489	Desmoglein-3 CAR p
18	36.4	8	23	AB454490	Desmoglein-3 CAR p
19	36.4	8	23	AB454494	Desmoglein-3 CAR p
20	36.4	8	23	AB454495	Desmoglein-3 CAR p
21	36.4	8	23	AB455000	Desmoglein-3 CAR p
22	36.4	8	23	AB461175	Desmoglein-3 CAR p
23	36.4	8	23	AB461176	Desmoglein-1 CAR s
24	36.4	8	23	AB461181	Desmoglein-1 CAR s
25	36.4	8	23	AB461187	Desmoglein-1 CAR s
26	36.4	8	23	AB461194	Desmoglein-1 CAR s
27	36.4	8	23	AB46203	Desmoglein-1 CAR s
28	36.4	8	23	AB46204	Desmoglein-1 CAR s
29	36.4	8	23	AB46209	Desmoglein-1 CAR s
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31	36.4	8	23	AB46222	Desmoglein-1 CAR s
32	36.4	8	23	AB46231	Desmoglein-1 CAR s
33	36.4	8	23	AB46232	Desmoglein-1 CAR s
34	36.4	8	23	AB46237	Desmoglein-1 CAR s
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49	36.4	8	23	AB46326	Desmoglein-1 CAR s
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51	36.4	8	23	AB46333	Desmoglein-1 CAR s
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53	36.4	8	23	AB46455	Desmoglein-3 CAR s
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56	36.4	8	23	AB46465	Desmoglein-3 CAR s
57	36.4	8	23	AB46479	Desmoglein-3 CAR s
58	36.4	8	23	AB46480	Desmoglein-3 CAR s
59	36.4	8	23	AB46483	Desmoglein-3 CAR s
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61	36.4	8	23	AB46503	Desmoglein-3 CAR s
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70	36.4	8	23	AB46552	Desmoglein-3 CAR s
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74	36.4	8	23	AB46584	Desmoglein-3 CAR s
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78	36.4	8	23	ABP56988	E. tenella EtMIC4/
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80	36.4	9	17	AAW49326	Human leucocyte an
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85	4	36.4	9	22	AAJ00984	Hepatitis C virus	158	4	36.4	9	23	ABR46530	Desmoglein-3	CAR	
86	4	36.4	9	22	AAJ01387	Hepatitis C virus	159	4	36.4	9	23	ABR46532	Desmoglein-3	CAR	
87	4	36.4	9	22	AAJ01799	Hepatitis C virus	160	4	36.4	9	23	ABR46533	Desmoglein-3	CAR	
88	4	36.4	9	22	AAJ02182	Hepatitis C virus	161	4	36.4	9	23	ABR46538	Desmoglein-3	CAR	
89	4	36.4	9	22	AAJ02315	Hepatitis C virus	162	4	36.4	9	23	ABR46544	Desmoglein-3	CAR	
90	4	36.4	9	22	AAJ02679	Hepatitis C virus	163	4	36.4	9	23	ABR46553	Desmoglein-3	CAR	
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92	4	36.4	9	23	ABG34116	Antigenic peptide	165	4	36.4	9	23	ABR46556	Desmoglein-3	CAR	
93	4	36.4	9	23	ABG34118	Antigenic peptide	166	4	36.4	9	23	ABR46557	Desmoglein-3	CAR	
94	4	36.4	9	23	ABG35101	Pancreatic targeti	167	4	36.4	9	23	ABR46562	Desmoglein-3	CAR	
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96	4	36.4	9	23	ABR45451	Desmoglein-1	CAR p	169	4	36.4	9	23	ABR46590	Desmoglein-3	CAR
97	4	36.4	9	23	ABR45457	Desmoglein-1	CAR p	170	4	36.4	9	23	ABR46591	Desmoglein-3	CAR
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102	4	36.4	9	23	ABR45497	Desmoglein-3	CAR p	175	4	36.4	10	18	AAW42662	Antigenic decapept	
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106	4	36.4	9	23	ABR46178	Desmoglein-1	CAR s	179	4	36.4	10	18	AAW32734	Human platelet gly	
107	4	36.4	9	23	ABR46182	Desmoglein-1	CAR s	180	4	36.4	10	18	AAW32745	Human platelet gly	
108	4	36.4	9	23	ABR46183	Desmoglein-1	CAR s	181	4	36.4	10	20	AAW47961	Immunogenic peptid	
109	4	36.4	9	23	ABR46188	Desmoglein-1	CAR s	182	4	36.4	10	21	AAW27126	Human CASB619 prot	
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111	4	36.4	9	23	ABR46205	Desmoglein-1	CAR s	184	4	36.4	10	22	AAW95686	Human complementar	
112	4	36.4	9	23	ABR46206	Desmoglein-1	CAR s	185	4	36.4	10	22	AAW95688	Human complementar	
113	4	36.4	9	23	ABR46210	Desmoglein-1	CAR s	186	4	36.4	10	22	AAW96942	Human complementar	
114	4	36.4	9	23	ABR46211	Desmoglein-1	CAR s	187	4	36.4	10	22	AAW96942	Human complementar	
115	4	36.4	9	23	ABR46216	Desmoglein-1	CAR s	188	4	36.4	10	22	AAW84251	Arabidopsis thalia	
116	4	36.4	9	23	ABR46223	Desmoglein-1	CAR s	189	4	36.4	10	22	AAW84253	Arabidopsis thalia	
117	4	36.4	9	23	ABR46233	Desmoglein-1	CAR s	190	4	36.4	10	22	AAW85696	Saccharomyces cere	
118	4	36.4	9	23	ABR46234	Desmoglein-1	CAR s	191	4	36.4	10	22	AAW85720	Saccharomyces cere	
119	4	36.4	9	23	ABR46238	Desmoglein-1	CAR s	192	4	36.4	10	22	AAJ00296	Hepatitis C virus	
120	4	36.4	9	23	ABR46239	Desmoglein-1	CAR s	193	4	36.4	10	22	AAJ00493	Hepatitis C virus	
121	4	36.4	9	23	ABR46244	Desmoglein-1	CAR s	194	4	36.4	10	22	AAJ00721	Hepatitis C virus	
122	4	36.4	9	23	ABR46251	Desmoglein-1	CAR s	195	4	36.4	10	22	AAJ01245	Hepatitis C virus	
123	4	36.4	9	23	ABR46261	Desmoglein-1	CAR s	196	4	36.4	10	22	AAJ01480	Hepatitis C virus	
124	4	36.4	9	23	ABR46262	Desmoglein-1	CAR s	197	4	36.4	10	22	AAJ01897	Hepatitis C virus	
125	4	36.4	9	23	ABR46266	Desmoglein-1	CAR s	198	4	36.4	10	22	AAJ02055	Hepatitis C virus	
126	4	36.4	9	23	ABR46267	Desmoglein-1	CAR s	199	4	36.4	10	22	AAJ02316	Hepatitis C virus	
127	4	36.4	9	23	ABR46272	Desmoglein-1	CAR s	200	4	36.4	10	22	AAJ02403	Hepatitis C virus	
128	4	36.4	9	23	ABR46279	Desmoglein-1	CAR s	201	4	36.4	10	22	AAJ02622	Hepatitis C virus	
129	4	36.4	9	23	ABR46289	Desmoglein-1	CAR s	202	4	36.4	10	22	AAJ02760	Hepatitis C virus	
130	4	36.4	9	23	ABR46290	Desmoglein-1	CAR s	203	4	36.4	10	22	AAJ03912	Hepatitis C virus	
131	4	36.4	9	23	ABR46294	Desmoglein-1	CAR s	204	4	36.4	10	22	AAJ286640	Cell adhesion mole	
132	4	36.4	9	23	ABR46295	Desmoglein-1	CAR s	205	4	36.4	10	23	AAU99409	Human ECSM4 peptid	
133	4	36.4	9	23	ABR46300	Desmoglein-1	CAR s	206	4	36.4	10	23	ABR45503	Desmoglein-3	CAR p
134	4	36.4	9	23	ABR46302	Desmoglein-1	CAR s	207	4	36.4	10	23	ABR45504	Desmoglein-3	CAR p
135	4	36.4	9	23	ABR46328	Desmoglein-1	CAR s	208	4	36.4	10	23	ABR45505	Desmoglein-3	CAR p
136	4	36.4	9	23	ABR46329	Desmoglein-1	CAR s	209	4	36.4	10	23	ABR45506	Desmoglein-3	CAR p
137	4	36.4	9	23	ABR46335	Desmoglein-1	CAR s	210	4	36.4	10	23	ABR46184	Desmoglein-1	CAR s
138	4	36.4	9	23	ABR46336	Desmoglein-1	CAR s	211	4	36.4	10	23	ABR46185	Desmoglein-1	CAR s
139	4	36.4	9	23	ABR46346	Desmoglein-3	CAR s	212	4	36.4	10	23	ABR46189	Desmoglein-1	CAR s
140	4	36.4	9	23	ABR46457	Desmoglein-3	CAR s	213	4	36.4	10	23	ABR46190	Desmoglein-1	CAR s
141	4	36.4	9	23	ABR46458	Desmoglein-3	CAR s	214	4	36.4	10	23	ABR46196	Desmoglein-1	CAR s
142	4	36.4	9	23	ABR46460	Desmoglein-3	CAR s	215	4	36.4	10	23	ABR46197	Desmoglein-1	CAR s
143	4	36.4	9	23	ABR46461	Desmoglein-3	CAR s	216	4	36.4	10	23	ABR46212	Desmoglein-1	CAR s
144	4	36.4	9	23	ABR46466	Desmoglein-3	CAR s	217	4	36.4	10	23	ABR46213	Desmoglein-1	CAR s
145	4	36.4	9	23	ABR46472	Desmoglein-3	CAR s	218	4	36.4	10	23	ABR46217	Desmoglein-1	CAR s
146	4	36.4	9	23	ABR46481	Desmoglein-3	CAR s	219	4	36.4	10	23	ABR46218	Desmoglein-1	CAR s
147	4	36.4	9	23	ABR46482	Desmoglein-3	CAR s	220	4	36.4	10	23	ABR46224	Desmoglein-1	CAR s
148	4	36.4	9	23	ABR46484	Desmoglein-3	CAR s	221	4	36.4	10	23	ABR46225	Desmoglein-1	CAR s
149	4	36.4	9	23	ABR46485	Desmoglein-3	CAR s	222	4	36.4	10	23	ABR46240	Desmoglein-1	CAR s
150	4	36.4	9	23	ABR46490	Desmoglein-3	CAR s	223	4	36.4	10	23	ABR46241	Desmoglein-1	CAR s
151	4	36.4	9	23	ABR46496	Desmoglein-3	CAR s	224	4	36.4	10	23	ABR46245	Desmoglein-1	CAR s
152	4	36.4	9	23	ABR46505	Desmoglein-3	CAR s	225	4	36.4	10	23	ABR46246	Desmoglein-1	CAR s
153	4	36.4	9	23	ABR46506	Desmoglein-3	CAR s	226	4	36.4	10	23	ABR46252	Desmoglein-1	CAR s
154	4	36.4	9	23	ABR46508	Desmoglein-3	CAR s	227	4	36.4	10	23	ABR46253	Desmoglein-1	CAR s
155	4	36.4	9	23	ABR46509	Desmoglein-3	CAR s	228	4	36.4	10	23	ABR46268	Desmoglein-1	CAR s
156	4	36.4	9	23	ABR46514	Desmoglein-3	CAR s	229	4	36.4	10	23	ABR46269	Desmoglein-1	CAR s

224	4	36.4	10	23	ABB46273	Desmoglein-1 CAR S	302	4	36.4	11	23	ABB46475	Desmoglein-3 CAR S
230	4	36.4	10	23	ABB46274	Desmoglein-1 CAR S	303	4	36.4	11	23	ABB46493	Desmoglein-3 CAR S
231	4	36.4	10	23	ABB46280	Desmoglein-1 CAR S	304	4	36.4	11	23	ABB46494	Desmoglein-3 CAR S
232	4	36.4	10	23	ABB46281	Desmoglein-1 CAR S	305	4	36.4	11	23	ABB46498	Desmoglein-3 CAR S
233	4	36.4	10	23	ABB46296	Desmoglein-1 CAR S	306	4	36.4	11	23	ABB46499	Desmoglein-3 CAR S
234	4	36.4	10	23	ABB46297	Desmoglein-1 CAR S	307	4	36.4	11	23	ABB46517	Desmoglein-3 CAR S
235	4	36.4	10	23	ABB46301	Desmoglein-1 CAR S	308	4	36.4	11	23	ABB46518	Desmoglein-3 CAR S
236	4	36.4	10	23	ABB46302	Desmoglein-1 CAR S	309	4	36.4	11	23	ABB46522	Desmoglein-3 CAR S
237	4	36.4	10	23	ABB46308	Desmoglein-1 CAR S	310	4	36.4	11	23	ABB46523	Desmoglein-3 CAR S
238	4	36.4	10	23	ABB46309	Desmoglein-1 CAR S	311	4	36.4	11	23	ABB46541	Desmoglein-3 CAR S
239	4	36.4	10	23	ABB46362	Desmoglein-3 CAR S	312	4	36.4	11	23	ABB46542	Desmoglein-3 CAR S
240	4	36.4	10	23	ABB46463	Desmoglein-3 CAR S	313	4	36.4	11	23	ABB46546	Desmoglein-3 CAR S
241	4	36.4	10	23	ABB46467	Desmoglein-3 CAR S	314	4	36.4	11	23	ABB46547	Desmoglein-3 CAR S
242	4	36.4	10	23	ABB46468	Desmoglein-3 CAR S	315	4	36.4	11	23	ABB46565	Desmoglein-3 CAR S
243	4	36.4	10	23	ABB46473	Desmoglein-3 CAR S	316	4	36.4	11	23	ABB46566	Desmoglein-3 CAR S
244	4	36.4	10	23	ABB46486	Desmoglein-3 CAR S	317	4	36.4	11	23	ABB46570	Desmoglein-3 CAR S
245	4	36.4	10	23	ABB46487	Desmoglein-3 CAR S	318	4	36.4	11	23	ABB46571	Desmoglein-3 CAR S
246	4	36.4	10	23	ABB46491	Desmoglein-3 CAR S	319	4	36.4	11	24	ABP60263	Synthetic peptide
247	4	36.4	10	23	ABB46492	Desmoglein-3 CAR S	320	4	36.4	12	20	AAW90055	Rhodococcus sp. M4
248	4	36.4	10	23	ABB46497	Desmoglein-3 CAR S	321	4	36.4	12	22	AAW65549	N-terminal modifie
249	4	36.4	10	23	ABB46510	Desmoglein-3 CAR S	322	4	36.4	12	23	AAW51191	HGF/SF antibody-b1
250	4	36.4	10	23	ABB46511	Desmoglein-3 CAR S	323	4	36.4	12	23	ABB46476	Desmoglein-3 CAR S
251	4	36.4	10	23	ABB46515	Desmoglein-3 CAR S	324	4	36.4	12	23	ABB46477	Desmoglein-3 CAR S
252	4	36.4	10	23	ABB46516	Desmoglein-3 CAR S	325	4	36.4	12	23	ABB46500	Desmoglein-3 CAR S
253	4	36.4	10	23	ABB46521	Desmoglein-3 CAR S	326	4	36.4	12	23	ABB46501	Desmoglein-3 CAR S
254	4	36.4	10	23	ABB46534	Desmoglein-3 CAR S	327	4	36.4	12	23	ABB46524	Desmoglein-3 CAR S
255	4	36.4	10	23	ABB46535	Desmoglein-3 CAR S	328	4	36.4	12	23	ABB46525	Desmoglein-3 CAR S
256	4	36.4	10	23	ABB46539	Desmoglein-3 CAR S	329	4	36.4	12	23	ABB46548	Desmoglein-3 CAR S
257	4	36.4	10	23	ABB46540	Desmoglein-3 CAR S	330	4	36.4	12	23	ABB46549	Desmoglein-3 CAR S
258	4	36.4	10	23	ABB46545	Desmoglein-3 CAR S	331	4	36.4	12	23	ABB46572	Desmoglein-3 CAR S
259	4	36.4	10	23	ABB46558	Desmoglein-3 CAR S	332	4	36.4	12	23	ABB46573	Desmoglein-3 CAR S
260	4	36.4	10	23	ABB46559	Desmoglein-3 CAR S	333	4	36.4	12	24	ABP60227	Synthetic peptide
261	4	36.4	10	23	ABB46563	Desmoglein-3 CAR S	334	4	36.4	13	20	AAV34065	Histone H1 isoform
262	4	36.4	10	23	ABB46564	Desmoglein-3 CAR S	335	4	36.4	13	21	AAV57363	Human histone H1.5
263	4	36.4	10	23	ABB46565	Desmoglein-3 CAR S	336	4	36.4	13	22	AAU04989	N-terminal peptide
264	4	36.4	10	23	ABB46597	Desmoglein-3 CAR S	337	4	36.4	13	22	AAW74179	BCL2 Bhl domain mu
265	4	36.4	10	23	ABB46598	Desmoglein-3 CAR S	338	4	36.4	13	23	AAU86049	Human glucocerebro
266	4	36.4	11	15	AAW55834	Meningococcal OMP	339	4	36.4	14	14	AAW32965	Mastoparan analogu
267	4	36.4	11	18	AAW34126	LiFA-1 beta subunit	340	4	36.4	14	14	AAW32978	Mastoparan analogu
268	4	36.4	11	18	AAW34129	LiFA-1 beta subunit	341	4	36.4	14	14	AAW32960	Mastoparan analogu
269	4	36.4	11	20	AAW74420	ILJ loop peptide KU	342	4	36.4	14	18	AAW32306	Leishmania immunog
270	4	36.4	11	20	AAW84054	Human V3 loop HIV	343	4	36.4	14	20	AAV55119	ATCC HB 11646 mono
271	4	36.4	11	22	AAJ00171	Hepatitis C virus	344	4	36.4	14	21	AAW26724	ATM kinase substra
272	4	36.4	11	22	AAJ00737	Hepatitis C virus	345	4	36.4	14	21	AAW86855	Human haematopoiet
273	4	36.4	11	22	AAJ01286	Hepatitis C virus	346	4	36.4	14	22	AAW98716	Human peptide #199
274	4	36.4	11	22	AAJ01538	Hepatitis C virus	347	4	36.4	14	22	AAW00343	Human protein frag
275	4	36.4	11	22	AAJ02159	Hepatitis C virus	348	4	36.4	14	22	AAW00344	Human protein frag
276	4	36.4	11	22	AAJ02474	Hepatitis C virus	349	4	36.4	14	24	ABP60225	Synthetic peptide
277	4	36.4	11	22	AAJ02672	Hepatitis C virus	350	4	36.4	15	18	AAW29480	Peptide #1 derived
278	4	36.4	11	22	AAJ02807	Hepatitis C virus	351	4	36.4	15	18	AAW29481	Peptide #2 derived
279	4	36.4	11	23	AAW46191	Desmoglein-1 CAR S	352	4	36.4	15	18	AAW29486	Peptide #7 derived
280	4	36.4	11	23	AAW46192	Desmoglein-1 CAR S	353	4	36.4	15	18	AAW29488	Peptide #9 derived
281	4	36.4	11	23	AAW46198	Desmoglein-1 CAR S	354	4	36.4	15	18	AAW38936	Peptide resembling
282	4	36.4	11	23	AAW46199	Desmoglein-1 CAR S	355	4	36.4	15	20	AAV34043	Histone H1S-3 deri
283	4	36.4	11	23	AAW46219	Desmoglein-1 CAR S	356	4	36.4	15	20	AAV34044	Histone H1S-3 deri
284	4	36.4	11	23	AAW46220	Desmoglein-1 CAR S	357	4	36.4	15	20	AAV34050	Histone H1S-3 deri
285	4	36.4	11	23	AAW46225	Desmoglein-1 CAR S	358	4	36.4	15	20	AAV34052	Histone H1S-3 deri
286	4	36.4	11	23	AAW46227	Desmoglein-1 CAR S	359	4	36.4	15	20	AAV34063	Histone H1 isoform
287	4	36.4	11	23	AAW46247	Desmoglein-1 CAR S	360	4	36.4	15	20	AAV34064	Histone H1 isoform
288	4	36.4	11	23	AAW46248	Desmoglein-1 CAR S	361	4	36.4	15	20	AAW73962	Antigenic fragment
289	4	36.4	11	23	AAW46254	Desmoglein-1 CAR S	362	4	36.4	15	21	AAV98869	HLA class II bindi
290	4	36.4	11	23	AAW46255	Desmoglein-1 CAR S	363	4	36.4	15	21	AAV98870	HLA class II bindi
291	4	36.4	11	23	AAW46275	Desmoglein-1 CAR S	364	4	36.4	15	21	AAV57341	Human histone H1 p
292	4	36.4	11	23	AAW46276	Desmoglein-1 CAR S	365	4	36.4	15	21	AAV57342	Human histone H1 p
293	4	36.4	11	23	AAW46282	Desmoglein-1 CAR S	366	4	36.4	15	21	AAV57348	Human histone H1 p
294	4	36.4	11	23	AAW46283	Desmoglein-1 CAR S	367	4	36.4	15	21	AAV57350	Human histone H1 p
295	4	36.4	11	23	AAW46303	Desmoglein-1 CAR S	368	4	36.4	15	21	AAV57361	Human histone H1.5
296	4	36.4	11	23	AAW46304	Desmoglein-1 CAR S	369	4	36.4	15	21	AAV57362	Human histone H1.5
297	4	36.4	11	23	AAW46310	Desmoglein-1 CAR S	370	4	36.4	15	22	AAW64552	Human sugar transp
298	4	36.4	11	23	AAW46311	Desmoglein-1 CAR S	371	4	36.4	15	22	AAW64608	Human X chromosome
299	4	36.4	11	23	AAW46319	Desmoglein-3 CAR S	372	4	36.4	15	22	AAW88656	HER2/NEU DR superm
300	4	36.4	11	23	AAW46340	Desmoglein-3 CAR S	373	4	36.4	15	22	AAW89039	Her2/neu DR superm
301	4	36.4	11	23	AAW463474	Desmoglein-3 CAR S	374	4	36.4	15	22	AAW89040	Her2/neu DR superm


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XX OS Synthetic.
XX AC WO2000:8801-A2.
XX DT 06 APR-2000.
XX DE 23 SEP-1999; 99WO-DK00500.
XX PF 29 SEP 1998; 98DK-0001232.
XX PR 29 APR-1999; 99DK-0000592.
XX XX
XX PA (RONN/) RONN L C B.
XX PA (BOCK/) BOCK E.
XX PA (HOLM/) HOLM A.
XX PA (OLSE/) OLSEN M.
XX PA (OSTE/) OSTERGAARD S.
XX PA (JENS/) JENSEN P H.
XX PA (POUL/) POULSEN F M.
XX PA (SORO/) SOROKA V.
XX PA (RALE/) RALETS I.
XX PA (BERE/) BEREZIN V.
XX XX
XX PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
XX PI Poulsen FM, Soroka V, Ralets I, Berezin V;
XX XX
XX DR WPI: 2000-29311/25.
XX XX
XX PT Compositions that bind neural cell adhesion molecules useful for
XX PT treating disorders of the nervous system and muscles e.g. Alzheimer's
XX PT and Parkinson's diseases
XX XX
XX PS Claim 20; page 82; 119pp; English.
XX XX
XX CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
XX CC NCAM is found in three forms, two of which are transmembrane forms, while
XX CC the third is attached via a lipid anchor to the cell membrane. All three
XX CC NCAM forms have an extracellular structure consisting five immunoglobulin
XX CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the
XX CC N-terminal. The present sequence represents a peptide which binds to the
XX CC NCAM Ig1 domain. The peptide can be used in a compound which binds to
XX CC NCAM-Ig1/Ig2 domains, and is capable of stimulating or promoting neurite
XX CC outgrowth from NCAM presenting cells, and is also capable of promoting the
XX CC proliferation of NCAM presenting cells. The compound may be used in
XX CC the treatment of normal, degenerated or damaged NCAM presenting cells.
XX CC The compound may in particular be used to treat diseases of the central
XX CC and peripheral nervous systems such as post operative nerve damage,
XX CC traumatic nerve damage, impaired myelination of nerve fibres, conditions
XX CC resulting from a stroke, Parkinson's disease, Alzheimer's disease,
XX CC dementia, sclerosis, nerve degeneration associated with diabetes,
XX CC mellitus, disorders affecting the circadian clock or neuro-muscular
XX CC transmission and schizophrenia. Conditions affecting the muscles may also
XX CC be treated with the compound, such as conditions associated with impaired
XX CC function of neuromuscular connections (e.g. genetic or traumatic shock or
XX CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
XX CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
XX CC liver and bowel may also be treated using the compound. The compound is
XX CC learn, and to stimulate the memory of a subject.
XX XX
XX SC Sequence 11 AA:
XX
XX Query Match 100.0%; Score 11; Lb 21; Length 11;
XX Best Local Similarity 100.0%; Fred. No. 1.4e-05;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AKALNWGAKPK 11
XX DB 1 AKALNWGAKPK 11
XX
XX RESULT 2
XX AAY88563

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ID AAY88563 standard: peptide: 11 AA.
XX AC AAY88563;
XX DT 07-AUG-2000 (first entry)
XX DE NCAM Ig1 binding peptide D4 used as a control peptide.
XX XX
XX KW NCAM: neural cell adhesion molecule; Ig1: immunoglobulin domain 1;
XX KW neurite outgrowth promoter; proliferation; nerve damage; sclerosis;
XX KW impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;
XX KW Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;
XX KW treatment; prosthetic nerve guide; treatment; nervous system.
XX OS Synthetic.
XX PN WO2000:8801-A2.
XX XX
XX PD 06-APR-2000.
XX XX
XX PF 23-SEP-1999; 99WO-DK00500.
XX XX
XX PR 29-SEP-1998; 98DK-0001232.
XX PR 29-APR-1999; 99DK-0000592.
XX XX
XX PA (RONN/) RONN L C B.
XX PA (BOCK/) BOCK E.
XX PA (HOLM/) HOLM A.
XX PA (OLSE/) OLSEN M.
XX PA (OSTE/) OSTERGAARD S.
XX PA (JENS/) JENSEN P H.
XX PA (POUL/) POULSEN F M.
XX PA (SORO/) SOROKA V.
XX PA (RALE/) RALETS I.
XX PA (BERE/) BEREZIN V.
XX XX
XX PI Ronn LCB, Bock E, Holm A, Olsen M, Ostergaard S, Jensen PH;
XX PI Poulsen FM, Soroka V, Ralets I, Berezin V;
XX XX
XX DR WPI: 2000-29311/25.
XX XX
XX PT Compositions that bind neural cell adhesion molecules useful for
XX PT treating disorders of the nervous system and muscles e.g. Alzheimer's
XX PT and Parkinson's diseases
XX PS Example 5; Fig 7; 119pp; English.
XX XX
XX CC Neural cell adhesion molecule (NCAM) is a cellular adhesion molecule.
XX CC NCAM is found in three forms, two of which are transmembrane forms, while
XX CC the third is attached via a lipid anchor to the cell membrane. All three
XX CC NCAM forms have an extracellular structure consisting five immunoglobulin
XX CC domains (Ig domains). The Ig domains are numbered 1 to 5 from the
XX CC N-terminal. The invention relates to a compound containing a peptide
XX CC which binds to the NCAM Ig1 domain. The compound binds to NCAM-Ig1/Ig2
XX CC domains, and is capable of stimulating or promoting neurite outgrowth
XX CC from NCAM presenting cells, and is also capable of promoting the
XX CC proliferation of NCAM presenting cells. The present sequence represents a
XX CC control peptide used in the identification of those binding peptides
XX CC which can be used in the compound. The compound may be used in the
XX CC treatment of normal, degenerated or damaged NCAM presenting cells. The
XX CC compound may in particular be used to treat diseases of the central and
XX CC peripheral nervous systems such as post operative nerve damage, traumatic
XX CC nerve damage, impaired myelination of nerve fibres, conditions resulting
XX CC from a stroke, Parkinson's disease, Alzheimer's disease, dementia,
XX CC sclerosis, nerve degeneration associated with diabetes mellitus,
XX CC disorders affecting the circadian clock or neuro-muscular transmission
XX CC and schizophrenia. Conditions affecting the muscles may also be treated
XX CC with the compound, such as conditions associated with impaired function
XX CC of neuromuscular connections (e.g. genetic or traumatic shock or
XX CC traumatic atrophic muscle disorders). Conditions of the gonads, pancreas
XX CC (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
XX CC liver and bowel may also be treated using the compound. The compound is
XX CC used in a prosthetic nerve guide, and also to stimulate the ability to

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CC learn, and to stimulate the memory of a subject.

XX Sequence 11 AA;
SQ
Query Match 100.0%; Score 11; DB 21; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARAALNWGAKPK 11
DB 1 ARAALNWGAKPK 11

RESULT 4
AB659331
ID ARG69331 standard; Peptide: 11 AA.
XX AC ARG69331;
XX DT 21-OCT-2002 (first entry)
XX DE Human neural cell adhesion molecule (NCAM) peptide #3
XX KW Human: neural cell adhesion molecule; NCAM; heart muscle cell survival;
KW acute myocardial infarction; central nervous system disorder; stroke;
KW peripheral nervous system disorder; postoperative nerve damage;
KW traumatic nerve damage; spinal cord injury; nerve fiber; schizophrenia;
KW postischemic damage; multifactorial dementia; multiple sclerosis;
KW nerve degeneration; diabetes mellitus; neuro-muscular degeneration;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease;
KW atrophic muscle disorder; gonad degeneration; nephrosis.

XX OS Homo sapiens.
XX WO200247719-A2.
XX DT 20-JUN-2002.
XX PD 12-DEC-2001; 2001WO-DK00822.
XX PF 12-DEC-2000; 2000DK-0001863.
XX PR (ENKA) ENKAM PHARM AS.
XX PA Roek E. Berezin V. Kohler LB;
XX DT 2002-583473/62.
XX WIPI: 2002-583473/62.

XX Use of a compound comprising a peptide of neural cell adhesion molecule, in the preparation of a medicament for prevention death of cells presenting NCAM or NCAM ligand and related central nervous system diseases

XX Claim 26; Page 39; 57pp; English.

XX The invention relates to use of a compound (1) comprising a peptide which comprises at least 5 contiguous amino acid residues of a sequence of the neural cell adhesion molecule (NCAM), its fragment, variant or its mimic, for the preparation of a medicament for preventing death of cells presenting the NCAM or an NCAM ligand (1) is useful in the preparation of a medicament for preventing death of cells presenting the NCAM or an NCAM ligand. The medicament is for the stimulation of the survival of heart muscle cells, such as survival after acute myocardial infarction. The medicament is for the treatment of diseases or conditions of the central and peripheral nervous system, such as postoperative nerve damage, traumatic nerve damage, etc. resulting from spinal cord injury. Impaired myelination of nerve fibres, postischemic damage, etc. resulting from a stroke, multifactorial dementia, multiple sclerosis, nerve degeneration associated with diabetes mellitus, neuro-muscular degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease and Huntington's disease. The medicament is for the treatment of diseases or conditions of the muscles including conditions with impaired function of neuro-muscular connections, such as genetic or traumatic atrophic

CC muscle disorders, and for the treatment of diseases of conditions of various organs, such as degenerative conditions of the gonads, pancreas (e.g. diabetes mellitus type I and II) and kidney (e.g. nephrosis).
CC AB659329-AB659352 represent human NCAM peptides of the invention.

XX SQ Sequence 11 AA;
Query Match 100.0%; Score 11; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARAALNWGAKPK 11
DB 1 ARAALNWGAKPK 11

RESULT 4
AAW75820
ID AAW75820 standard; peptide: 11 AA.
XX AC AAW75820;
XX DT 27-OCT-1998 (first entry)
XX DE Mouse mast cell protease (mMCP-6) susceptible peptide 14.
XX KW Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma;
KW trypsinase-6 protein; inflammatory disorder; allergic rhinitis; urticaria;
KW antioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis;
KW hyperproliferative skin disease; peptic ulcer; hyperresponsiveness;
KW inflammatory skin condition.

XX CS Synthetic.
XX OS Mus SP.
XX PN WO9833812 A1.
XX PD 06-AUG-1998.
XX PF 30-JAN-1998; 98WO-0501865.
XX PR 05-FEB-1997; 97JS-0037090.
XX PA (BGM) BRIGHAM 6 WOMENS HOSPITAL.
XX DT Huang C. Stevens RL;
XX WIPI: 1998-437390/37.
XX DT Trypsinase 6 complex inhibitory peptides - used to treat mast cell-mediated inflammatory disorders e.g. asthma
XX Examples: Page 26; 69pp; English.

XX Sequences shown in AAW75807 to AAW75835 represent mouse mast cell protease (mMCP-6) susceptible peptides obtained in the absence of heparin. The invention provides sequences shown in AAW63160 to AAW63169 that are inhibitors of mMCP-6. These trypsinase-6 complex inhibitor peptides can be used for treating a mast cell-mediated inflammatory disorder. The inhibitors can be used to treat inflammatory disorders including asthma, allergic rhinitis, urticaria and antioedema, eczematous dermatitis (atopic dermatitis), hyperproliferative skin disease, anaphylaxis, peptic ulcers, inflammatory bowel disorder, hyperresponsiveness and inflammatory skin conditions.

XX SQ Sequence 11 AA;
Query Match 36.4%; Score 4; DB 19; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARAAL 4
DB 1

```

DB      4 ARAL 7

RESULT 5
AAJ01170
ID      AAJ01170 standard; Peptide; 8 AA.
AC      AAJ01170.
XX
XX      02-JUL-2001 (first entry)
XX
XX      Hepatitis C virus epitope #116.
XX
XX      Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA binding motif;
KW      antiviral.
XX
XX      Hepatitis C virus.
OS
XX      WO200121189-A1.
PN
XX      29-MAR-2001.
PD
XX
XX      19-JUL-2000; 2000WO-US19774.
XX
XX      19-JUL-1999; 99US-0357737.
XX      (EPIM ) EPIIMMUNE INC.
XX
XX      Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI      Baker DM, Cellis E, Kubo RT, Grey HM;
XX
XX      WPI: 2001-308046/32.
XX
XX      A new composition useful as a vaccines against hepatitis C virus -
PT
XX      Disclosure; Page 130; 214pp; English.
PS
XX      The present invention describes a composition comprising a prepared
CC      hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC      These are derived from HCV HLA-binding motifs. They are useful in
CC      vaccines for the prevention and treatment of HCV infection in humans. The
CC      present sequence is an epitope used in the disclosure of the invention.
XX
XX      Sequence 8 AA;
SQ
XX
XX      Query Match      36.4%; Score 4; DB 22; Length 8;
XX      Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARAL 4
DB      1 ARAL 4

RESULT 6
AAJ02158
ID      AAJ02158 standard; Peptide; 8 AA.
AC      AAJ02158.
XX
XX      02-JUL 2001 (first entry)
XX
XX      Hepatitis C virus epitope #2149.
XX
XX      Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW      antiviral.
XX
XX      Hepatitis C virus.
OS
XX      WO200121189-A1.
PN
XX      29-MAR-2001.
PD
XX
XX      19-JUL-2000; 2000WO-US19774.
XX
XX      19-JUL-1999; 99US-0357737.
XX      (EPIM-) EPIIMMUNE INC.
XX
XX      Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI      Baker DM, Cellis E, Kubo RT, Grey HM;
XX
XX      WPI: 2001-308046/32.
XX
XX      A new composition useful as a vaccines against hepatitis C virus -
PT
XX      Disclosure; Page 154; 214pp; English.
PS
XX      The present invention describes a composition comprising a prepared
CC      hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC      These are derived from HCV HLA-binding motifs. They are useful in
CC      vaccines for the prevention and treatment of HCV infection in humans. The
CC      present sequence is an epitope used in the disclosure of the invention.
XX
XX      Sequence 8 AA;
SQ
XX
XX      Query Match      36.4%; Score 4; DB 22; Length 8;
XX      Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARAL 4
DB      1 ARAL 4

RESULT 7
AAJ02181
ID      AAJ02181 standard; Peptide; 8 AA.
AC      AAJ02181.
XX
XX      02-JUL-2001 (first entry)
XX
XX      Hepatitis C virus epitope #2172.
XX
XX      Hepatitis C virus; HCV; epitope; vaccine; immunogen; HLA-binding motif;
KW      antiviral.
XX
XX      Hepatitis C virus.
OS
XX      WO200121189-A1.
PN
XX      29-MAR-2001.
PD
XX
XX      19-JUL-2000; 2000WO-US19774.
XX
XX      19-JUL-1999; 99US-0357737.
XX      (EPIM-) EPIIMMUNE INC.
XX
XX      Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI      Baker DM, Cellis E, Kubo RT, Grey HM;
XX
XX      WPI: 2001-308046/32.
XX
XX      A new composition useful as a vaccines against hepatitis C virus -
PT
XX      Disclosure; Page 154; 214pp; English.
PS
XX      The present invention describes a composition comprising a prepared
CC      hepatitis C virus (HCV) epitope such as those given in AAJ00010-AAJ04121.
CC      These are derived from HCV HLA-binding motifs. They are useful in
CC      vaccines for the prevention and treatment of HCV infection in humans. The
CC      present sequence is an epitope used in the disclosure of the invention.
XX
XX      Sequence 8 AA;
SQ

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Query Match          36.4%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
DB 4 ARAL 7

RESULT 8
ID AAJ02671 standard; Peptide: 8 AA.
XX AC AAJ02671;
XX DT 02-JUL-2001 (first entry)
XX DE Hepatitis C virus epitope #2662.
XX KW Hepatitis C virus; HCV; epitope: vaccine; immunization; HLA binding motif;
XX KW antiviral.
XX OS Hepatitis C virus.
XX PN W020012189-A1.
XX PD 29 MAR 2001.
XX PF 19-JUL-2000; 2000WO-US19774.
XX PR 19-JUL-1999; 99US-0357737.
XX PA (EPIM-) EPIMUNE INC.
XX PI Sette A, Sidney J, Southwood S, Livingston BB, Chesnut R;
XX PI Baker DM, Cells E, Kubo RT, Grey HM;
XX WK WPI: 2001-109046/32.
XX PI A new composition useful as a vaccine against hepatitis C virus
XX PS Disclosure: Page 166; 214pp; English.
XX CC The present invention describes a composition comprising a prepared
XX CC hepatitis C virus (HCV) epitope such as those given in AAJ03010-AAJ04121.
XX CC These are derived from HCV HLA-binding motifs. They are useful in
XX CC vaccines for the prevention and treatment of HCV infection in humans. The
XX CC present sequence is an epitope used in the disclosure of the invention.
XX SQ Sequence 8 AA;

Query Match          36.4%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
DB 3 ARAL 6

RESULT 9
ID ABB84505 standard; Protein; 8 AA.
XX AC ABB84505;
XX DT 09-JAN-2003 (first entry)
XX DE Encephalomyocarditis virus autocatalytic peptide cleavage site #2.
XX KW Replicon; structural region; vaccine; subgenomic replicon; gene therapy;
XX KW structural protein; C protein; PreM protein; E protein; immunisation.

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XX OS Encephalomyocarditis virus.
XX PN W0200272803-A2.
XX PD 19-SEP-2002.
XX PF 21-FEB-2002; 2002WO-US06962.
XX PR 09-MAR-2001; 2001US-274584P.
XX PA (USSR) US DEPT HEALTH & HUMAN SERVICES.
XX PI Pang X, Dayton AI, Zhang M;
XX PD WPI: 2002-723344/78.
XX DT New subgenomic replicon of dengue virus origin comprising a deletion
XX DT for the sequence coding for C, PreM and/or E structural proteins
XX DT useful as vaccines for immunization against dengue virus infection
XX PS Disclosure: Page 12; 66pp; English.
XX CC This invention describes a novel subgenomic replicon of dengue virus
XX CC origin comprising a deletion for the sequence coding for C, PreM and E
XX CC (DeltaCME), for PreM and E (DeltaME), or for E (DeltaE) structural
XX CC proteins, and/or which is adapted to receive at least a nucleotide
XX CC sequence without disrupting its replication capabilities. The products
XX CC of the invention can be used for constructing (1) a vaccine or a
XX CC therapeutic comprising the subgenomic replicon and a carrier; (2) a
XX CC dengue virus-like particle comprising the subgenomic replicon, and
XX CC structural proteins of the homologous dengue virus, which encapsulates
XX CC the subgenomic replicon; and (3) methods of immunisation and treatment
XX CC comprising administering to the individual the subgenomic replicon or
XX CC the dengue virus like particle cited above. The subgenomic replicons are
XX CC useful in gene therapy as vaccines for immunisation against dengue virus
XX CC infection. This sequence represents an Encephalomyocarditis virus strain
XX CC B autocatalytic peptide cleavage site which can be added to the
XX CC subgenomic replicon of the invention to optimise expression of desired
XX CC foreign proteins.
XX SQ Sequence 8 AA;

Query Match          36.4%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 4 AKPK 7

RESULT 10
ID AAG79508 standard; peptide: 8 AA.
XX AC AAG79508;
XX DT 29-NOV-2002 (first entry)
XX DE C. trachomatis epitopic peptide #1.
XX KW Epitope: Chlamydia trachomatis; serovar; medicine; infection; human.
XX KW Chlamydia trachomatis.
XX OS Chlamydia trachomatis.
XX PN W0200265129-A2.
XX PD 22-AUG-2002.
XX PF 12-FEB-2002; 2002WO-GB00600.
XX PR 12-FEB-2001; 2001GB-0003387.

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CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue. For enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.

XX
 SQ Sequence 8 AA:

Query Match 36.4% Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 IIII
 DB 3 RALN 6

RESULT 13
 ABB45448
 ID ABB45448 standard; Peptide: 8 AA.
 AC ABB45448;
 DT 10 JAN-2002 (first entry)
 DE Desmoglein 1 CAR peptide SEQ ID No 167.
 KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis;
 XX Synthetic;
 OS W:2003172956-A2.
 PN 04-OCT 2001.
 PP 27-MAR-2001; 2001WO-1851400.
 XX 27-MAR-2003; 2000US-0535852.
 PA (ADBE) ADHEREX TECHNOLOGIES INC.
 PI Blaschuk OW, Symonds JM, Gour RJ;
 XX WPI: 2002-025778/03.
 DR
 XX
 PT Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis.
 XX
 PS Claim 15; Page 95; 127pp; English.

The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45441-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.

XX
 SQ Sequence 8 AA:

Query Match 36.4% Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 IIII
 DB 3 RALN 6

RESULT 15
 ABB45455

Query Match 36.4% Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 IIII
 DB 3 RALN 6

RESULT 14
 ABB45449
 ID ABB45449 standard; Peptide: 8 AA.
 AC ABB45449;
 DT 30-JAN-2002 (first entry)
 DE Desmoglein 1 CAR peptide SEQ ID No 168.
 KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis;
 XX Synthetic;
 OS W:2003172956-A2.
 PN 04-OCT 2001.
 PP 27-MAR-2001; 2001WO-1851400.
 XX 27-MAR-2003; 2000US-0535852.
 PA (ADBE) ADHEREX TECHNOLOGIES INC.
 PI Blaschuk OW, Symonds JM, Gour RJ;
 XX WPI: 2002-025778/03.
 DR
 XX
 PT Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis.
 XX
 PS Claim 15; Page 95; 127pp; English.

The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45441-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.

XX
 SQ Sequence 8 AA:

Query Match 36.4% Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 IIII
 DB 3 RALN 6

RESULT 15
 ABB45455

XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX Blaschuk OW, Symonds JM, Gour BJ;
 XX WPI: 2002-025778/03.
 XX
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX
 XX Claim 15; Page 96; 127pp; English.
 XX
 XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 XX Sequence 8 AA;
 XX
 XX Query Match 36.4%; Score 4; DB 23; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 2 RALN 5
 XX IIII
 XX Db 2 RALN 5
 XX
 XX RESULT 18
 XX ABB45490
 XX ID ABB45490 standard; Peptide: 8 AA.
 XX AC ABB45490;
 XX DT 30-JAN-2002 (first entry)
 XX DE Desmoglein-3 CAR peptide SEQ ID NO 205.
 XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis.
 XX OS Synthetic.
 XX PN WO200172956-A2.
 XX PD 04-OCT-2001.
 XX PF 27-MAR-2001; 2001WO-1B01400.
 XX PR 27-MAR-2000; 2000US-0535852.
 XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX PI Blaschuk OW, Symonds JM, Gour BJ;
 XX WPI: 2002-025778/03.
 XX
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX

PS Claim 15; Page 96; 127pp; English.
 XX
 XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 XX Sequence 8 AA;
 XX
 XX Query Match 36.4%; Score 4; DB 23; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 2 RALN 5
 XX IIII
 XX Db 2 RALN 5
 XX
 XX RESULT 19
 XX ABB45494
 XX ID ABB45494 standard; Peptide: 8 AA.
 XX AC ABB45494;
 XX DT 30-JAN-2002 (first entry)
 XX DE Desmoglein-3 CAR peptide SEQ ID NO 213.
 XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis.
 XX OS Synthetic.
 XX PN WO200172956-A2.
 XX PD 04-OCT-2001.
 XX PF 27-MAR-2001; 2001WO-1B01400.
 XX PR 27-MAR-2000; 2000US-0535852.
 XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX PI Blaschuk OW, Symonds JM, Gour BJ;
 XX WPI: 2002-025778/03.
 XX
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX
 XX Claim 15; Page 96; 127pp; English.
 XX
 XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to

CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA;

Query Match

Best Local Similarity 36.4%; Score 4; DB 23; Length 8;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 III
 DB 3 RALN 6

RESULT 20

ABB45495
 ID ABB45495 standard; Peptide: 8 AA.

AC ABB45495;

DT 10-JAN-2002 (first entry)

DE Desmoqlein-3 CAR peptide SEQ ID NO 214

XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytotatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis.

XX Synthetic.

OS WO200172956-A2.

PN 04-OCT-2001.

XX 27-MAR-2001; 2001WO-IB01400.

XX 27-MAR-2000; 2000US-0535852.

PR (ADHE-) ADHEREX TECHNOLOGIES INC.

PA Blaschuk GW, Symonds JM, Gour BJ,

XX WPI; 2002-025778/03.

XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PI mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -

XX Claim 15; Page 96; 127pp; English.

XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX

SQ Sequence 8 AA;

Query Match

Best Local Similarity 36.4%; Score 4; DB 23; Length 8;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 III
 DB 3 RALN 6

RESULT 21

ABB45500
 ID ABB45500 standard; Peptide: 8 AA.

AC ABB45500;

DT 30-JAN-2002 (first entry)

DE Desmoqlein-3 CAR peptide SEQ ID NO 219.

XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytotatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis.

XX Synthetic.

OS WO200172956-A2.

PN 04-OCT-2001.

XX 27-MAR-2001; 2001WO-IB01400.

XX 27-MAR-2000; 2000US-0535852.

PR (ADHE-) ADHEREX TECHNOLOGIES INC.

PA Blaschuk GW, Symonds JM, Gour BJ,

XX WPI; 2002-025778/03.

XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PI mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -

XX Claim 15; Page 96; 127pp; English.

XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.

SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 23; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 III
 DB 4 RALN 7

RESULT 22

ABB46175
 ID ABB46175 standard; Peptide: 8 AA.

AC ABB46175;

XX

```

DT 30-JAN-2002 (first entry)
DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 919.
XX
XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
KW skin graft; organ implant; autoimmune blistering disorder; cancer;
KW apoptosis; cyclic.
XX
OS Synthetic.
XX
XX WO200172956-A2.
XX
XX PD 04-OCT-2001.
XX
XX PF 27-MAR-2001; 2001WO-1B01400.
XX
XX PR 27-MAR-2000; 2000US-0535852.
XX
XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX PI Blaschuk OW, Symonds JM, Gout BJ;
XX WPI: 2002-025778/03.
XX
XX PT Modulating agents for inhibiting or enhancing desmosomal cadherin
PT mediated cell adhesion, useful for facilitating wound healing and/or
PT reducing scar tissue, treating cancer and inducing apoptosis.
XX
XX PS Claim 18; Page 100; 127pp; English.
XX
XX CC The invention relates to modulating agents for inhibiting or enhancing
CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
CC (AB45341-AB47262), a non-peptide mimetic of a desmosomal cadherin CAR
CC sequence, a substance such as an antibody or antigen-binding fragment
CC that specifically binds a desmosomal cadherin CAR sequence and/or a
CC polynucleotide encoding a polypeptide that comprises a desmosomal
CC cadherin CAR sequence or analogue. The modulating agents have
CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
CC facilitate wound healing and/or reduce scar tissue, for enhancing
CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
CC treating an autoimmune blistering disorder and to treat cancer
CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX
XX SQ Sequence 8 AA;
XX
XX Query Match 36.4%; Score 4; DB 23; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 RAIN 5
XX IIII
XX DB 2 RAIN 5
XX
XX RESULT 24
XX AB45181
XX ID AB45181 Standard; Peptide; # AA.
XX
XX AC AB45181;
XX
XX DT 30-JAN-2002 (first entry)
XX
XX DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 925.
XX
XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
KW skin graft; organ implant; autoimmune blistering disorder; cancer;
KW apoptosis; cyclic.
XX
XX OS Synthetic.
XX
XX XX WO200172956-A2.
XX
XX XX PD 04-OCT-2001.
XX
XX XX PF 27-MAR-2001; 2001WO-1B01400.
XX
XX XX PR 27-MAR-2000; 2000US-0535852.
XX
XX XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
XX
XX XX PI Blaschuk OW, Symonds JM, Gout BJ;

```

XX WPI: 2002-025778/03.
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer, and inducing apoptosis.
 XX Claim 18: Page 100; 127pp; English.
 XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX Sequence 8 AA:
 SQ
 Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RALN 5
 ID IIII
 DB 3 RALN 6
 Desmoqlein-1 CAR sequence cyclic peptide SEQ ID NO 931.
 Desmosomal cadherin: cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX Synthetic.
 XX WO200172956-A2.
 XX 04-OCT-2001.
 XX 27-MAR-2001; 2001WO-1B01400.
 XX 27-MAR-2000; 2000US-0535852.
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX Blaschuk OW, Symonds JM, Gour BJ;
 WPI: 2002-025778/03.
 Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer, and inducing apoptosis.
 XX Claim 18: Page 100; 127pp; English.
 XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX Sequence 8 AA:
 SQ
 Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RALN 5
 ID IIII
 DB 3 RALN 6
 Desmoqlein-1 CAR sequence cyclic peptide SEQ ID NO 931.
 Desmosomal cadherin: cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX Synthetic.
 XX WO200172956-A2.
 XX 04-OCT-2001.
 XX 27-MAR-2001; 2001WO-1B01400.
 XX 27-MAR-2000; 2000US-0535852.
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX Blaschuk OW, Symonds JM, Gour BJ;
 WPI: 2002-025778/03.
 Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer, and inducing apoptosis.
 XX Claim 18: Page 100; 127pp; English.
 XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent

CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX Sequence 9 AA:
 SQ
 Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RALN 5
 ID IIII
 DB 4 RALN 7
 Desmoqlein-1 CAR sequence cyclic peptide SEQ ID NO 938.
 Desmosomal cadherin: cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX Synthetic.
 XX WO200172956-A2.
 XX 04-OCT-2001.
 XX 27-MAR-2001; 2001WO-1B01400.
 XX 27-MAR-2000; 2000US-0535852.
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX Blaschuk OW, Symonds JM, Gour BJ;
 WPI: 2002-025778/03.
 Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis.
 XX Claim 18: Page 100; 127pp; English.
 XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.


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XX SQ Sequence 8 AA:
Query Match 36.4%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
DB 4 RALN 7

RESULT 27
ABB46203
ID ABB46203 standard; Peptide: 8 AA.
XX AC ABB46203;
XX DT 30-JAN-2002 (first entry)
XX DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 947.
XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
XX KW cytosstatic; antiapoptotic; wound healing; reduce scar tissue;
XX KW skin graft; organ implant; autoimmune blistering disorder; cancer;
XX KW apoptosis; cyclic.
XX OS Synthetic.
XX PN WO200172956-A2.
XX PD 04-OCT 2001.
XX PF 27-MAR-2001; 2001WO-1B01400.
XX PR 27-MAR-2000; 2000US-0535852.
XX PA (ADHEX) ADHEREX TECHNOLOGIES INC.
XX PI Blaschuk OW, Symonds JM, Gour RJ;
XX DR WPI: 2002-025778/G3.
XX PT Modulating agents for inhibiting or enhancing desmosomal cadherin
XX PT mediated cell adhesion, useful for facilitating wound healing and/or
XX PT reducing scar tissue, treating cancer and inducing apoptosis.
XX PS Claim 13; Page 100; 127pp; English.
XX CC The invention relates to modulating agents for inhibiting or enhancing
XX CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
XX CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
XX CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
XX CC sequence, a substance such as an antibody or antigen-binding fragment
XX CC that specifically binds a desmosomal cadherin CAR sequence and/or a
XX CC polynucleotide encoding a desmosomal cadherin CAR sequence and/or a
XX CC cadherin CAR sequence or analogue. The modulating agents have
XX CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
XX CC facilitate wound healing and/or reduce scar tissue, for enhancing
XX CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
XX CC treating an autoimmune blistering disorder and to treat cancer
XX CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX SQ Sequence 8 AA:
Query Match 36.4%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
DB 2 RALN 5

RESULT 28
ABB46204
ID ABB46204 standard; Peptide: 8 AA.
XX AC ABB46204;
XX DT 30-JAN-2002 (first entry)
XX DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 948.
XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
XX KW cytosstatic; antiapoptotic; wound healing; reduce scar tissue;
XX KW skin graft; organ implant; autoimmune blistering disorder; cancer;
XX KW apoptosis; cyclic.
XX OS Synthetic.
XX PN WO200172956-A2.
XX PD 04-OCT 2001.
XX PF 27-MAR-2001; 2001WO-1B01400.
XX PR 27-MAR-2000; 2000US-0535852.
XX PA (ADHEX) ADHEREX TECHNOLOGIES INC.
XX PI Blaschuk OW, Symonds JM, Gour RJ;
XX DR WPI: 2002-025778/G3.
XX PT Modulating agents for inhibiting or enhancing desmosomal cadherin
XX PT mediated cell adhesion, useful for facilitating wound healing and/or
XX PT reducing scar tissue, treating cancer and inducing apoptosis.
XX PS Claim 18; Page 100; 127pp; English.
XX CC The invention relates to modulating agents for inhibiting or enhancing
XX CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
XX CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
XX CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
XX CC sequence, a substance such as an antibody or antigen-binding fragment
XX CC that specifically binds a desmosomal cadherin CAR sequence and/or a
XX CC polynucleotide encoding a desmosomal cadherin CAR sequence and/or a
XX CC cadherin CAR sequence or analogue. The modulating agents have
XX CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
XX CC facilitate wound healing and/or reduce scar tissue, for enhancing
XX CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
XX CC treating an autoimmune blistering disorder and to treat cancer
XX CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX SQ Sequence 8 AA:
Query Match 36.4%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
DB 2 RALN 5

RESULT 29
ABB46209
ID ABB46209 standard; Peptide: 8 AA.
XX AC ABB46209;
XX DT 30-JAN-2002 (first entry)
XX DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 953.
XX SQ Sequence 8 AA:
Query Match 36.4%; Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
DB 2 RALN 5

```


PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 PS Claim 18: Page 100; 127pp; English.
 XX
 CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue. For enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer;
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 4 RALN 7
 ||||
 ||||

RESULT 32
 ABB46231
 ID ABB46231 standard; Peptide: 8 AA.
 XX
 AC ABB46231;
 XX
 XX 30 JAN-2002 (first entry)
 XX
 DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 975.
 XX
 KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX
 OS Synthetic.
 XX
 PN W0200172956-A2.
 XX
 PD 04 OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-1B01400.
 XX
 PR 27-MAR-2000; 2000US-0535852.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Symonds JM, Gour BJ;
 XX
 DR WPI: 2002-025778/03.
 XX
 PT Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX
 PS Claim 18: Page 100; 127pp; English.
 XX
 CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer;
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA;

CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 2 RALN 5
 ||||
 ||||

RESULT 33
 ABB46232
 ID ABB46232 standard; Peptide: 8 AA.
 XX
 AC ABB46232;
 XX
 XX 30 JAN-2002 (first entry)
 XX
 DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 976.
 XX
 KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX
 OS Synthetic.
 XX
 PN W0200172956-A2.
 XX
 PD 04 OCT-2001.
 XX
 PF 27-MAR-2001; 2001WO-1B01400.
 XX
 PR 27-MAR-2000; 2000US-0535852.
 XX
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX
 PI Blaschuk OW, Symonds JM, Gour BJ;
 XX
 DR WPI: 2002-025778/03.
 XX
 PT Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX
 PS Claim 18: Page 100; 127pp; English.
 XX
 CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA;

Query Match 36.4%; Score 4; DB 23; Length 8;


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XX  US      Synthesia Inc.
XX  PN      WO200172956-A2.
XX  PD      04-OCT-2001.
XX  PF      27-MAR-2001: 2001WO-IB01400.
XX  PR      27-MAR-2000: 2000US-0535852.
XX  PA      (ADHEX) ADHEREX TECHNOLOGIES INC.
XX  PI      Blaschuk OW, Symonds JM, Gour BJ.
XX  DR      WPI: 2002-025778/03.
XX  PT      Modulating agents for inhibiting or enhancing desmosomal cadherin
PT      mediated cell adhesion, useful for facilitating wound healing and/or
PT      reducing scar tissue, treating cancer and inducing apoptosis.
XX  PS      Claim 18: Page 100; 127pp, English.
XX  CC      The invention relates to modulating agents for inhibiting or enhancing
CC      desmosomal cadherin mediated cell adhesion, comprising a modulating agent
CC      comprising a desmosomal cadherin cell adhesion recognition CAR sequence
CC      (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
CC      sequence, a substance such as an antibody or antigen-binding fragment
CC      that specifically binds a desmosomal cadherin CAR sequence and/or a
CC      polynucleotide encoding a polypeptide that comprises a desmosomal
CC      cadherin CAR sequence or analogue. The modulating agents have
CC      immunosuppressive, cytostatic and antiapoptotic activity and are used to
CC      facilitate wound healing and/or reduce scar tissue, for enhancing
CC      adhesion of foreign tissue implants (e.g. skin graft or organ implant),
CC      treating an autoimmune blistering disorder and to treat cancer
CC      (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX  SQ      Sequence 8 AA:
XX  QY      2 RALN 5
XX  DB      1111
XX  DB      2 RALN 5
XX  RESULT 36
XX  ID      ABB46259
XX  AC      ABB46259
XX  DT      30-JAN-2002 (first entry)
XX  DE      Desmosomal CAR sequence cyclic peptide SEQ ID NO 1004.
XX  KW      Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
XX  KW      cytostatic; antiapoptotic; wound healing; reduce scar tissue;
XX  KW      skin graft; organ implant; autoimmune blistering disorder; cancer;
XX  KW      apoptosis; cyclic
XX  QS      Synthetic.
XX  PN      WO200172956-A2.
XX  PD      04-OCT-2001.
XX  PF      27-MAR-2001: 2001WO-IB01400.
XX  PR      27-MAR-2000: 2000US-0535852.
XX  PA      (ADHEX) ADHEREX TECHNOLOGIES INC.
XX  PI      Blaschuk OW, Symonds JM, Gour BJ.
XX  DR      WPI: 2002-025778/03.
XX  PT      Modulating agents for inhibiting or enhancing desmosomal cadherin
PT      mediated cell adhesion, useful for facilitating wound healing and/or
PT      reducing scar tissue, treating cancer and inducing apoptosis.
XX  PS      Claim 18, Page 100; 127pp, English.

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XX  US      Synthesia Inc.
XX  PN      WO200172956-A2.
XX  PD      04-OCT-2001.
XX  PF      27-MAR-2001: 2001WO-IB01400.
XX  PR      27-MAR-2000: 2000US-0535852.
XX  PA      (ADHEX) ADHEREX TECHNOLOGIES INC.
XX  PI      Blaschuk OW, Symonds JM, Gour BJ.
XX  DR      WPI: 2002-025778/03.
XX  PT      Modulating agents for inhibiting or enhancing desmosomal cadherin
PT      mediated cell adhesion, useful for facilitating wound healing and/or
PT      reducing scar tissue, treating cancer and inducing apoptosis.
XX  PS      Claim 18: Page 100; 127pp, English.
XX  CC      The invention relates to modulating agents for inhibiting or enhancing
CC      desmosomal cadherin mediated cell adhesion, comprising a modulating agent
CC      comprising a desmosomal cadherin cell adhesion recognition CAR sequence
CC      (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
CC      sequence, a substance such as an antibody or antigen-binding fragment
CC      that specifically binds a desmosomal cadherin CAR sequence and/or a
CC      polynucleotide encoding a polypeptide that comprises a desmosomal
CC      cadherin CAR sequence or analogue. The modulating agents have
CC      immunosuppressive, cytostatic and antiapoptotic activity and are used to
CC      facilitate wound healing and/or reduce scar tissue, for enhancing
CC      adhesion of foreign tissue implants (e.g. skin graft or organ implant),
CC      treating an autoimmune blistering disorder and to treat cancer
CC      (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX  SQ      Sequence 8 AA:
XX  QY      2 RALN 5
XX  DB      1111
XX  DB      2 RALN 7
XX  RESULT 37
XX  ID      ABB46259
XX  AC      ABB46259
XX  DT      30-JAN-2002 (first entry)
XX  DE      Desmosomal CAR sequence cyclic peptide SEQ ID NO 1004.
XX  KW      Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
XX  KW      cytostatic; antiapoptotic; wound healing; reduce scar tissue;
XX  KW      skin graft; organ implant; autoimmune blistering disorder; cancer;
XX  KW      apoptosis; cyclic
XX  QS      Synthetic.
XX  PN      WO200172956-A2.
XX  PD      04-OCT-2001.
XX  PF      27-MAR-2001: 2001WO-IB01400.
XX  PR      27-MAR-2000: 2000US-0535852.
XX  PA      (ADHEX) ADHEREX TECHNOLOGIES INC.
XX  PI      Blaschuk OW, Symonds JM, Gour BJ.
XX  DR      WPI: 2002-025778/03.
XX  PT      Modulating agents for inhibiting or enhancing desmosomal cadherin
PT      mediated cell adhesion, useful for facilitating wound healing and/or
PT      reducing scar tissue, treating cancer and inducing apoptosis.
XX  PS      Claim 18, Page 100; 127pp, English.

```

XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA:

Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 2 RALN 5

RESULT 49
 ABB46265
 ID ABB46265 standard; Peptide: 8 AA.
 XX ABB46265:
 AC ABB46265:
 XX
 XX 30-JAN-2002 (first entry)
 XX Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 1459.

XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX
 XX Synthetic.
 OS
 XX WO200172956 A2.
 XX 04-OCT-2001.
 XX 27-MAR-2001; 2001WO 1B01400.
 XX 27-MAR-2000; 2000US-0535852.
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX Blaschuk OW, Symonds JM, Gour PJ.
 WPI: 2002-025778/03.
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX
 XX Claim 18; Page 100; 127pp; English.

XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing

CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA:

Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 3 RALN 6

RESULT 49
 ABB46271
 ID ABB46271 standard; Peptide: 8 AA.
 XX ABB46271:
 AC ABB46271:
 XX
 XX 30-JAN-2002 (first entry)
 XX Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 1015.

XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX
 XX Synthetic.
 OS
 XX WO200172956-A2.
 XX 04-OCT-2001.
 XX 27-MAR-2001; 2001WO 1B01400.
 XX 27-MAR-2000; 2000US-0535852.
 XX (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX Blaschuk OW, Symonds JM, Gour PJ.
 WPI: 2002-025778/03.
 XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX
 XX Claim 18; Page 100; 127pp; English.

XX The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX
 SQ Sequence 8 AA:

Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5

```

XX      4 RALN 7
DE      1111
XX      10-JAN 2002 (first entry)
KW      Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 1032.
KW      Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW      cytostatic; antiapoptotic; wound healing; reduce scar tissue;
KW      skin graft; organ implant; autoimmune blistering disorder; cancer;
KW      apoptosis; cyclic.
XX      Synthetic.
OS      WO200172956-A2.
XX      04-OCT 2001.
XX      27-MAR-2001; 2001WO-1801400.
XX      27-MAR-2000; 2000US-0545852.
XX      (ADHE-) ADHEREX TECHNOLOGIES INC.
XX      Blaschuk OW, Symonds JM, Gour RJ:
XX      WPI: 2002-025778/03.
XX      Modulating agents for inhibiting or enhancing desmosomal cadherin
XX      mediated cell adhesion, useful for facilitating wound healing and/or
XX      reducing scar tissue, treating cancer and inducing apoptosis -
XX      Claim 18; Page 101; 127pp; English.
XX      The invention relates to modulating agents for inhibiting or enhancing
XX      desmosomal cadherin mediated cell adhesion, comprising a modulating agent
XX      comprising a desmosomal cadherin cell adhesion recognition CAR sequence
XX      (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
XX      sequence, a substance such as an antibody or antigen-binding fragment
XX      that specifically binds a desmosomal cadherin CAR sequence and/or a
XX      polynucleotide encoding a polypeptide that comprises a desmosomal
XX      cadherin CAR sequence or analogue. The modulating agents have
XX      immunosuppressive, cytostatic and antiapoptotic activity and are used to
XX      facilitate wound healing and/or reduce scar tissue, for enhancing
XX      adhesion of foreign tissue implants (e.g. skin graft or organ implant),
XX      treating an autoimmune blistering disorder and to treat cancer
XX      (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX      Sequence 8 AA:
XX      Query Match: 36.4%, Score 4; DB 23; Length 8;
XX      Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      QY      2 RALN 5
XX      DB      1111
XX      2 RALN 5
XX      RESULT 43
XX      ABB46288
XX      ID      ABB46288 standard; Peptide; 8 AA.
XX      AC      ABB46288;
XX      XX      30-JAN-2002 (first entry)
XX      DE      Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 1032.
XX      KW      Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
XX      KW      cytostatic; antiapoptotic; wound healing; reduce scar tissue;
XX      KW      skin graft; organ implant; autoimmune blistering disorder; cancer;
XX      KW      apoptosis; cyclic.
XX      OS      Synthetic.
XX      PN      WO200172956-A2.
XX      04-OCT 2001.
XX      27-MAR-2001; 2001WO-1801400.
XX      27-MAR-2000; 2000US-0545852.
XX      (ADHE-) ADHEREX TECHNOLOGIES INC.
XX      Blaschuk OW, Symonds JM, Gour RJ:
XX      WPI: 2002-025778/03.
XX      Modulating agents for inhibiting or enhancing desmosomal cadherin
XX      mediated cell adhesion, useful for facilitating wound healing and/or
XX      reducing scar tissue, treating cancer and inducing apoptosis -
XX      Claim 18; Page 100; 127pp; English.
XX      The invention relates to modulating agents for inhibiting or enhancing
XX      desmosomal cadherin mediated cell adhesion, comprising a modulating agent
XX      comprising a desmosomal cadherin cell adhesion recognition CAR sequence
XX      (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
XX      sequence, a substance such as an antibody or antigen-binding fragment
XX      that specifically binds a desmosomal cadherin CAR sequence and/or a
XX      polynucleotide encoding a polypeptide that comprises a desmosomal
XX      cadherin CAR sequence or analogue. The modulating agents have
XX      immunosuppressive, cytostatic and antiapoptotic activity and are used to
XX      facilitate wound healing and/or reduce scar tissue, for enhancing
XX      adhesion of foreign tissue implants (e.g. skin graft or organ implant),
XX      treating an autoimmune blistering disorder and to treat cancer
XX      (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX      Sequence 8 AA:
XX      Query Match: 36.4%, Score 4; DB 23; Length 8;
XX      Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX      Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      QY      2 RALN 5
XX      DB      1111
XX      4 RALN 7
XX      RESULT 42
XX      ABB46287
XX      ID      ABB46287 standard; Peptide; 8 AA.
XX      AC      ABB46287;
XX      XX      30-JAN 2002 (first entry)

```

XX PD 04-OCT-2001.
 XX XX
 XX PF 27-MAR-2001; 2001WO-IB01400.
 XX PR 27-MAR-2000; 2000US-0535852.
 XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX PI Blaschuk OW, Symonds JM, Gour BJ;
 XX XX WPI: 2002-025778/03.
 XX XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX XX Claim 18; Page 101; 127pp; English.
 XX CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX XX
 XX SQ Sequence 8 AA;
 Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RALN 5
 DB IIII
 2 RALN 5
 RESULT: 44
 ABB46293
 ID ABB46293 standard; Peptide: 8 AA.
 XX AC ABB46293;
 XX DT 10-JAN-2002 (first entry)
 XX DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 1037.
 XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX OS Synthetic.
 XX PN W0200172956-A2.
 XX PD 04-OCT-2001.
 XX PF 27-MAR-2001; 2001WO-IB01400.
 XX XX 27-MAR-2000; 2000US-0535852.
 XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX PI Blaschuk OW, Symonds JM, Gour BJ;
 XX XX WPI: 2002-025778/03.
 XX XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX XX Claim 18; Page 101; 127pp; English.
 XX CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX XX

DR WPI: 2002-025778/03.
 XX XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX XX Claim 18; Page 101; 127pp; English.
 XX CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX XX
 XX SQ Sequence 8 AA;
 Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RALN 5
 DB IIII
 3 RALN 6
 RESULT: 45
 ABB46299
 ID ABB46299 standard; Peptide: 8 AA.
 XX AC ABB46299;
 XX DT 30-JAN-2002 (first entry)
 XX DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 1043.
 XX KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX OS Synthetic.
 XX PN W0200172956-A2.
 XX PD 04-OCT-2001.
 XX PF 27-MAR-2001; 2001WO-IB01400.
 XX XX 27-MAR-2000; 2000US-0535852.
 XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.
 XX PI Blaschuk OW, Symonds JM, Gour BJ;
 XX XX WPI: 2002-025778/03.
 XX XX Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX XX Claim 18; Page 101; 127pp; English.
 XX CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC comprising a desmosomal cadherin

CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX

SQ Sequence 8 AA:
 Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 4 RALN 7

RESULT 46
 ABB46306
 ID ABB45306 standard; Peptide: 8 AA.
 AC ABB46306;
 DT 30-JAN-2002 (first entry)
 DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 1050.
 KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX Synthetic.
 OS WO200172956-A2.
 PN 04 OCT-2001.
 PD 27-MAR-2001; 2001WO-1801400.
 PE 27-MAR-2000; 2000US-0535852.
 PR (ADHE-) ADHEREX TECHNOLOGIES INC.
 PA Blaschuk OW, Symonds JM, Gour RJ;
 PI WPI: 2002 025778/03.
 PT Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX Claim 18; Page 101; 127pp; English.
 CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX

SQ Sequence 8 AA:
 Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 4 RALN 7

RESULT 47
 ABB46321
 ID ABB46321 standard; Peptide: 8 AA.
 AC ABB46321;
 DT 30-JAN-2002 (first entry)
 DE Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 1065.
 KW Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
 KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
 KW skin graft; organ implant; autoimmune blistering disorder; cancer;
 KW apoptosis; cyclic.
 XX Synthetic.
 OS WO200172956-A2.
 PN 04 OCT-2001.
 PD 27-MAR-2001; 2001WO-1801400.
 PE 27-MAR-2000; 2000US-0545852.
 PR (ADHE-) ADHEREX TECHNOLOGIES INC.
 PA Blaschuk OW, Symonds JM, Gour RJ;
 PI WPI: 2002 025778/03.
 PT Modulating agents for inhibiting or enhancing desmosomal cadherin
 PT mediated cell adhesion, useful for facilitating wound healing and/or
 PT reducing scar tissue, treating cancer and inducing apoptosis -
 XX Claim 18; Page 101; 127pp; English.
 CC The invention relates to modulating agents for inhibiting or enhancing
 CC desmosomal cadherin mediated cell adhesion, comprising a modulating agent
 CC comprising a desmosomal cadherin cell adhesion recognition CAR sequence
 CC (ABB45341-ABB47262), a non-peptide mimetic of a desmosomal cadherin CAR
 CC sequence, a substance such as an antibody or antigen-binding fragment
 CC that specifically binds a desmosomal cadherin CAR sequence and/or a
 CC polynucleotide encoding a polypeptide that comprises a desmosomal
 CC cadherin CAR sequence or analogue. The modulating agents have
 CC immunosuppressive, cytostatic and antiapoptotic activity and are used to
 CC facilitate wound healing and/or reduce scar tissue, for enhancing
 CC adhesion of foreign tissue implants (e.g. skin graft or organ implant),
 CC treating an autoimmune blistering disorder and to treat cancer
 CC (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
 XX

SQ Sequence 8 AA:
 Query Match 36.4%; Score 4; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RALN 5
 DB 2 RALN 5

```

RESULT 48
AB46322
ID AB46322 standard; Peptide: 8 AA.
XX
XX A0446322;
XX
XX 10 JAN-2002 (first entry)
XX
XX Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 1071.
XX
XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
KW skin graft; organ implant; autoimmune blistering disorder; cancer;
KW apoptosis; cyclic.
XX
XX Synthetic.
XX
XX W0200172956.A2.
XX
XX 04 OCT-2001.
XX
XX 27-MAR-2001; 2001WO1801400.
XX
XX 27-MAR-2000; 2000US-0535852.
XX
XX (ABRE-) ADHEREX TECHNOLOGIES INC.
XX
XX Blaschuk GW, Symonds JM, Gour BJ;
XX WPI: 2002-025778/03.
XX
XX Modulating agents for inhibiting or enhancing desmosomal cadherin
mediated cell adhesion, useful for facilitating wound healing and/or
reducing scar tissue, treating cancer and inducing apoptosis.
XX
XX Claim 18; Page 101; 127pp; English.
XX
XX The invention relates to modulating agents for inhibiting or enhancing
desmosomal cadherin mediated cell adhesion, comprising a modulating agent
comprising a desmosomal cadherin cell adhesion recognition CAR sequence
(AB45341-AB47262), a non-peptide mimetic of a desmosomal cadherin CAR
sequence, a substance such as an antibody or antigen-binding fragment
that specifically binds a desmosomal cadherin CAR sequence and/or a
polynucleotide encoding a polypeptide that comprises a desmosomal
cadherin CAR sequence or analogue. The modulating agents have
immunosuppressive, cytostatic and antiapoptotic activity and are used to
facilitate wound healing and/or reduce scar tissue, for enhancing
adhesion of foreign tissue implants (e.g. skin graft or organ implant),
treating an autoimmune blistering disorder and to treat cancer
(e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX
XX Sequence 8 AA:
SQ
Query Match 36.4% Score 4; DB 23; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RAIN 5
ID 1111
XX 1 RAIN 4
RESULT 49
AB46326
ID AB46326 standard; Peptide: 8 AA.
XX
XX A0446326;
XX
XX 10 JAN-2002 (first entry)
XX
XX Desmoglein-1 CAR sequence cyclic peptide SEQ ID NO 1071.
XX
XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
KW skin graft; organ implant; autoimmune blistering disorder; cancer;
KW apoptosis; cyclic.
XX
XX Synthetic.
XX
XX W0200172956.A2.
XX
XX 04 OCT-2001.
XX
XX 27-MAR-2001; 2001WO1801400.
XX
XX Desmosomal cadherin; cell adhesion; CAR sequence; immunosuppressive;
KW cytostatic; antiapoptotic; wound healing; reduce scar tissue;
KW skin graft; organ implant; autoimmune blistering disorder; cancer;
KW apoptosis; cyclic.
XX
XX Synthetic.
XX
XX W0200172956.A2.
XX
XX 04 OCT-2001.
XX
XX 27-MAR-2001; 2001WO1801400.

```

```

XX      27-MAR-2000: 2000US-0535852.
XX
XX      (AHEX-) ADHREX TECHNOLOGIES INC
XX
XX      Blaschuk GW, Symonds JM, Scott WJ;
XX      WPI: 2002-025778/03.
XX
XX      Modulating agents for inhibiting or enhancing desmosomal cadherin
XX      mediated cell adhesion, useful for facilitating wound healing and/or
XX      reducing scar tissue, treating cancer and inflicting apoptosis
XX
XX      Claim 18; Page 101; 127pp; English
XX
XX      The invention relates to modulating agents for inhibition of adherens
XX      desmosomal cadherin mediated cell adhesion, comprising a modulating agent
XX      comprising a desmosomal cadherin cell adhesion recognition CAR sequence
XX      (AHB4344-ABN47262), a non peptide moiety of a desmosomal cadherin CAR
XX      sequence, a substance such as an antibody or anti-heparin binding fragment
XX      that specifically binds a desmosomal cadherin CAR sequence and/or a
XX      polynucleotide encoding a polypeptide that comprises a desmosomal
XX      cadherin CAR sequence or analogue, the modulating agents have
XX      immunosuppressive, cytostatic and antiproliferative activity and are used to
XX      facilitate wound healing and/or reduce scar tissue, for enhancing
XX      adhesion of foreign tissue implants (e.g. skin graft or organ implant),
XX      treating an autoimmune blistering disorder and to treat cancer
XX      (e.g. carcinoma, leukaemia or melanoma) and induce apoptosis.
XX
XX      Sequence: 8 AA;
XX
XX      Query Match: 36.4%; Score 4; IP 24; Length 9;
XX      Best Local Similarity: 100.0%; Pos'd Seq. % 6.00%;
XX      Matches: 4; Conservative 0; Mismatched 3; Gaps 0;
XX
XX      2 PALN 5
XX      |||||
XX      3 PALN 6
XX
XX      Search completed: September 30, 2003, 1:24:37
XX      Job File: 146.1667.secs

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cdm protein protein search, using sw mode.

Run on: September 30, 2003, 10:57:04 : Search time 41.567 Seconds
(without alignments)
62.639 Million cell updates/sec

Title: us-09-787-443-3

Perfect score: 11

Sequence: 1 ARALNWGAAPK li

Scoring table: 0LIG0

Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 25852604 residues

Word size: 0

Total number of hits satisfying chosen parameters: 3459

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: listing first 500 summaries

Database:

SPTREMBL_23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_ordanelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriophage:
17: sp_archaeap:

Prod. No. is the number of results printed. The number to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Query			SUMMARY			Description
	Score	Match	Length	DB	ID		
1	4	36.4	15	13	P81334		P81333 ozoorthychn
2	3	27.3	8	4	Q9UCN4		Q9UCN4 homo sapien
3	3	27.3	9	2	Q9R7ER		Q9R7E8 escherichia
4	3	27.3	9	4	Q166C5		Q166C5 homo sapien
5	3	27.3	9	8	Q9T2L0		Q9T2L0 spinacia ol
6	3	27.3	9	8	Q9T2L0		Q9T2L0 spinacia ol
7	3	27.3	10	3	Q8J0C2		Q8J0C2 encephalito
8	3	27.3	10	4	Q8T2A2		Q8T2A2 homo sapien
9	3	27.3	10	5	Q8WPE7		Q8WPE7 skogsberqia
10	3	27.3	10	11	Q9LWZ3		Q9LWZ3 rattus sp.
11	3	27.3	10	12	Q9Q0W3		Q9Q0W3 polymovaviru
12	3	27.3	10	12	Q8JV70		Q8JV70 polymovaviru
13	3	27.3	10	12	Q9Q0W1		Q9Q0W1 polymovaviru
14	3	27.3	10	12	Q8J26E		Q8J26E polymovaviru
15	3	27.3	10	12	Q63147		Q63147 herpes simp
16	3	27.3	10	12	Q9Q0V9		Q9Q0V9 polymovaviru

Q8JV84 polymovaviru
Q9Q0W7 polymovaviru
Q8JV66 polymovaviru
Q9Q0V7 polymovaviru
Q8JV82 polymovaviru
Q8JV76 polymovaviru
Q8JV74 polymovaviru
Q9Q0X7 polymovaviru
Q8JV78 polymovaviru
Q9Q0W5 polymovaviru
Q9Q0X3 polymovaviru
Q9Q0X5 polymovaviru
Q9Q0X3 polymovaviru
Q9Q0X1 polymovaviru
Q9Q0X9 polymovaviru
Q8JV72 polymovaviru
Q8CD88 homo sapien
Q9TWX6 dictyosteli
Q9TQX9 equus cabal
Q9VH3 rattus sp.
Q9VH3 rattus sp.
P94011 arabidopsis
Q34770 borrelia af
Q34622 borrelia bu
Q96P10 homo sapien
Q9U7D6 neospora ca
Q97122 toxoplasma
Q9GJU2 ovis aries
Q62355 mus musculu
Q9CU06 mus musculu
Q8CIW3 mus musculu
Q69394 pseudorabie
Q8X4F5 escherichia
Q8192 ashbya goss
Q16232 homo sapien
Q9FUX5 symphoricar
P83291 arabidopsis
Q99PB8 mus musculu
Q8CFB7 mus musculu
Q85662 reovirus (t
Q85718 reovirus (t
O10228 human immun
O10232 human immun
O10233 human immun
O10227 human immun
O10226 human immun
O8UT17 human immun
Q9F598 micrococci
Q9F564 escherichia
Q9F5K5 comamonas a
Q8N0N6 brachiostio
P92076 euhadra her
Q9T202 chlamydomon
Q9SQ16 oryza sativ
Q941J1 zea mays (m
Q9FYV6 gossypium h
Q8AXQ9 xenopus lae
Q9Q090 human immun
Q97098 human immun
Q97098 human immun
Q97099 human immun
Q97092 human immun
Q97094 human immun
Q9F5R2 shigella dy
P77556 escherichia
Q32560 escherichia
Q9Z1E9 neisseria m
Q9F4M3 enterococcu
Q9URB9 saccharomyc
Q15889 homo sapien
Q15900 homo sapien

90	2	18.2	8	4	015888	Q15888 homo sapien	163	2	18.2	9	8	094NB1	Q94nb1 microcebus
91	2	18.2	8	4	090J50	Q90j50 homo sapien	164	2	18.2	9	8	09TNF4	Q9tnf4 magnolia sc
92	2	18.2	8	5	P82685	P82685 periplaneta	165	2	18.2	9	8	09THL7	Q9thl7 magnolia si
93	2	18.2	8	5	P82686	P82686 periplaneta	166	2	18.2	9	8	09TNE0	Q9tne0 michelia co
94	2	18.2	8	5	P82687	P82687 periplaneta	167	2	18.2	9	8	095GN1	Q95gn1 pelargonium
95	2	18.2	8	5	P82688	P82688 periplaneta	168	2	18.2	9	8	09TNE4	Q9tne4 magnolia sa
96	2	18.2	8	5	P82689	P82689 periplaneta	169	2	18.2	9	8	095DS6	Q95ds6 magnolia wi
97	2	18.2	8	6	Q9TRX8	Q9trx8 bos taurus	170	2	18.2	9	8	094NB2	Q94nb2 microcebus
98	2	18.2	8	6	Q8WNS1	Q8wns1 bos taurus	171	2	18.2	9	8	09TNF6	Q9tnf6 magnolia gr
99	2	18.2	8	8	Q19957	Q19957 gossypium h	172	2	18.2	9	8	09THL5	Q9thl5 magnolia li
100	2	18.2	8	8	Q19961	Q19961 gossypium d	173	2	18.2	9	8	09TNF1	Q9tnf1 magnolia he
101	2	18.2	8	8	Q19958	Q19958 gossypium b	174	2	18.2	9	8	094VH4	Q94vh4 varanus gla
102	2	18.2	8	8	Q9TD02	Q9td02 terranotos	175	2	18.2	9	8	095DT3	Q95dt3 magnolia il
103	2	18.2	8	8	Q19960	Q19960 gossypium m	176	2	18.2	9	8	094VH4	Q94vh4 varanus gla
104	2	18.2	8	8	Q19959	Q19959 gossypium t	177	2	18.2	9	8	095DS2	Q95ds2 magnolia fr
105	2	18.2	8	8	Q19956	Q19956 gossypium a	178	2	18.2	9	8	094V18	Q94v18 varanus ere
106	2	18.2	8	8	Q8WGC7	Q8wgc7 petriolisthe	179	2	18.2	9	8	09T3P4	Q9t3p4 magnolia ma
107	2	18.2	8	9	Q8SBJ0	Q8sbj0 bacterioph	180	2	18.2	9	8	094NA9	Q94na9 daubentonia
108	2	18.2	8	9	Q8H9K4	Q8h9k4 bacterioph	181	2	18.2	9	8	09THL8	Q9thl8 magnolia of
109	2	18.2	8	9	Q8H9K1	Q8h9k1 bacterioph	182	2	18.2	9	8	09TNE2	Q9tne2 magnolia ac
110	2	18.2	8	9	Q8H9J9	Q8h9j9 bacterioph	183	2	18.2	9	8	09TNF5	Q9tnf5 magnolia gu
111	2	18.2	8	9	Q8H9J7	Q8h9j7 bacterioph	184	2	18.2	9	8	09TNE3	Q9tne3 magnolia ko
112	2	18.2	8	9	Q8H9J5	Q8h9j5 bacterioph	185	2	18.2	9	8	09TNE1	Q9tne1 magnolia li
113	2	18.2	8	9	Q8H9J3	Q8h9j3 bacterioph	186	2	18.2	9	8	09TNE3	Q9tne3 magnolia st
114	2	18.2	8	9	Q8H9J1	Q8h9j1 bacterioph	187	2	18.2	9	6	Q9TND9	Q9tnd9 michelia fl
115	2	18.2	8	9	Q8H9J9	Q8h9j9 bacterioph	188	2	18.2	9	8	09THL6	Q9thl6 magnolia si
116	2	18.2	8	9	Q8H9J8	Q8h9j8 bacterioph	189	2	18.2	9	8	095DS4	Q95ds4 magnolia do
117	2	18.2	8	9	Q8H9J6	Q8h9j6 bacterioph	190	2	18.2	9	8	09TNF3	Q9tnf3 magnolia sh
118	2	18.2	8	9	Q8H9J4	Q8h9j4 bacterioph	191	2	18.2	9	8	09TNE8	Q9tne8 magnolia de
119	2	18.2	8	9	Q8H9J3	Q8h9j3 bacterioph	192	2	18.2	9	8	08W8W5	Q8w8w5 diadema set
120	2	18.2	8	9	Q8H9J2	Q8h9j2 bacterioph	193	2	18.2	9	8	095DS7	Q95ds7 magnolia si
121	2	18.2	8	9	Q8H9H6	Q8h9h6 bacterioph	194	2	18.2	9	8	09THL9	Q9thl9 magnolia fr
122	2	18.2	8	9	Q8H9H5	Q8h9h5 bacterioph	195	2	18.2	9	8	09TNE6	Q9tne6 magnolia de
123	2	18.2	8	9	Q8H9H3	Q8h9h3 bacterioph	196	2	18.2	9	8	09TNF2	Q9tnf2 magnolia ta
124	2	18.2	8	10	Q40659	Q40659 gryza sativ	197	2	18.2	9	8	09T3P3	Q9t3p3 magnolia vi
125	2	18.2	8	10	Q42507	Q42507 trititum ae	198	2	18.2	9	8	09TNE7	Q9tne7 magnolia ni
126	2	18.2	8	11	Q9VER02	Q9ver02 mus musculu	199	2	18.2	9	8	094XE6	Q94xe6 tectocoris
127	2	18.2	8	11	Q9JLD7	Q9jld7 mesocricetu	200	2	18.2	9	8	095DR9	Q95dr9 manglietia
128	2	18.2	8	11	Q90615	Q90615 mus musculu	201	2	18.2	9	8	094NB0	Q94nb0 microcebus
129	2	18.2	8	11	Q9QV44	Q9qv44 rattus sp.	202	2	18.2	9	8	Q8W8W6	Q8w8w6 diadema ant
130	2	18.2	8	11	Q9R4R8	Q9r4r8 mus musculu	203	2	18.2	9	8	Q95DR8	Q95dr8 michelia ma
131	2	18.2	8	11	Q9QVK5	Q9qvks rattus sp.	204	2	18.2	9	8	Q31653	Q31653 anser caeru
132	2	18.2	8	11	Q62528	Q62528 mus spretus	205	2	18.2	9	11	Q8R514	Q8r514 rattus norv
133	2	18.2	8	12	Q9WJ33	Q9wj33 pseudorabie	206	2	18.2	9	11	Q924N8	Q924n8 mus musculu
134	2	18.2	8	13	Q9SP69	Q9sp69 gallus gail	207	2	18.2	9	11	Q9QVH9	Q9qvhi9 mus sp. sup
135	2	18.2	8	13	Q8JFNE	Q8jfn6 gallus gail	208	2	18.2	9	11	Q9QVH0	Q9qvht0 mus musculu
136	2	18.2	9	1	Q50832	Q50832 methanococc	209	2	18.2	9	11	Q61723	Q61723 mus musculu
137	2	18.2	9	2	Q9E214	Q9e214 sodalis glo	210	2	18.2	9	11	Q61723	Q61723 mus musculu
138	2	18.2	9	2	P72145	P72145 pseudomonas	211	2	18.2	9	12	Q69473	Q69473 human herpe
139	2	18.2	9	2	Q53914	Q53914 streptomyce	212	2	18.2	9	12	Q69473	Q69473 human herpe
140	2	18.2	9	2	Q57428	Q57428 aeromonas s	213	2	18.2	9	12	Q71067	Q71067 hepatitis b
141	2	18.2	9	2	Q45852	Q45852 clostridium	214	2	18.2	9	12	Q82622	Q82622 avian infec
142	2	18.2	9	2	Q93LE4	Q93le4 hellobacilli	215	2	18.2	9	12	P90359	P90359 barley mild
143	2	18.2	9	2	Q44377	Q44377 aeromonas t	216	2	18.2	9	12	Q71069	Q71069 canine dist
144	2	18.2	9	2	Q44468	Q44468 aeromonas v	217	2	18.2	9	12	Q92766	Q92766 canine dist
145	2	18.2	9	2	Q91735	Q91735 streptomyc	218	2	18.2	9	12	Q84333	Q84333 simian viru
146	2	18.2	9	2	P72149	P72149 pseudomonas	219	2	18.2	9	12	Q71068	Q71068 canine dist
147	2	18.2	9	2	Q43928	Q43928 aeromonas f	220	2	18.2	9	12	Q89491	Q89491 murine minu
148	2	18.2	9	2	Q43001	Q43001 aeromonas c	221	2	18.2	9	13	Q91A14	Q91a14 gallus gall
149	2	18.2	9	2	Q51765	Q51765 pseudomonas	222	2	18.2	9	13	Q8JFA7	Q8jfa7 ficedula al
150	2	18.2	9	4	Q15999	Q15999 homo sapien	223	2	18.2	9	13	Q8JFA6	Q8jfa6 ficedula hy
151	2	18.2	9	4	Q9H461	Q9h461 homo sapien	224	2	18.2	9	13	Q92009	Q92009 gallus gall
152	2	18.2	9	4	Q15892	Q15892 homo sapien	225	2	18.2	9	13	Q8AYL5	Q8ayl5 carassius a
153	2	18.2	9	4	Q9UCN5	Q9ucn5 homo sapien	226	2	18.2	9	15	Q50843	Q50843 methanococc
154	2	18.2	9	5	Q91WD6	Q91wd6 leptinotars	227	2	18.2	10	1	Q50843	Q50843 methanococc
155	2	18.2	9	5	Q9TVF1	Q9tvf1 trypanosoma	228	2	18.2	10	2	Q9F9H5	Q9f9h5 hellobacte
156	2	18.2	9	5	Q9MW43	Q9mw43 homo sapien	229	2	18.2	10	2	Q9F9H5	Q9f9h5 hellobacte
157	2	18.2	9	8	Q95DS5	Q95ds5 magnolia sa	230	2	18.2	10	2	Q47651	Q47651 escherichia
158	2	18.2	9	8	Q8WFS4	Q8wfs4 diadema mex	231	2	18.2	10	2	Q47651	Q47651 escherichia
159	2	18.2	9	8	Q95DS0	Q95ds0 manglietia	232	2	18.2	10	2	Q96352	Q96352 marinobacte
160	2	18.2	9	8	Q9TNF0	Q9tnf0 magnolia tr	233	2	18.2	10	2	P96421	P96421 neisseria g
161	2	18.2	9	8	Q95DS1	Q95ds1 manglietia	234	2	18.2	10	2	Q93LE5	Q93le5 photobacter
162	2	18.2	9	8	Q9TNE9	Q9tne9 magnolia co	235	2	18.2	10	2	Q9R5N6	Q9r5n6 clostridium

236	2	18.2	10	2	P96423	P96423 pseudomonas	309	2	18.2	10	15	Q90KJ0	Q90KJ0 human immun
237	2	18.2	10	2	Q8KH9	Q8KH9 clostridium	310	2	18.2	11	2	Q68237	Q68237 borrelia bu
238	2	18.2	10	2	Q47475	Q47475 escherichia	311	2	18.2	11	2	Q9A1Z7	Q9A1Z7 carsonella
239	4	18.2	10	2	Q8RSU1	Q8RSU1 helicobacte	312	2	18.2	11	2	Q8KKN1	Q8KKN1 escherichia
240	2	18.2	10	2	Q9F5W1	Q9F5W1 vibrio chol	313	2	18.2	11	2	Q8KHL0	Q8KHL0 streptococc
241	2	18.2	10	2	Q9K343	Q9K343 escherichia	314	2	18.2	11	2	Q9R4B1	Q9R4B1 streptococc
242	2	18.2	10	2	Q95421	Q95421 escherichia	315	2	18.2	11	2	Q9X5S6	Q9X5S6 streptomyce
243	2	18.2	10	2	Q8R171	Q8R171 anaplasma p	316	2	18.2	11	2	Q9S618	Q9S618 prochloroco
244	2	18.2	10	2	Q47691	Q47691 escherichia	317	2	18.2	11	2	Q9F0Z3	Q9F0Z3 escherichia
245	2	18.2	10	2	Q96306	Q96306 aeromonas s	318	2	18.2	11	2	Q47600	Q47600 escherichia
246	2	18.2	10	2	Q83067	Q83067 bacillus ce	319	2	18.2	11	2	Q87882	Q87882 mycobacteri
247	2	18.2	10	2	Q83160	Q83160 anabaena sp	320	2	18.2	11	2	Q9R4Z2	Q9R4Z2 mycoplasma
248	2	18.2	10	2	Q83154	Q83154 anabaena sp	321	2	18.2	11	2	Q9S518	Q9S518 pasteurella
249	2	18.2	10	2	Q82386	Q82386 streptococc	322	2	18.2	11	2	Q47604	Q47604 escherichia
250	2	18.2	10	2	Q8GDX0	Q8GDX0 escherichia	323	2	18.2	11	2	Q47345	Q47345 escherichia
251	2	18.2	10	4	Q8NEK0	Q8NEK0 homo sapien	324	2	18.2	11	2	Q47420	Q47420 escherichia
252	2	18.2	10	4	Q9R369	Q9R369 homo sapien	325	2	18.2	11	2	Q8KKA1	Q8KKA1 streptococc
253	2	18.2	10	4	Q9UNF2	Q9UNF2 homo sapien	326	2	18.2	11	2	Q56411	Q56411 escherichia
254	2	18.2	10	4	Q14096	Q14096 homo sapien	327	2	18.2	11	2	Q47059	Q47059 escherichia
255	2	18.2	10	4	Q9UCS3	Q9UCS3 homo sapien	328	2	18.2	11	2	Q9R446	Q9R446 neisseria g
256	2	18.2	10	4	Q9UJ48	Q9UJ48 homo sapien	329	2	18.2	11	2	Q8GMU3	Q8GMU3 acinetobact
257	2	18.2	10	4	Q9U8R6	Q9U8R6 homo sapien	330	2	18.2	11	3	Q60005	Q60005 aspergillus
258	2	18.2	10	5	Q91W31	Q91W31 fusinus fer	331	2	18.2	11	3	Q60007	Q60007 emericella
259	2	18.2	10	5	Q25356	Q25356 locusta mig	332	2	18.2	11	3	Q60192	Q60192 aspergillus
260	2	18.2	10	5	Q8WFL6	Q8WFL6 oikopleura	333	2	18.2	11	3	Q6C1R7	Q6C1R7 saccharomyc
261	2	18.2	10	5	Q82383	Q82383 drosophila	334	2	18.2	11	3	Q60006	Q60006 aspergillus
262	2	18.2	10	6	Q91S43	Q91S43 sus scrofa	335	2	18.2	11	4	Q60614	Q60614 homo sapien
263	2	18.2	10	6	Q8WFO4	Q8WFO4 atelies belz	336	2	18.2	11	4	Q14759	Q14759 homo sapien
264	2	18.2	10	6	Q95NB1	Q95NB1 eulemur ful	337	2	18.2	11	4	Q9UCP2	Q9UCP2 homo sapien
265	2	18.2	10	6	Q95NH0	Q95NH0 eulemur ful	338	2	18.2	11	4	Q9KX38	Q9KX38 homo sapien
266	2	18.2	10	6	Q8SPN8	Q8SPN8 macaca mula	339	2	18.2	11	4	Q60761	Q60761 homo sapien
267	2	18.2	10	6	Q95M70	Q95M70 trichosurus	340	2	18.2	11	4	Q73811	Q73811 homo sapien
268	2	18.2	10	6	Q83205	Q83205 ovis aries	341	2	18.2	11	4	Q15997	Q15997 homo sapien
269	2	18.2	10	8	Q9XMB4	Q9XMB4 acgilops ta	342	2	18.2	11	4	Q96QF8	Q96QF8 homo sapien
270	2	18.2	10	8	Q912P3	Q912P3 rattus sp.	343	2	18.2	11	4	Q9UCP5	Q9UCP5 homo sapien
271	2	18.2	10	8	Q912P4	Q912P4 rattus sp.	344	2	18.2	11	4	Q9UE69	Q9UE69 homo sapien
272	2	18.2	10	8	Q95D00	Q95D00 magnolia po	345	2	18.2	11	4	Q9HCN5	Q9HCN5 homo sapien
273	2	18.2	10	8	Q95D58	Q95D58 magnolia de	346	2	18.2	11	5	Q26092	Q26092 pisaster oc
274	2	18.2	10	8	Q95D58	Q95D58 magnolia sp	347	2	18.2	11	5	Q95PX6	Q95PX6 caenorhabdi
275	2	18.2	10	8	Q91347	Q91347 ophisaurus	348	2	18.2	11	5	Q9NFX0	Q9NFX0 drosophila
276	2	18.2	10	8	Q8W8C2	Q8W8C2 anolis punc	349	2	18.2	11	5	Q95J20	Q95J20 eulemur ful
277	2	18.2	10	8	Q91G32	Q91G32 ophisaurus	350	2	18.2	11	6	Q95NB6	Q95NB6 eulemur ful
278	2	18.2	10	8	Q95D53	Q95D53 magnolia me	351	2	18.2	11	6	Q95J19	Q95J19 eulemur ful
279	2	18.2	10	8	Q8WDB8	Q8WDB8 anolis iran	352	2	18.2	11	7	Q77914	Q77914 oreochromis
280	2	18.2	10	8	Q8W8C3	Q8W8C3 anolis nite	353	2	18.2	11	7	Q9UEX7	Q9UEX7 homo sapien
281	2	18.2	10	8	Q91368	Q91368 gerthomotis	354	2	18.2	11	7	Q78118	Q78118 oreochromis
282	2	18.2	10	8	Q8W8C4	Q8W8C4 anolis punc	355	2	18.2	11	7	Q77872	Q77872 oreochromis
283	2	18.2	10	8	Q95AR2	Q95AR2 magnolia pa	356	2	18.2	11	7	Q78120	Q78120 oreochromis
284	2	18.2	10	8	Q95UT1	Q95UT1 magnolia yo	357	2	18.2	11	7	Q77873	Q77873 oreochromis
285	2	18.2	10	8	Q95UR7	Q95UR7 magnolia sc	358	2	18.2	11	7	Q77871	Q77871 oreochromis
286	2	18.2	10	8	Q8WDB4	Q8WDB4 anomobryum	359	2	18.2	11	8	Q9G622	Q9G622 salea horsf
287	2	18.2	10	9	Q38217	Q38217 lactococcus	360	2	18.2	11	8	Q95E14	Q95E14 dendrochilu
288	2	18.2	10	10	Q95926	Q95926 glycine max	361	2	18.2	11	8	Q9G359	Q9G359 japalura fl
289	2	18.2	10	10	Q41788	Q41788 zea mays (m	362	2	18.2	11	8	Q9G649	Q9G649 otocryptis
290	2	18.2	10	10	Q94119	Q94119 zea mays (m	363	2	18.2	11	8	Q9G528	Q9G528 acanthosaur
291	2	18.2	10	10	Q9R938	Q9R938 nicotiana t	364	2	18.2	11	8	Q94VH7	Q94VH7 varanus gil
292	2	18.2	10	10	Q82414	Q82414 nicotiana t	365	2	18.2	11	8	Q9G619	Q9G619 ceratophora
293	2	18.2	10	11	Q9QVK8	Q9QVK8 mus sp. mep	366	2	18.2	11	8	Q8WER7	Q8WER7 ceratophora
294	2	18.2	10	11	Q70580	Q70580 mus musculu	367	2	18.2	11	8	Q8WD50	Q8WD50 ceratophora
295	2	18.2	10	11	Q9R320	Q9R320 mus musculu	368	2	18.2	11	8	Q35374	Q35374 paramacium
296	2	18.2	10	11	Q8RHN2	Q8RHN2 mus musculu	369	2	18.2	11	8	Q9G5X1	Q9G5X1 trapelus pe
297	2	18.2	10	12	Q9UJ48	Q9UJ48 hepatitis q	370	2	18.2	11	8	Q9G5X1	Q9G5X1 trapelus pe
298	2	18.2	10	12	Q9UJ48	Q9UJ48 hepatitis q	371	2	18.2	11	8	Q9G682	Q9G682 cheilosania
299	2	18.2	10	12	Q9UJ48	Q9UJ48 hepatitis q	372	2	18.2	11	8	Q9G655	Q9G655 japalura tr
300	2	18.2	10	12	Q9UJ48	Q9UJ48 hepatitis q	373	2	18.2	11	8	Q9G637	Q9G637 calotes lio
301	2	18.2	10	13	Q9P507	Q9P507 alligator m	374	2	18.2	11	9	Q38415	Q38415 bacterioph
302	2	18.2	10	13	Q9P507	Q9P507 alligator m	375	2	18.2	11	10	Q66626	Q66626 solanum tub
303	2	18.2	10	13	Q73588	Q73588 gallus gall	376	2	18.2	11	10	Q65901	Q65901 leavenworth
304	2	18.2	10	13	Q73594	Q73594 gallus gall	377	2	18.2	11	10	Q8RV30	Q8RV30 zea mays (m
305	2	18.2	10	13	Q82C80	Q82C80 limnodynast	378	2	18.2	11	10	Q9S8X4	Q9S8X4 glycine max
306	2	18.2	10	13	Q82C80	Q82C80 limnodynast	379	2	18.2	11	10	Q93784	Q93784 gossypium h
307	2	18.2	10	15	Q85598	Q85598 moloney mur	380	2	18.2	11	10	Q9T019	Q9T019 brassica ol
308	2	18.2	10	15	Q85619	Q85619 moloney mur	381	2	18.2	11	10	Q941R5	Q941R5 pinus radia

382	2	18.2	11	11	Q99JC3	Q99JC3 rattus sp.	455	2	18.2	12	8	Q95EL0	Q95el0 dendrochilu
383	2	18.2	11	11	Q99AM6	Q99AM6 mus musculus	456	2	18.2	12	8	Q95EK0	Q95ek0 dendrochilu
384	2	18.2	11	11	Q99N81	Q99N81 mus musculus	457	2	18.2	12	8	Q95EL6	Q95el6 dendrochilu
385	2	18.2	11	11	Q9JLE6	Q9JLE6 rattus norv	458	2	18.2	12	8	Q95EM2	Q95em2 dendrochilu
386	2	18.2	11	11	Q9JLH5	Q9JLH5 mus musculus	459	2	18.2	12	8	Q31851	Q31851 arbidopsis
387	2	18.2	11	12	Q86866	Q86866 lymphocytic	460	2	18.2	12	8	Q95EK8	Q95ek8 dendrochilu
388	2	18.2	11	12	Q84084	Q84084 leucania sp	461	2	18.2	12	8	Q95EL2	Q95el2 dendrochilu
389	2	18.2	11	12	Q85806	Q85806 lymphocytic	462	2	18.2	12	8	Q95EM0	Q95em0 dendrochilu
390	2	18.2	11	12	Q86874	Q86874 feline cali	463	2	18.2	12	8	Q95E13	Q95e13 dendrochilu
391	2	18.2	11	12	Q84247	Q84247 poliovaviru	464	2	18.2	12	8	Q03816	Q03816 metasequoia
392	2	18.2	11	13	Q98511	Q98511 lute rubrip	465	2	18.2	12	8	Q95EL8	Q95e18 dendrochilu
393	2	18.2	11	13	Q9AX69	Q9AX69 oreochromis	466	2	18.2	12	8	Q95EK6	Q95ek6 dendrochilu
394	2	18.2	11	13	Q9AX68	Q9AX68 oreochromis	467	2	18.2	12	8	Q95EK2	Q95ek2 dendrochilu
395	2	18.2	11	15	Q93410	Q93410 mouse mamma	468	2	18.2	12	8	Q03815	Q03815 abies alba
396	2	18.2	11	15	Q85620	Q85620 honey murr	469	2	18.2	12	8	Q95EJ1	Q95e11 dendrochilu
397	2	18.2	12	2	Q9K5F7	Q9K5F7 helicobacte	470	2	18.2	12	8	Q95E12	Q95e12 dendrochilu
398	2	18.2	12	2	Q9K149	Q9K149 fischerella	471	2	18.2	12	8	P92457	P92457 ephebra sp.
399	2	18.2	12	2	Q9R5F5	Q9R5F5 helicobacte	472	2	18.2	12	8	Q95E18	Q95e18 dendrochilu
400	2	18.2	12	2	Q9L8H8	Q9L8H8 enterococc	473	2	18.2	12	8	Q95EK4	Q95ek4 dendrochilu
401	2	18.2	12	2	Q9R7F1	Q9R7F1 staphylococ	474	2	18.2	12	8	P92454	P92454 cymas revol
402	2	18.2	12	2	Q8K6T5	Q8K6T5 campylobact	475	2	18.2	12	8	Q95EL4	Q95el4 dendrochilu
403	2	18.2	12	2	Q9K1H4	Q9K1H4 enterococc	476	2	18.2	12	8	P82164	P82164 spinacia ol
404	2	18.2	12	2	Q9X6Y0	Q9X6Y0 aquilex pyr	477	2	18.2	12	8	Q36668	Q36668 pinus sylve
405	2	18.2	12	2	Q46747	Q46747 escherichia	478	2	18.2	12	8	Q37791	Q37791 larix eurol
406	2	18.2	12	2	Q9L8H6	Q9L8H6 enterococc	479	2	18.2	12	8	Q36669	Q36669 pinus sylve
407	2	18.2	12	2	Q9L4M9	Q9L4M9 streptococc	480	2	18.2	12	8	Q37790	Q37790 larix eurol
408	2	18.2	12	2	Q05328	Q05328 sphingomora	481	2	18.2	12	8	Q8H093	Q8H093 bryum donia
409	2	18.2	12	3	Q01275	Q01275 neurospora	482	2	18.2	12	8	Q8HB27	Q8HB27 picea glauc
410	2	18.2	12	3	Q8J0A7	Q8J0A7 saccharomyc	483	2	18.2	12	8	Q8HB26	Q8HB26 picea maria
411	2	18.2	12	4	Q9UMR0	Q9UMR0 homo sapien	484	2	18.2	12	8	Q8HB25	Q8HB25 picea ruben
412	2	18.2	12	4	Q96PH0	Q96PH0 homo sapien	485	2	18.2	12	10	Q8L3X3	Q8L3X3 pinus radia
413	2	18.2	12	4	Q9UC37	Q9UC37 homo sapien	486	2	18.2	12	10	Q8SAS2	Q8SAS2 pinus sylve
414	2	18.2	12	4	Q16452	Q16452 homo sapien	487	2	18.2	12	10	Q93X21	Q93X21 zea mays (m
415	2	18.2	12	4	Q9UMZ9	Q9UMZ9 homo sapien	488	2	18.2	12	10	Q945C3	Q945C3 crypthecodi
416	2	18.2	12	4	Q9HB04	Q9HB04 homo sapien	489	2	18.2	12	10	Q9S938	Q9S938 beta vulgar
417	2	18.2	12	4	Q9HB32	Q9HB32 homo sapien	490	2	18.2	12	10	Q9FSA9	Q9FSA9 silene aega
418	2	18.2	12	4	Q9UMZ8	Q9UMZ8 homo sapien	491	2	18.2	12	10	Q9AXW1	Q9AXW1 brassica na
419	2	18.2	12	4	Q13865	Q13865 homo sapien	492	2	18.2	12	10	Q8SAS3	Q8SAS3 pinus sylve
420	2	18.2	12	4	Q9HAX3	Q9HAX3 homo sapien	493	2	18.2	12	10	P83196	P83196 oryza sativ
421	2	18.2	12	4	Q9NR17	Q9NR17 homo sapien	494	2	18.2	12	10	P82325	P82325 pisum sativ
422	2	18.2	12	5	Q8MYG1	Q8MYG1 drosophila	495	2	18.2	12	10	P82328	P82328 pisum sativ
423	2	18.2	12	5	Q9TWV4	Q9TWV4 lymnaea sta	496	2	18.2	12	11	Q8H6B6	Q8H6B6 hordeum vul
424	2	18.2	12	5	C61574	C61574 estertagia	497	2	18.2	12	11	Q8K303	Q8K303 mus musculu
425	2	18.2	12	6	Q9LHY4	Q9LHY4 sus sp. ias	498	2	18.2	12	11	Q35868	Q35868 mus musculu
426	2	18.2	12	6	Q8MJL0	Q8MJL0 suainus fu	499	2	18.2	12	11	Q9QVK4	Q9QVK4 rattus sp.
427	2	18.2	12	6	Q9LHY4	Q9LHY4 bos taurus	500	2	18.2	12	15	Q12110	Q12110 caprine art
428	2	18.2	12	6	Q8MJL6	Q8MJL6 callithrix							
429	2	18.2	12	6	Q9LHY4	Q9LHY4 callithrix							
430	2	18.2	12	6	Q9LHY4	Q9LHY4 bos taurus							
431	2	18.2	12	6	Q9X5V1	Q9X5V1 sus scrofa							
432	2	18.2	12	6	Q8MJL7	Q8MJL7 callithrix							
433	2	18.2	12	6	Q8MJL9	Q8MJL9 leontopitue							
434	2	18.2	12	6	Q8MJL6	Q8MJL6 cebuella py							
435	2	18.2	12	6	Q95NB4	Q95NB4 eulemur fu							
436	2	18.2	12	6	Q97NT8	Q97NT8 bos taurus							
437	2	18.2	12	6	Q8MJL3	Q8MJL3 saimiri sci							
438	2	18.2	12	6	Q8MJL1	Q8MJL1 ateles fusc							
439	2	18.2	12	6	Q8MJL2	Q8MJL2 cebus apeli							
440	2	18.2	12	6	Q8MJL4	Q8MJL4 aotus azara							
441	2	18.2	12	6	Q91T29	Q91T29 saguinus oe							
442	2	18.2	12	6	Q91T17	Q91T17 bos taurus							
443	2	18.2	12	6	P83127	P83127 bos indicus							
444	2	18.2	12	7	Q77891	Q77891 oreochromis							
445	2	18.2	12	7	Q77920	Q77920 pseudotroph							
446	2	18.2	12	7	C77890	C77890 oreochromis							
447	2	18.2	12	7	Q77889	Q77889 oreochromis							
448	2	18.2	12	8	Q8MES0	Q8MES0 anoda crist							
449	2	18.2	12	8	Q9T203	Q9T203 bos taurus							
450	2	18.2	12	8	Q95EJ8	Q95EJ8 dendrochilu							
451	2	18.2	12	8	Q95E16	Q95E16 dendrochilu							
452	2	18.2	12	8	Q9XN16	Q9XN16 malva nega							
453	2	18.2	12	8	Q9XN16	Q9XN16 pyletella i							
454	2	18.2	12	8	Q95E15	Q95E15 dendrochilu							

ALIGNMENTS

RESULT 1

P83333 PRELIMINARY: PRT: 15 AA.

ID P83333
AC P83333
DT 01-JUN-2002 (TREMBLE1. 21, Created)
DT 01-JUN-2002 (TREMBLE1. 21, Last sequence update)
DT 01-OCT-2002 (TREMBLE1. 22, Last annotation update)
DE Lyszyme C. III (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
[1]
RN TISSUE=Skin mucus;
RC Fernandes J.M.O., Kemp G.D., Smith V.J.;
RA "Characterisation of two muramidases from skin mucus of rainbow trout".
RL Submitted (Apr-2002) to the SWISS-PROT data bank.
CC !- FUNCTION: LYSOZYMES HAVE PRIMARILY A BACTERIOLYTIC FUNCTION; THOSE

CC IN TISSUES AND BODY FLUIDS ARE ASSOCIATED WITH THE MONOCYTE
 CC MACROPHAGE SYSTEM AND ENHANCE THE ACTIVITY OF IMMUNOAGENTS.
 CC -P- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4 BETA-LINKAGES BETWEEN N-
 CC ACETYL-D-GLUCOSAMINE AND N-ACETYL-MURAMIC ACID IN PEPTIDOGLYCAN
 CC HETEROPOLYMERS OF THE PROKARYOTES CELL WALLS.
 CC -P- MASS SPECTROMETRY: MW-14235; METRO-60 MALDI;
 CC -P- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
 DR INTERPT: IPRO01916; Glyco_Hydro_22;
 DR PROSITE: PS00128; LACTALBUMIN-LYSOZYME, PARTIAL
 KW Hydrolase; Glycosidase; Bacteriolytic enzyme
 FT NON_TER 15
 SQ SEQUENCE 15 AA: 1665 MW: 40FE1BE2FA8B870 CRC64:
 Query Match 36.4%; Score 4; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.4e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AKAL 4
 DB 9 AKAL 12
 RESULT 2
 Q9UCN4 PRELIMINARY: PRT: 8 AA.
 AC Q9UCN4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Cell-surface heparin/HEPARANSULFATE binding protein peptide 3
 DE (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 GN NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE
 RX MEDLINE:92291055; PubMed:1601862;
 RA Raboudi N., Julian J., Rohde L.H., Carson E.D.
 RT "Identification of cell-surface heparin/heparan sulfate-binding
 RT proteins of a human uterine epithelial cell line (K056)."
 RL J. Biol. Chem. 267:11930-11939(1992)
 SQ SEQUENCE 8 AA: 689 MW: 80B833D054097E CRC64:
 Query Match 27.3%; Score 3; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GAK 9
 DB 2 GAK 4
 RESULT 3
 Q9R7E8 PRELIMINARY: PRT: 4 AA.
 AC Q9R7E8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE KdsB (Fragment).
 GN KdsB.
 CC Escherichia coli.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;
 CC Enterobacteriaceae; Escherichia.
 GN NCBI_TaxID:562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:95180691; PubMed:7875564;
 RA Roseow C., Roberts J.S., Jiang K.
 RT "Isolation from recombinant Escherichia coli, and characterization of
 RT CMP-Kds synthetase, involved in the expression of the capsular K5

RT polysaccharide (K-Cks).";
 DR FEMS Microbiol. Lett. 125:159-164(1995).
 DR EMBL: S76943; AAB3585.1;
 FT plasmid.
 FT NON_TER 1
 SQ SEQUENCE 9 AA: 899 MW: 3EBBH72042C33DD8 CRC64:
 Query Match 27.3%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 GAK 9
 DB 2 GAK 4
 RESULT 4
 Q16605 PRELIMINARY: PRT: 9 AA.
 ID Q16605;
 AC Q16605;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Glutathione S-transferase 2 (Fragment).
 GN GSTA2 OR GST2.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 GN NCBI_TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:88330756; PubMed:3138230;
 RA Chow N.W., Whang-Peng J., Kao-Shan C.S., Tam M.F., Lai H.C., Tu C.P.;
 RT "Human glutathione S transferases. The Ha multigene family encodes
 RT products of different but overlapping substrate specificities.";
 RL J. Biol. Chem. 263:12797-12800(1988).
 DR EMBL: M21867; AAA52617.1;
 DR EMBL: M21866; AAA35938.1;
 FT NON_TER 9
 SQ SEQUENCE 9 AA: 1116 MW: D168E72327633B1D CRC64:
 Query Match 27.3%; Score 3; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 KPK 11
 DB 4 KPK 6
 RESULT 5
 Q9T2L0 PRELIMINARY: PRT: 9 AA.
 ID Q9T2L0;
 AC Q9T2L0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE LHC II-LIGHT-harvesting chlorophyll protein II (Fragment).
 GN Spinacia oleracea (Spinach).
 CC Chloroplast.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.
 GN NCBI_TaxID:3562;
 RN [1]
 RP SEQUENCE
 RX MEDLINE:91373386; PubMed:1894641;
 RA Michel H., Griffin P.R., Shabanowitz J., Hunt D.F., Bennett J.;
 RT "Tandem mass spectrometry identifies sites of three post-translational
 RT modifications of spinach light-harvesting chlorophyll protein II.
 RT Proteolytic cleavage, acetylation, and phosphorylation.";
 RL J. Biol. Chem. 266:17584-17591(1991).
 FT NON_TER 1


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ID Q91W23 PRELIMINARY; PRT: 10 AA.
AC Q91W23;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Luteinizing hormone/chorionic gonadotropin receptor homolog
DE (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE=96147985; PubMed=8571710;
RA Shen Q.X., Liu H.H., Chen W.Y., Bahl C.P.;
RT "Cloning and overexpression of rat ovary LH/hCG receptor cDNA in
RT insect cells";
RL Shih Yen Sheng Wu Hsueh Pao 28:283-290(1995).
DR EMBL: S80660; AAB50710.1; -.
KW Chorion; Receptor.
FT NON_TER 1
FT SEQUENCE 10 AA; 1129 MW; 09A5F22DC417760 CRC64;

Query Match 27.3%; Score 3; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAL 4
DB 6 RAL 8

RESULT 11
ID Q9Q0W9 PRELIMINARY; PRT: 10 AA.
AC Q9Q0W9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-UMEA3;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119350; AAF24106.1; -.
FT NON_TER 1
FT SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 12
ID Q8JV70 PRELIMINARY; PRT: 10 AA.
AC Q8JV70;
DT 01-OCT-2002 (TrEMBLrel. 22, Created);
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-USA 6;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,

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OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-USA 5;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL: AF304387; AAM97804.1; -.
FT NON_TER 1
FT SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 13
ID Q9Q0W1 PRELIMINARY; PRT: 10 AA.
AC Q9Q0W1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CSFB;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119354; AAF24114.1; -.
FT NON_TER 1
FT SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 14
ID Q8JV68 PRELIMINARY; PRT: 10 AA.
AC Q8JV68;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-USA 6;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,

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RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
KI gastrointestinal tract after exposure to virions or viral DNA.";
KL J. Virol. 75:10290-10299(2001).
DR EMBL: AF304388; AAM97806.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 15
Q69347 ID Q69347 PRELIMINARY: PRT: 10 AA.
AC Q69347;
DT 01-NOV-1996 (TREMBlrel. 0; Created)
DI 01-NOV-1996 (TREMBlrel. 01; Last sequence update)
DE 01-DEC-2001 (TREMBlrel. 19; Last annotation update)
DE Hypothetical 1.1 kDa protein.
OS Herpes simplex virus (type 1 / strain KOS)
OC Viruses: dsDNA viruses, no RNA stage; Herpesviridae;
NC Alphaherpesvirinae; Simplexvirus.
CX NCBI_TaxID=10306;
[1]
KP SEQUENCE FROM N.A.
RC STRAIN=KOS;
RX MEDLINE=86068025; PubMed=2999787;
RA Gibbs J.S., Chlou H.C., Hall J.D., Mount D.W., Retondo M.J.,
RT "Sequencing and mapping analyses of the herpes simplex virus DNA
KI polymerase gene predict a C-terminal substrate binding domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7969-7973(1985).
DR EMBL: M10792; AAA66437.1; -.
KW Hypothetical protein.
SQ SEQUENCE 10 AA; 1057 MW; C45DF775BDC420B CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AKA 3
DB 3 AKA 5

RESULT 16
Q690V9 ID Q690V9 PRELIMINARY: PRT: 10 AA.
AC Q690V9;
DT 01-MAY-2000 (TREMBlrel. 13; Created)
DI 01-MAY-2000 (TREMBlrel. 13; Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13; Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses: dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
[1]
KP SEQUENCE FROM N.A.
RC STRAIN=CSFE;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
KI populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119355; AAF24116.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

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Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 17
Q8JV84 ID Q8JV84 PRELIMINARY: PRT: 10 AA.
AC Q8JV84;
DT 01-OCT-2002 (TREMBlrel. 22; Created)
DI 01-OCT-2002 (TREMBlrel. 22; Last sequence update)
DE 01-OCT-2002 (TREMBlrel. 22; Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses: dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
[1]
KP SEQUENCE FROM N.A.
RC STRAIN=G1;
RX MEDLINE=21465052; PubMed=11581397;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RT "Potential transmission of human polyomaviruses through the
KI gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL: AF303943; AAM97790.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1180 MW; 4CD6A977AF1A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 18
Q900W7 ID Q900W7 PRELIMINARY: PRT: 10 AA.
AC Q900W7;
DT 01-MAY-2000 (TREMBlrel. 13; Created)
DI 01-MAY-2000 (TREMBlrel. 13; Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13; Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses: dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
[1]
KP SEQUENCE FROM N.A.
RC STRAIN=NANCY2;
RX MEDLINE=20087544; PubMed=10618230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
KI populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119351; AAF24108.1; -.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

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RESULT 19
Q8JV66 PRELIMINARY; PRT; 10 AA.
ID Q8JV66;
AC Q8JV66;
DT 01-OCT-2002 (TReMBLrel..22, Created)
DT 01-OCT-2002 (TReMBLrel..22, Last sequence update)
DE 01-OCT-2002 (TReMBLrel..22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSF K;
RX MEDLINE=21465052; PubMed=11581397;
RA Bojill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions of viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL: AF304389; AAM97808.1; -.
FT NON_TER 1
FT SEQUENCE 10 AA; 1167 MW; 4C06A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB [1]
3 KPK 5

RESULT 20
Q8JV76 PRELIMINARY; PRT; 10 AA.
ID Q8JV76;
AC Q8JV76;
DT 01-MAY-2000 (TReMBLrel..13, Created)
DT 01-MAY-2000 (TReMBLrel..13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel..13, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSF2;
RX MEDLINE=2007544; PubMed=10618230;
RA Bojill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewerage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119356; AAF24118.1; -.
FT NON_TER 1
FT SEQUENCE 10 AA; 1167 MW; 4C06A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB [1]
3 KPK 5

RESULT 21
Q8JV82 PRELIMINARY; PRT; 10 AA.
ID Q8JV82;
AC Q8JV82;
DT 01-OCT-2002 (TReMBLrel..22, Created)
DT 01-OCT-2002 (TReMBLrel..22, Last sequence update)

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DT 01-OCT-2002 (TReMBLrel..22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL;
RX MEDLINE=21465052; PubMed=11581397;
RA Bojill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions of viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL: AF303944; AAM97792.1; -.
FT NON_TER 1
FT SEQUENCE 10 AA; 1167 MW; 4C06A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB [1]
3 KPK 5

RESULT 22
Q8JV76 PRELIMINARY; PRT; 10 AA.
ID Q8JV76;
AC Q8JV76;
DT 01-OCT-2002 (TReMBLrel..22, Created)
DT 01-OCT-2002 (TReMBLrel..22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel..22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA2;
RX MEDLINE=21465052; PubMed=11581397;
RA Bojill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to virions of viral DNA.";
RL J. Virol. 75:10290-10299(2001).
DR EMBL: AF303947; AAM97798.1; -.
FT NON_TER 1
FT SEQUENCE 10 AA; 1167 MW; 4C06A97771A32763 CRC64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB [1]
3 KPK 5

RESULT 23
Q8JV74 PRELIMINARY; PRT; 10 AA.
ID Q8JV74;
AC Q8JV74;
DT 01-OCT-2002 (TReMBLrel..22, Created)
DT 01-OCT-2002 (TReMBLrel..22, Last sequence update)
DT 01-OCT-2002 (TReMBLrel..22, Last annotation update)
DE Large T antigen (Fragment).
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.

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KC STRAIN-USA3;
RX MEDLINE-21465052; PubMed-11591397;
RA Bo111-Mas S., Formiga-Cruz M., Clemente-Casares P., Calatell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to viruses of viral RNA.";
RL J. Virol. 75:10290-10299(2001);
DR EMBL: AF303948; AAM97800.1;
FT NON_TER
SQ SEQUENCE 10 AA: 1167 MW: 4006497771A32763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 9 KPK 11
DB 3 KPK 5

RESULT 24
Q900X7 PRELIMINARY: PRT: 10 AA.
AC Q900X7;
DT 01-MAY-2000 (TrEMBLrel. 13; Created);
DI 01-MAY-2000 (TrEMBLrel. 13; Last sequence update);
DE Large T antigen (Fragment);
OS Polyomavirus JC;
OC Viruses; dSDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN-BCN2;
RA MEDLINE-20087544; PubMed-10618230;
RA Bo111-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000);
DR EMBL: AF119346; AAF4098.1;
FT NON_TER
SQ SEQUENCE 10 AA: 1180 MW: 4006497771A32763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 9 KPK 11
DB 3 KPK 5

RESULT 25
Q8J078 PRELIMINARY: PRT: 10 AA.
AC Q8J078;
DI 01-OCT-2002 (TrEMBLrel. 22; Created);
DI 01-OCT-2002 (TrEMBLrel. 22; Last sequence update);
DE Large T antigen (Fragment);
OS Polyomavirus JC;
OC Viruses; dSDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN-USA1;
RA MEDLINE-21465052; PubMed-11591397;
RA Bo111-Mas S., Formiga-Cruz M., Clemente-Casares P., Calatell F.,
RA Girones R.;
RT "Potential transmission of human polyomaviruses through the
RT gastrointestinal tract after exposure to viruses of viral RNA.";
RL J. Virol. 75:10290-10299(2001);
DR EMBL: AF303948; AAM97796.1;
FT NON_TER
SQ SEQUENCE 10 AA: 1167 MW: 4006497771A32763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 9 KPK 11
DB 3 KPK 5

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FT NON_TER
SQ SEQUENCE 10 AA: 1183 MW: 4006496731A32763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 9 KPK 11
DB 3 KPK 5

RESULT 26
Q900W5 PRELIMINARY: PRT: 10 AA.
AC Q900W5;
DT 01-MAY-2000 (TrEMBLrel. 13; Created);
DT 01-MAY-2000 (TrEMBLrel. 13; Last sequence update);
DT 01-MAY-2000 (TrEMBLrel. 13; Last annotation update);
DE Large T antigen (Fragment);
OS Polyomavirus JC;
OC Viruses; dSDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN-PRETORIA3;
RX MEDLINE-20087544; PubMed-10618230;
RA Bo111-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000);
DR EMBL: AF119352; AAF24110.1;
FT NON_TER
SQ SEQUENCE 10 AA: 1167 MW: 4006497771A32763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 9 KPK 11
DB 3 KPK 5

RESULT 27
Q900X3 PRELIMINARY: PRT: 10 AA.
AC Q900X3;
DI 01-MAY-2000 (TrEMBLrel. 13; Created);
DI 01-MAY-2000 (TrEMBLrel. 13; Last sequence update);
DI 01-MAY-2000 (TrEMBLrel. 13; Last annotation update);
DE Large T antigen (Fragment);
OS Polyomavirus JC;
OC Viruses; dSDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN-BCN8;
RX MEDLINE-20087544; PubMed-10618230;
RA Bo111-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
RT populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000);
DR EMBL: AF119448; AAF24102.1;
FT NON_TER
SQ SEQUENCE 10 AA: 1167 MW: 4006497771A32763 CRC64;

Query Match 27.3% Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 9 KPK 11
DB 3 KPK 5

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Db          3 KPK 5

RESULT 28
Q9Q0X5      PRELIMINARY;      PRT:      10 AA.
AC Q9Q0X5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DI 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Large T antigen (Fragment);
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN BCN16;
RX Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
   populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119347; AAF24100.1;
FT NON_TER
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match      27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          9 KPK 11
Db          111
          3 KPK 5

RESULT 29
Q9Q0W3      PRELIMINARY;      PRT:      10 AA.
AC Q9Q0W3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DI 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Large T antigen (Fragment);
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN PRETORIAL;
RX MEDLINE:20087544; PubMed-10612230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
   populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119353; AAF24112.1;
FT NON_TER
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match      27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          9 KPK 11
Db          111
          3 KPK 5

RESULT 30
Q9JUV80     PRELIMINARY;      PRT:      10 AA.
AC Q9JUV80;
DI 01-OCT-2002 (TREMBlrel. 22, Created)
DE Large T antigen (Fragment);
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN BCN16;
RX MEDLINE:20087544; PubMed-10612230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
   populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119353; AAF24112.1;
FT NON_TER
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match      27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          9 KPK 11
Db          111
          3 KPK 5

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UT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Large T antigen (Fragment);
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-E2;
RX MEDLINE:21455052; PubMed-11581497;
RA Bofill-Mas S., Formiga-Cruz M., Clemente-Casares P., Calafell F.,
   Girones R.;
RT "Potential transmission of human polyomaviruses through the
   gastrointestinal tract after exposure to virions or viral DNA.";
RL J. Virol. 75:19290-19299(2001).
DR EMBL; AF303945; AAM97794.1;
FT NON_TER
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match      27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          9 KPK 11
Db          111
          3 KPK 5

RESULT 31
Q9Q0X1      PRELIMINARY;      PRT:      10 AA.
AC Q9Q0X1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DI 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Large T antigen (Fragment);
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BCN15;
RX MEDLINE:20087544; PubMed-10612230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
   populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119349; AAF24104.1;
FT NON_TER
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match      27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          9 KPK 11
Db          111
          3 KPK 5

RESULT 32
Q9Q0X9      PRELIMINARY;      PRT:      10 AA.
AC Q9Q0X9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DI 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE Large T antigen (Fragment);
OS Polyomavirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomavirus.
CX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BCN16;
RX MEDLINE:20087544; PubMed-10612230;
RA Bofill-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polyomaviruses in human
   populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL; AF119349; AAF24104.1;
FT NON_TER
SQ SEQUENCE 10 AA; 1167 MW; 4CD6A97771A32763 CRC64;

Query Match      27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          9 KPK 11
Db          111
          3 KPK 5

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RA MEDLINE:20087544; PubMed=10518240;
RA Botilli-Mas S., Pina S., Girones R.;
RT "Documenting the epidemiologic patterns of polioviruses in human
R populations by studying their presence in urban sewage.";
RL Appl. Environ. Microbiol. 66:238-245(2000).
DR EMBL: AF119345; AAF24096.1;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4006A97771A42763 CR*64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 33
ID Q8JV72 PRELIMINARY: PRT; 16 AA.
AC Q8JV72
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DI 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DI 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Large T antigen (Fragment).
OS Poliovirus JC.
OC Viruses; dsDNA viruses, no RNA stage; Polymoviridae; Polymovavirus.
OX NCBI_TaxID=10632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USA 4;
RX MEDC:NE-21465C52; PubMed=11561347;
RA Botilli-Mas S., Formiga-Cruz M., Clemente-Gusares E., Calatell F.,
RA Girones R.;
RT "Potential transmission of human polioviruses through the
RT gastrointestinal tract after exposure to viruses of viral DNA.";
RL J. Virol. 75:10290-10295(2001).
DR EMBL: AF304386; AAM97802.1;
FT NON_TER 1
SQ SEQUENCE 10 AA; 1167 MW; 4706A97771A42763 CR*64;

Query Match 27.3%; Score 3; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 3 KPK 5

RESULT 34
ID Q8TDAB PRELIMINARY: PRT; 11 AA.
AC Q8TDAB
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DI 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Glutathione synthetase (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Cho Y. W., Lee Y.-Y., Lim C.-J.;
RT "Cloning and characterization of glutathione synthetase gene from
RT human placenta DNA.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL: AF485789; AAL91591.1;
FT NON_TER 11
SQ SEQUENCE 11 AA; 1235 MW; 1CB2831E59F6474 CR*64;

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Query Match 27.3%; Score 3; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NMG 7
DB 4 NMG 6

RESULT 35
ID Q9IWX6 PRELIMINARY: PRT; 11 AA.
AC Q9IWX6
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Juvenile hormone binding protein, JHBP-12.5 kDa CNBR peptide
DE (Fragment).
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Spingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7140;
RN [1]
RP SEQUENCE
RX MEDLINE=92134256; PubMed=1734862;
RA Touhara K., Prestwich G.D.;
RT "Binding site mapping of a photoaffinity-labeled juvenile hormone
RT binding protein.";
RL Biochem. Biophys. Res. Commun. 182:466-473(1992).
FT NON_TER 11
SQ SEQUENCE 11 AA; 1071 MW; D232A98E705045BD CR*64;

Query Match 27.3%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9
DB 9 GAK 11

RESULT 36
ID Q23876 PRELIMINARY: PRT; 11 AA.
AC Q23876
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-NOV-1998 (TrEMBLrel. 01, Last annotation update)
DE Actin 4.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX NCBI_TaxID=44869;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=82260445; PubMed=6286214;
RA McKown M., Firtel R.A.;
RT "Actin multigene family of Dictyostelium.";
RL Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
DR EMBL: K02957; AAA33150.1;
DR EMBL: K02956; AAA33150.1; JOINED.
SQ SEQUENCE 11 AA; 1205 MW; 728B4C14C6C2CAAB CR*64;

Query Match 27.3%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ALN 5
DB 8 ALN 10

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RESULT 37
Q9TOS9          PRELIMINARY;      PRT:      11 AA.
AC Q9TOS9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Transferrin (Fragment).
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Giffard J.M., Brandon R.B., Bell T.K.;
RT "Further identification of single nucleotide polymorphisms in the
RT equine transferrin gene."
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AF185800; AAF05495.1;
DR EMBL: AF185797; AAF05492.1;
DR EMBL: AF185798; AAF05493.1;
DR EMBL: AF185799; AAF05494.1;
FT NON_TER 11
SQ SEQUENCE 11 AA; 1231 MW; 6586121E2DC4905D CRC64;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KAK 4
DB 6 KAL 8

RESULT 38
Q9QVH3          PRELIMINARY;      PRT:      11 AA.
AC Q9QVH3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Chromogranin-B, CGB-GLUCAGONOMA peptide (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Scuriognathia; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92064871; PubMed=1954899;
RA Nielsen E., Wellinder B.S., Madsen A.L.;
RT "Chromogranin-B, a putative precursor of eight novel rat glucagonoma
RT peptides through processing at mono-, di-, or tri-basic residues."
RL Endocrinology 129:3147-3156(1991).
DR InterPro: IPR001990; Granin.
DR Pfam: PF01271; Granin; 1.
FT NON_TER 1
FT NON_TER 11
SQ SEQUENCE 11 AA; 1342 MW; 6C82C37374525AAB CRC64;

Query Match 27.3%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NWG 7
DB 7 NWG 9

RESULT 39
Q8VLX8          PRELIMINARY;      PRT:      12 AA.
AC Q8VLX8;
DT 01-MAR-2002 (TREMBlrel. 20, Created)

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DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Lysyl-tRNA synthetase (Fragment).
GN LYSS.
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OC Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RA Spada S., Fembroke J.T., Wall J.G.;
RT "Cloning and characterisation of the czrB metal cation efflux protein
RT from T. thermophilus."
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AJ307316; CAC83721.1;
KW Aminoacyl-tRNA synthetase.
FT NON_TER 1
SQ SEQUENCE 12 AA; 1327 MW; 5D2A33E27ECDD813 CRC64;

Query Match 27.3%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 2 KPK 4

RESULT 40
P94011          PRELIMINARY;      PRT:      12 AA.
ID P94011;
AC P94011;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Elongation factor EF-1 alpha A4 (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA SPRAIN-cv. Columbia; TISSUE-Green siliques;
RA Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.;
RL Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
DR EMBL: Z27066; CAA81582.1;
FT NON_TER 1
SQ SEQUENCE 12 AA; 1229 MW; CEDA9EA59422CDDD CRC64;

Query Match 27.3%; Score 3; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9
DB 10 GAK 12

RESULT 41
O34770          PRELIMINARY;      PRT:      13 AA.
ID O34770;
AC O34770;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE GUAA (Fragment).
GN GUAA.
OS Borrelia afzelii.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=29518;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN PKO, VS461, and J11;
RX MEDLINE-97426044; PubMed-9282748;
RA Tilly K., Casjens S., Stevenson H., Bono J.L., Samuels D.S., Hogan D.,
  Rosa P.;
RI "The Borrelia burgdorferi circular plasmid cp26: conservation of
  plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-374(1997).
DR EMBL: U93698; AAC45530.1; -.
DR EMBL: U93695; AAC45524.1; -.
DR EMBL: U94697; AAC45528.1; -.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1421 MW; 08FAR3950E195720 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.2e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARA 3
   III
Db 3 ARA 5

RESULT 42
Q34622 PRELIMINARY; PRT; 13 AA.
AC Q34622;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DI 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DI 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
EF GUAA (Fragment).
GN GUAA.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=135;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN-C139, UN127CL9-2, and 25015;
RX MEDLINE-97426044; PubMed-9282748;
RA Tilly K., Casjens S., Stevenson H., Bono J.L., Samuels D.S., Hogan D.,
  Rosa P.;
RI "The Borrelia burgdorferi circular plasmid cp26: conservation of
  plasmid structure and targeted inactivation of the ospC gene.";
RL Mol. Microbiol. 25:361-374(1997).
DR EMBL: U93694; AAC45522.1; -.
DR EMBL: U04280; AAC45543.1; -.
DR EMBL: U04282; AAC45541.1; -.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1407 MW; 08FAR3950E09C720 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.2e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARA 3
   III
Db 3 ARA 5

RESULT 43
Q96PT0 PRELIMINARY; PRT; 13 AA.
AC Q96PT0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

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DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Epilysin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21167821; PubMed-1121198;
RA Lohi J., Wilson C.L., Roby J.D., Parks W.C.;
RI "Epilysin, a novel human matrix metalloproteinase (MMP-28) expressed
  in testis and keratinocytes and in response to injury.";
RL J. Biol. Chem. 276:10134-10144(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-21458570; PubMed-11574168;
RA Lilman S.A., Keski-Oja J., Lohi J.;
RI "Promoter characterization of the human and mouse epilysin (MMP-28)
  genes.";
RL Gene 275:185-194(2001).
DR EMBL: AF336346; AAL15619.1; -.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1440 MW; 2F1EE783D61E2728 CRC64;

Query Match 27.3%; Score 3; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.2e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAL 4
   III
Db 10 RAL 12

RESULT 44
Q907D6 PRELIMINARY; PRT; 13 AA.
AC Q907D6;
DI 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Ycf24 protein (fragment).
GN YCF24.
OS Neospora caninum.
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
  Neosporida.
OX NCBI_TaxID=29176;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC1;
RX MEDLINE-20074141; PubMed-10508442;
RA Lang-Unnasch N., Aiello D.P.;
RI "Sequence evidence for an altered genetic code in the Neospora caninum
  plasmid.";
RL Int. J. Parasitol. 29:1557-1562(1999).
DR EMBL: AF138960; AAF14260.1; -.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1532 MW; CC8DB4011FCDC40D CRC64;

Query Match 27.3%; Score 3; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.2e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARA 3
   III
Db 6 ARA 8

RESULT 45
Q97122 PRELIMINARY; PRT; 13 AA.
AC Q97122;
DI 01-MAY-1999 (TrEMBLrel. 10, Created)
DI 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)

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BT 01-MAY-1999 (TRENBLREL. 10, Last annotation update)
DE YCF24.
GN Tokoplasma gondii.
OS Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriidae; Sarcocystidae;
OC Tokoplasma
OC Tokoplasma
GX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RH:
RA Atello D.P., Lang-Unnasch N.J.
RT "Analysis of the rpoB gene product of Tokoplasma gondii."
RL Submitted (SEP-1998) to the EMBL/GenBank/Trna databases.
DR EMBL: AF095904; AAD17841.1;
FT NON_TER 1
SQ SEQUENCE 13 AA: 1532 MW: 3090640115167430.76664;

Query Match 27.3% Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARA 3
DB 6 ARA 8

RESULT 46
Q9GJC2 ID Q9GJC2 PRELIMINARY; PRT; 13 AA.
AC Q9GJC2
DT 01-MAR-2001 (TRENBLREL. 15, Created)
DT 01-MAR-2001 (TRENBLREL. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLREL. 16, Last annotation update)
DE Calpastatin (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
GX NCBI_TaxID=9440;
RN [1]
RP SEQUENCE FROM N.A.
RA Noneman D., Geesink G.H., Kachmarian M.
RT "Differential splicing and protein isoforms of calpastatin."
RL Submitted (OCT-1999) to the EMBL/GenBank/Trna databases.
DR EMBL: AF192536; AAC31688.1;
DR EMBL: AF192535; AAC31687.1;
FT NON_TER 1
SQ SEQUENCE 13 AA: 1335 MW: 41671309666.63663;

Query Match 27.3% Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 4 KPK 6

RESULT 47
Q62455 ID Q62455 PRELIMINARY; PRT; 13 AA.
AC Q62455
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Trypsin (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
GX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-A/1;
RX MEDLINE=87066713; Pubmed=3641189;
RA Stevenson B.J., Hagenbuechle C., Wellauer P.K.;
RT "Sequence organisation and transcriptional regulation of the mouse
elastase II and trypsin genes."
RL Nucleic Acids Res 14:8307-8330(1986).
DR EMBL: X04580; CAA28248.1;
DR MGD: MGI:102757; Try4.
FT NON_TER 13
SQ SEQUENCE 13 AA: 1346 MW: 20554200214D729 CRC64;

Query Match 27.3% Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAI 4
DB 2 RAI 4

RESULT 48
Q9CU06 ID Q9CU06 PRELIMINARY; PRT; 13 AA.
AC Q9CU06
DT 01-JUN-2001 (TRENBLREL. 17, Created)
DT 01-JUN-2001 (TRENBLREL. 17, Last sequence update)
DT 01-JUN-2001 (TRENBLREL. 17, Last annotation update)
DE Zona pellucida binding protein (Fragment).
GX ZPBP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
GX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=21085660; Pubmed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kuenl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schraml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Bettei D., Bolunda N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gastlrich S., Hill D., Holtzmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni E., Mashima J., Mazzarelli J., Mombaerts P.,
Nordenskiöld P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
Hayashizaki Y.
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:585-590(2001).
DR EMBL: AK018876; BAB31470.1;
DR MGD: MGI:1855701; Zpbp.
FT NON_TER 1
SQ SEQUENCE 13 AA: 1404 MW: D6A4220999576842 CRC64;

Query Match 27.3% Score 3; DB 11; Length 13;
Best Local Similarity 100.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9
DB 8 GAK 10

RESULT 49
Q62455 ID Q62455 PRELIMINARY; PRT; 13 AA.
AC Q62455
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE Trypsin (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
GX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

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ID	QCUIW3	PRELIMINARY:	ERT:	14 AA.
AC	QCUIW3			
DT	01-MAR-2003 (TRMBLrel. 23, created)			
DI	01-MAR-2003 (TRMBLrel. 23, last sequence update)			
DI	01-MAR-2003 (TRMBLrel. 23, last annotation update)			
DE	MORF4-related protein (Fragment).			
GN	TEX189			
GN	Mus musculus (Mouse).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Mammalia; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurostomatia; Muridae; Murinae; Mus.			
OX	NCBI_TaxID:10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN L29/S897			
RA	MEDLINE: 22220132; PubMed:12274461			
RA	Taniguchi K., Pereira-Smith O.,			
RI	"The genomic organization, promoter position and expression profile of			
RI	the mouse MORF4 gene."			
RL	Gene 294:215-215(2002).			
DR	EMBL: AY072694; AAL67900.1; -			
FT	NON-TER 13 13			
SQ	SEQUENCE 13 AA: 1544 MW: 980488/356276A (0004)			
Query Match 27.38; Score 3; 16 11; Length 14;				
Best Local Similarity 100.0%; Pctid No. 8; 400; 4;				
Matches	3;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	9 KPK 11			
IB	111			
IB	6 KPK 10			
RESULT 50				
Q69394	Q69394	PRELIMINARY:	ERT:	14 AA
AC	Q69394			
DT	01-NOV-1996 (TRMBLrel. 01, created)			
DI	01-NOV-1996 (TRMBLrel. 01, last sequence update)			
DI	01-NOV-1996 (TRMBLrel. 08, last annotation update)			
DE	Glycoprotein precursor (Fragment).			
OS	Pseudorabies virus.			
OC	Viruses; dsDNA viruses, to RNA stage; Herpesviridae;			
OC	Alphaherpesvirinae; Varicellovirinae.			
OX	NCBI_TaxID:10445;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE: 94227568; PubMed:8485640;			
RA	Ryan P., Robbins A., Whealy M., Enquist			
RI	"Overall signal sequence hydrophobicity, polarity, and the in vitro			
RI	translocation efficiency of a herpesvirus signal peptide."			
RL	Virus Genes 7:5-21(1993).			
DR	EMBL: M77773; AAA73134.1; -			
KW	Signal.			
FT	SIGNAL 1 12 POTENTIAL			
FT	CHAIN 13 >13 POTENTIAL			
FT	NON-TER 13 13			
SQ	SEQUENCE 13 AA: 1274 MW: 20366752/2666234 (0004)			
Query Match 27.38; Score 3; 16 12; Length 14;				
Best Local Similarity 100.0%; Pctid No. 8; 400; 4;				
Matches	3;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 ASA 3			
IB	111			
IB	5 ASA 7			

GenCore version 5.1.6

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OM protein - protein search, using SW model

Run on: September 30, 2003, 10:07:04 : Search time 6.26 Seconds

(without alignments)
82,767 Million cell updates/sec

Title: us-09-787-443-3

Perfect score: 11

Sequence: 1 ARALWGAQPK 11

Scoring table: GLI30

Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 9

Total number of hits satisfying chosen parameters: 707

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : SwissProt_41.*

Note: No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	13	1	CH60_CANFA
2	3	27.3	10	1	COXQ_SHEEP
3	3	27.3	10	1	HIF1_ROMM
4	3	27.3	10	1	HIF2_ROMM
5	3	27.3	11	1	RS30_ONCMY
6	3	27.3	15	1	FGF1_CANFA
7	2	18.2	8	1	ACT_THICK
8	2	18.2	8	1	AKH_MELM
9	2	18.2	8	1	ALB4_CYTO
10	2	18.2	8	1	ALB5_CYTO
11	2	18.2	8	1	FAR4_CANFA
12	2	18.2	8	1	FAR5_CANFA
13	2	18.2	8	1	GLUR_HUMAN
14	2	18.2	8	1	HIF1_PERAM
15	2	18.2	8	1	HIF2_PERAM
16	2	18.2	8	1	HIF_TENM
17	2	18.2	8	1	LCK1_LEUMA
18	2	18.2	8	1	LCK2_LEUMA
19	2	18.2	8	1	LCK3_LEUMA
20	2	18.2	8	1	LCK4_LEUMA
21	2	18.2	8	1	LCK5_LEUMA
22	2	18.2	8	1	LCK6_LEUMA
23	2	18.2	8	1	LCK7_LEUMA
24	2	18.2	8	1	LCK8_LEUMA
25	2	18.2	8	1	NS1_MYCTU
26	2	18.2	8	1	RQC1_PANBO
27	2	18.2	8	1	RS1_ERWCH
28	2	18.2	8	1	RS7_MYC11
29	2	18.2	8	1	RT34_RGVIN
30	2	18.2	8	1	UF06_MOUSE
31	2	18.2	8	1	WPI_PEAR1
32	2	18.2	9	1	CON2_CUNGE
33	2	18.2	9	1	COM_CONVE

P1859 calliphora
P43170 ascaris suu
P82661 panagrellus
P31799 locusta mig
P04277 homo sapien
P82003 bombyx mori
P82926 bos taurus
P01255 sus scrofa
P30092 homo sapien
P30422 bothrops ja
P10222 bothrops ja
P30426 bothrops in
P31351 viper a aspi
P83208 oncorhynch
P80328 oncorhynch
P80336 oryctolagus
P83317 penaeus mon
P83278 macrobrachi
P82660 panagrellus
P42560 mytilus edu
P14537 ceratotheri
P02728 homo sapien
P80677 chelyosoma
P04378 petromyzon
P30948 petromyzon
P16353 heliothis z
P10939 nauphoeta c
P14596 tabanus atr
P13270 jatropha mu
P81135 mycobacteri
P81863 pardachirus
P22103 homo sapien
P21996 rattus norv
P81084 pinus pinas
P29221 acholeplasm
P08608 scyllorhinu
P40752 urechis uni
P19118 nicotiana p
P30091 homo sapien
P32080 homo sapien
P80717 dictyoglu
P01021 akistodon
P82087 litoria cit
P82088 litoria cit
P81095 bacillus su
P56571 rattus norv
P83321 penaeus mon
P05624 thiermus the
P80580 klebsiella
P49820 canis fami
P41837 periplaneta
P80464 comamonas t
P13179 chandipura
P08616 uperoleia r
P28498 gadus morhu
P01290 equus cabal
P28499 oncorhynch
P22688 rana catesb
P29207 rana ridibu
P41333 scyllorhinu
P22691 rana catesb
P31933 homo sapien
P99013 saccharomyc
P83322 penaeus mon
P82021 litoria inf
P83327 oncorhynch
P83054 bacteroides
P22395 locusta mig
P80903 methanobact
P80662 physcomitre
Q46490 clover yell
Q47881 elm yellows
P80863 bacillus su

107	2	18.2	12	1	TKN_KASMA	P08613	kassia mac	180	2	18.2	15	1	IMA2_LOCHI	P38497	locusta mig
108	2	18.2	12	1	TKN_KASSE	P08611	kassia sen	181	2	18.2	15	1	LPL_THETH	P21234	thermus the
109	2	18.2	12	1	URZA_CATCO	P04558	catostomus	182	2	18.2	15	1	MAOX_CHICK	Q92060	gallus gall
110	2	18.2	12	1	VIAK_WSSV	P82006	white spot	183	2	18.2	15	1	MCRA_METTE	P22948	methanosarc
111	2	18.2	13	1	ADFB_TENMO	P83109	tenebrio mo	184	2	18.2	15	1	METK_MAIZE	P80616	zea mays (m
112	2	18.2	13	1	BPJ7_FUMA	P81754	leucophaea	185	2	18.2	15	1	MK1_PALPR	P80408	palomena pr
113	2	18.2	13	1	CHBP_FAKID	P42718	parapolybia	186	2	18.2	15	1	MK2A_PALPR	P80409	palomena pr
114	2	18.2	13	1	CRBL_VESAN	P17233	vespa anali	187	2	18.2	15	1	NU08_SOLTU	P80731	solanum tub
115	2	18.2	13	1	CRBL_VESCR	P01519	vespa crabr	188	2	18.2	15	1	NXSO_PSETE	P59073	pseudonaja
116	2	18.2	13	1	CRBL_VESIE	P17215	vespula iew	189	2	18.2	15	1	ODP3_SOLTU	P81420	solanum tub
117	2	18.2	13	1	CRBL_VESXA	P17234	vespa xanth	190	2	18.2	15	1	ONC1_ONCNY	P83287	oncorhynch
118	2	18.2	13	1	FIBB_HYLLA	P14472	lyctobates l	191	2	18.2	15	1	PC20_BRANA	P81096	brassica na
119	2	18.2	13	1	FIBB_HAB11	P14478	oryctolagus	192	2	18.2	15	1	PGKH_PHYPA	P80659	physcomitre
120	2	18.2	13	1	ITBS_BOVIN	P80747	bos taurus	193	2	18.2	15	1	PGTS_PELAC	P80564	pelobacter
121	2	18.2	13	1	IMAI_LOCHI	P38496	locusta mig	194	2	18.2	15	1	R13A_SPIOL	P82454	spinacia ol
122	2	18.2	13	1	MLA_ANCCA	P41589	anellus caro	195	2	18.2	15	1	RBS_PHYPA	P80657	physcomitre
123	2	18.2	13	1	MLA_CAMDRA	P01198	camelus dro	196	2	18.2	15	1	RL11_STRAU	Q94520	streptomyce
124	2	18.2	13	1	NEUT_BUFMA	P81796	buto marinu	197	2	18.2	15	1	RS10_BACST	P59683	bacillus st
125	2	18.2	13	1	NEUT_CHICK	P13724	gallus gall	198	2	18.2	15	1	RS20_BACST	P59681	bacillus st
126	2	18.2	13	1	NEUT_FANTE	P41536	rana tempor	199	2	18.2	15	1	SODM_ENTAE	P22799	enterobacte
127	2	18.2	13	1	NEUT_TRLVJ	P31745	trichosurus	200	2	18.2	15	1	SODM_STRGR	P80733	streptomyce
128	2	18.2	13	1	PSRP_PINPS	P81668	pinus pinas	201	2	18.2	15	1	TAI1_TREBR	P34070	tremella br
129	2	18.2	13	1	RPOC_MYCGA	P47716	mycoplasma	202	2	18.2	15	1	TRPA_LEUMA	P81753	leucophaea
130	2	18.2	13	1	RS19_ASHYP	Q44592	ash yellows	203	2	18.2	15	1	UBL1_MONDO	P50103	monodelphis
131	2	18.2	13	1	SODM_CANFA	P54712	canis famli	204	2	18.2	15	1	UC14_MAIZE	P80620	zea mays (m
132	2	18.2	13	1	TEGA_RANCA	P83307	rana japoni	205	2	18.2	15	1	UC17_MAIZE	P80623	zea mays (m
133	2	18.2	13	1	TEMC_FANTE	P56916	rana tempor	206	2	18.2	15	1	UC20_MAIZE	P80626	zea mays (m
134	2	18.2	13	1	TEMC_FANTE	P56919	rana tempor	207	2	18.2	15	1	UC23_MAIZE	P80629	zea mays (m
135	2	18.2	13	1	TEMC_RANTE	P56920	rana tempor	208	2	18.2	15	1	UC28_MAIZE	P80634	zea mays (m
136	2	18.2	13	1	TY13_PHYRO	P34096	phyllomedus	209	2	18.2	15	1	UE15_HORVU	P34938	hordeum vul
137	2	18.2	14	1	HGAT_MOUSE	P38649	m fistro-blo	210	2	18.2	15	1	UN04_PINPS	P81673	pinus pinas
138	2	18.2	14	1	GALI_CALGI	P20728	calotropis	211	2	18.2	15	1	VORA_METTM	P80907	methanobact
139	2	18.2	14	1	DHSL_ANACY	P17874	anabaena cy	212	2	18.2	15	1	YAA3_RHOPA	Q02006	rhodopseudo
140	2	18.2	14	1	SFTU_CANFA	P54835	canis famli	213	2	9.1	8	1	ACT_CARMA	P80709	carcinus ma
141	2	18.2	14	1	GR75_CANFA	P59502	canis famli	214	2	9.1	8	1	AKHG_GRYBI	P14086	gryllus bim
142	2	18.2	14	1	HY14_PTS	P01155	sus scrota	215	2	9.1	8	1	AKH_LIBAU	P25418	libellula a
143	2	18.2	14	1	KARA_BKAPL	P22442	bromelia pl	216	2	9.1	8	1	AKH_TABAT	P14595	tabanus atr
144	2	18.2	14	1	LPEK_BACLI	Q64403	bacillus li	217	2	9.1	8	1	AL12_CARMA	P81815	carcinus ma
145	2	18.2	14	1	LPM_RHIME	P18854	rhizobium m	218	2	9.1	8	1	AL15_CARMA	P81818	carcinus ma
146	2	18.2	14	1	LPM_SALTY	P03954	salmorella	219	2	9.1	8	1	AL16_CARMA	P81819	carcinus ma
147	2	18.2	14	1	MAST_PAKID	P42716	parapolybia	220	2	9.1	8	1	AL17_CARMA	P81820	carcinus ma
148	2	18.2	14	1	MAST_VESBA	P21654	vespa basal	221	2	9.1	8	1	AL18_CARMA	P81821	carcinus ma
149	2	18.2	14	1	MAST_VESCR	P01516	vespa crabr	222	2	9.1	8	1	ALL1_CYDPO	P82152	cydia pomon
150	2	18.2	14	1	MAST_VESIE	P01514	vespula iew	223	2	9.1	8	1	ALL3_CYDPO	P82154	cydia pomon
151	2	18.2	14	1	MAST_VESMA	P04265	vespa manda	224	2	9.1	8	1	ALL4_CALVO	P41840	calliphora
152	2	18.2	14	1	MAST_VESOR	P17248	vespa orien	225	2	9.1	8	1	ALL5_CALVO	P41841	calliphora
153	2	18.2	14	1	MPEX_METEM	P01515	vespa xanth	226	2	9.1	8	1	ALL6_CYDPO	P82157	cydia pomon
154	2	18.2	14	1	MY14_EUSEP	P58915	melibactact	227	2	9.1	8	1	ALL7_CARMA	P81809	carcinus ma
155	2	18.2	14	1	PSA2_PUSSA	P46979	eisenia ioe	228	2	9.1	8	1	ALL8_CARMA	P81811	carcinus ma
156	2	18.2	14	1	RS49_OLEPP	P42049	cucumis sat	229	2	9.1	8	1	ALL9_CARMA	P81812	carcinus ma
157	2	18.2	14	1	RS49_OLEPP	Q46428	clover grol	230	2	9.1	8	1	ANG2_BOTJA	Q10582	bothrops ja
158	2	18.2	14	1	RS19_LUWHI	Q46478	loolab whit	231	2	9.1	8	1	B4K_PORGI	P81886	porphyromon
159	2	18.2	14	1	SAP2_AKEPU	P11760	artacia pun	232	2	9.1	8	1	CAD1_ENTFA	P13268	enterococcu
160	2	18.2	14	1	TAT_HV1W2	P12509	human immu	233	2	9.1	8	1	CKN_MACSU	P30369	macropus eu
161	2	18.2	14	1	TAT_HV1ZP	P12511	human immu	234	2	9.1	8	1	CLP_THICU	P80488	thiobacillu
162	2	18.2	14	1	TKNM_PANMA	P40451	rana margar	235	2	9.1	8	1	COM2_CONPU	P58785	conus purpu
163	2	18.2	14	1	UC04_MAIZE	P80610	zea mays (m	236	2	9.1	8	1	COXG_RAT	P80430	rattus norv
164	2	18.2	14	1	UC34_MAIZE	P80640	zea mays (m	237	2	9.1	8	1	CPD1_ENTFA	P13269	enterococcu
165	2	18.2	14	1	UN07_CATA	P81452	clostridium	238	2	9.1	8	1	FAR1_PANRE	P41872	panagrellus
166	2	18.2	15	1	AH2_PROSE	P29260	prunus sero	239	2	9.1	8	1	FAR1_PENMO	P83316	penaeus mon
167	2	18.2	15	1	ASPI_LACSN	P82648	lactobacill	240	2	9.1	8	1	FAR2_MACRS	P83275	macrobrachi
168	2	18.2	15	1	C10A_RAF	P11720	rattus norv	241	2	9.1	8	1	FAR3_HOMAM	P83275	macrobrachi
169	2	18.2	15	1	CKX_WHEAT	P58763	triticum ae	242	2	9.1	8	1	FAR4_HOMAM	P41487	homarus ame
170	2	18.2	15	1	COX1_TROUB	P80978	thunmus obe	243	2	9.1	8	1	FAR7_ASCSU	P43171	ascariu suu
171	2	18.2	15	1	DOMM_TSECH	P19317	pseudomonas	244	2	9.1	8	1	FUSS_FUSSO	P81010	fusarium so
172	2	18.2	15	1	DIDH_PSESP	P80701	pseudomonas	245	2	9.1	8	1	LMT2_LOCHI	P22396	locusta mig
173	2	18.2	15	1	ECDA_LYMDI	P80938	lymantria d	246	2	9.1	8	1	LPK_LEUMA	P13049	leucophaea
174	2	18.2	15	1	EFIA_MICCR	P81266	microplitis	247	2	9.1	8	1	LPMS_STAP	P23211	staphylococ
175	2	18.2	15	1	ESTB_SUNGA	P81011	scirizaphis	248	2	9.1	8	1	NFB_BOVIN	P15507	bos taurus
176	2	18.2	15	1	FREZ_LITIN	P82022	litoria inf	249	2	9.1	8	1	ORMY_ORCLI	P82455	orconectes
177	2	18.2	15	1	GLN2_PINPS	P81107	pinus pinas	250	2	9.1	8	1	PLP_BRANA	P81707	brassica na
178	2	18.2	15	1	GTS_ASAGI	P83246	asaphis dic	251	2	9.1	8	1	PPK2_PERAM	P82692	periplaneta
179	2	18.2	15	1	LEC3_AXIPO	P28568	axinella po	252	2	9.1	8	1	PPK3_PERAM	P82618	periplaneta

253	1	9.1	8	1	CC26_MAIZE	P80632	zea mays (m	326	1	9.1	9	1	TK01_CALVO	P41517	calliphora
254	1	9.1	8	1	UH09_RAT	P56575	rattus norv	327	1	9.1	9	1	TKL1_LOEMI	P16223	locusta mig
255	1	9.1	8	1	UPA1_HUMAN	P30087	homo sapien	328	1	9.1	9	1	TRP4_LEUMA	P81736	leucophaea
256	1	9.1	8	1	UPAA_HUMAN	P30296	homo sapien	329	1	9.1	9	1	ULAD_HUMAN	P31929	homo sapien
257	1	9.1	8	1	VG02_HSV2H	P81780	herpes simp	330	1	9.1	9	1	ULAE_HUMAN	P31931	homo sapien
258	1	9.1	9	1	AL10_CAKMA	P81813	carcinus ma	331	1	9.1	9	1	ULAH_HUMAN	P31934	homo sapien
259	1	9.1	9	1	AL11_CAKMA	P81814	carcinus ma	332	1	9.1	9	1	ULAK_MOUSE	P99031	mus musculus
260	1	9.1	9	1	AL12_CHIRE	P82678	chlamydomon	333	1	9.1	9	1	UN19_CLOPA	P81355	clostridium
261	1	9.1	9	1	BS41_SERP2	P81375	serattia p.	334	1	9.1	9	1	UPA3_HUMAN	P30089	homo sapien
262	1	9.1	9	1	BUX_CLOPA	P81377	clostridium	335	1	9.1	9	1	UPA7_HUMAN	P30093	homo sapien
263	1	9.1	9	1	CCAP_CAKMA	P34556	carcinus ma	336	1	9.1	9	1	XY1A_STRSQ	P19149	streptomyce
264	1	9.1	9	1	CONE_CUNST	P05487	conus stria	337	1	9.1	9	1	YHFR_AZOV1	P25825	azotobacter
265	1	9.1	9	1	CONE_THUOB	P89975	thunus obe	338	1	9.1	10	1	AEGL_AGRVE	P83465	agrocyste ae
266	1	9.1	9	1	DI_NEPNO	P24615	nephrops ro	339	1	9.1	10	1	AH3_PRUSE	P29261	prunus sero
267	1	9.1	9	1	GNF1_LOEMI	P76134	locusta mig	340	1	9.1	10	1	AKHX_LOEMI	P81626	locusta mig
268	1	9.1	9	1	GSIP_RABIT	P01158	oryctolagus	341	1	9.1	10	1	AL19_CAKMA	P81822	carcinus ma
269	1	9.1	9	1	FAR1_CALVO	P41856	calliphora	342	1	9.1	10	1	AMPN_HELAM	P81731	helicoverpa
270	1	9.1	9	1	FAR2_CALVO	P41857	calliphora	343	1	9.1	10	1	ANG1_BOTJA	Q10581	bothrops ja
271	1	9.1	9	1	FAR2_PANRE	P41873	panagrellus	344	1	9.1	10	1	ANGT_BOVIN	P01017	bos taurus
272	1	9.1	9	1	FAR3_CALVO	P41858	calliphora	345	1	9.1	10	1	ANGT_CHICK	P01018	gallus gall
273	1	9.1	9	1	FAR3_MACRS	P83276	macrobrachi	346	1	9.1	10	1	APE_CAPGI	P80474	capnocytoph
274	1	9.1	9	1	FAR4_PENMO	P83318	penaeus mon	347	1	9.1	10	1	BRK_ONCMY	O9prz1	oncorhynchu
275	1	9.1	9	1	FAR4_PENMO	P83319	penaeus mon	348	1	9.1	10	1	CAJ2_LITCI	P82086	litoria cit
276	1	9.1	9	1	FAR5_CALVO	P41860	calliphora	349	1	9.1	10	1	CAER_LITXA	P56264	litoria xan
277	1	9.1	9	1	FAR5_PENMO	P83420	penaeus mon	350	1	9.1	10	1	COXH_ONCMY	P80331	oncorhynchu
278	1	9.1	9	1	FAR6_CALVO	P41861	calliphora	351	1	9.1	10	1	COXX_ONCMY	P80332	oncorhynchu
279	1	9.1	9	1	FAR6_MACRS	P83279	macrobrachi	352	1	9.1	10	1	COXX_RAT	P80431	rattus norv
280	1	9.1	9	1	FAR7_CALVO	P41862	calliphora	353	1	9.1	10	1	COXO_RAT	P80432	rattus norv
281	1	9.1	9	1	FAR8_MACRS	P83281	macrobrachi	354	1	9.1	10	1	COXO_THUOB	P80982	thunus obe
282	1	9.1	9	1	FAR9_ASIUS	P43172	ascaris suu	355	1	9.1	10	1	CU30_LOEMI	P11735	locusta mig
283	1	9.1	9	1	FAR9_CALVO	P41865	calliphora	356	1	9.1	10	1	ESL_LACCA	P81758	lactobacilli
284	1	9.1	9	1	FAR9_CALVO	P41868	calliphora	357	1	9.1	10	1	ESTA_SCHGA	P81012	schizaphis
285	1	9.1	9	1	FARP_CALSI	P38495	callinectes	358	1	9.1	10	1	FAR7_MACRS	P83280	macrobrachi
286	1	9.1	9	1	FIR3_EKPYA	P19346	erythroceba	359	1	9.1	10	1	FARC_CALVO	P41867	calliphora
287	1	9.1	9	1	FIR3_MACFC	P19345	macaca fusc	360	1	9.1	10	1	FARP_LOEMI	P38553	locusta mig
288	1	9.1	9	1	FIR8_PAPAN	P19344	papio anabi	361	1	9.1	10	1	FARP_WANSE	P18523	manduca sex
289	1	9.1	9	1	FIBB_PAPHA	P19343	papio hamad	362	1	9.1	10	1	GAJU_HUMAN	P01358	homo sapien
290	1	9.1	9	1	FIBB_THEGE	P19342	theropitheci	363	1	9.1	10	1	GONI_ALLMI	P37041	alligator m
291	1	9.1	9	1	FLAZ_TREHY	P80159	treponema h	364	1	9.1	10	1	GONI_CLOPA	P81749	clupea pall
292	1	9.1	9	1	FRE1_SARBU	P83350	sarcophaqa	365	1	9.1	10	1	GON2_CHEPR	P80678	chelyosoma
293	1	9.1	9	1	HJIC_KLEAE	P12361	kiebsiella	366	1	9.1	10	1	GON2_CHICK	P37043	gallus gall
294	1	9.1	9	1	IPYR_RHOVI	P82992	rhodopseudo	367	1	9.1	10	1	GON3_ONCRE	P20367	oncorhynchu
295	1	9.1	9	1	ISO_CYPCA	P42993	cypripus ca	368	1	9.1	10	1	GONL_SQUAC	P27429	squalus aca
296	1	9.1	9	1	KNL3_BOMVA	P83058	bombina var	369	1	9.1	10	1	GRP_RANRI	P23260	rana ridibu
297	1	9.1	9	1	LIT1_LITAU	P08945	litoria aur	370	1	9.1	10	1	GS09_BACSU	P80243	bacillus su
298	1	9.1	9	1	LITR_PHYRO	P08946	phyllomedus	371	1	9.1	10	1	LCMS_LEUMA	P21144	leucophaea
299	1	9.1	9	1	LMG3_LOEMI	P41489	locusta mig	372	1	9.1	10	1	LPK2_LOEMI	P41488	locusta mig
300	1	9.1	9	1	LEA_STAGH	P36884	staphylococ	373	1	9.1	10	1	LSK2_LEUMA	P09039	leucophaea
301	1	9.1	9	1	LMCI_BOVIN	P29177	bos taurus	374	1	9.1	10	1	MALE_KLEPN	Q05564	kiebsiella
302	1	9.1	9	1	MOSH_CLYJA	P19853	clypeaster	375	1	9.1	10	1	MOSQ_CLYJA	P19962	clypeaster
303	1	9.1	9	1	MOSH_CLYJA	P19854	clypeaster	376	1	9.1	10	1	MP2_MICOC	P81533	microplitis
304	1	9.1	9	1	NEF_HV725	P12481	human immun	377	1	9.1	10	1	NO40_TOBAC	P55962	nicotiana t
305	1	9.1	9	1	NEUO_CAVPO	P34966	cavia porce	378	1	9.1	10	1	ODP2_BOVIN	P11180	bos taurus
306	1	9.1	9	1	NSK1_SARBU	P41492	sarcophaqa	379	1	9.1	10	1	POPB_METTM	P80901	methanobact
307	1	9.1	9	1	OXYA_SGYCA	P42996	scyllorhinu	380	1	9.1	10	1	PPCK_FASHE	P80525	fasciola he
308	1	9.1	9	1	OXYA_SQUAC	P42999	squalus aca	381	1	9.1	10	1	PSBF_CAPAN	Q03367	capsicum an
309	1	9.1	9	1	OXYE_SGYCA	P42997	scyllorhinu	382	1	9.1	10	1	PVK_LOEMI	P83382	locusta mig
310	1	9.1	9	1	OXYE_HURE	P42995	bufo requia	383	1	9.1	10	1	Q20B_COMTE	P80465	comamonas t
311	1	9.1	9	1	OXYL_CYPCA	P23879	cypripus ca	384	1	9.1	10	1	Q20G_COMTE	P80466	comamonas t
312	1	9.1	9	1	OXYI_ESEFO	P42998	eisenia foe	385	1	9.1	10	1	RRPL_PHODV	P35946	phocine dis
313	1	9.1	9	1	OXYT_CATVC	P80027	octopus vul	386	1	9.1	10	1	RT02_BOVIN	P82923	bos taurus
314	1	9.1	9	1	OXYT_PALCI	P12878	oryctolagus	387	1	9.1	10	1	SLAP_BACGT	P49325	bacillus th
315	1	9.1	9	1	OXYT_PALCI	P42994	raja clavac	388	1	9.1	10	1	SP34_DICMU	P81545	dictyosteli
316	1	9.1	9	1	OXYV_SQUAC	P43000	squalus aca	389	1	9.1	10	1	SPI_HALRO	Q10997	halocynthia
317	1	9.1	9	1	PGJR_DIAAB	P81179	diaprepes a	390	1	9.1	10	1	SYK_CAMUP	Q46464	campylobact
318	1	9.1	9	1	PPH1_LNCES	P83380	lycopersico	391	1	9.1	10	1	TENK_RANTE	P56923	rana tempor
319	1	9.1	9	1	PPK1_PPERAM	P82591	periplaneta	392	1	9.1	10	1	TKL2_LOEMI	P16224	locusta mig
320	1	9.1	9	1	RE42_LITRU	P82075	litoria rub	393	1	9.1	10	1	TKL3_LOEMI	P30249	locusta mig
321	1	9.1	9	1	RS10_SERMA	Q68936	serrattia ma	394	1	9.1	10	1	TKL4_LOEMI	P30250	locusta mig
322	1	9.1	9	1	SAMP_MUSCA	P19095	musculus ca	395	1	9.1	10	1	TKNB_CHICK	P19851	gallus gall
323	1	9.1	9	1	SAP_STOVA	P24047	stomopreute	396	1	9.1	10	1	TKNB_ONCMY	P28500	oncorhynchu
324	1	9.1	9	1	TAL3_PICCA	P17440	pichia jadi	397	1	9.1	10	1	TKNB_RANCA	P22689	rana catesb
325	1	9.1	9	1	TAL3_PICCA	P17441	pichia jadi	398	1	9.1	10	1	TKNB_RANRI	P29135	rana ridibu

399	1	9.1	10	1	TKNC_RANCA	P22690 rana catesb	472	1	9.1	12	1	CD14_LITXA	P56246 litoria xan
400	1	9.1	10	1	TKNC_PIG	P01292 sus scrofa	473	1	9.1	12	1	CXAL_CONIM	P50983 conus imper
401	1	9.1	10	1	TKN_PHYBI	P08610C phylloredus	474	1	9.1	12	1	CXL3_CONMR	P58809 conus marmo
402	1	9.1	10	1	TKS1_AEGAE	P42634 acedus acgypt	475	1	9.1	12	1	CXST_CONTE	P58846 conus texti
403	1	9.1	10	1	TKS2_AEGAE	P42635 acedus acgypt	476	1	9.1	12	1	FARI_CALVO	P41869 calliphora
404	1	9.1	10	1	TKU1_UPEIN	P40751 urechis uni	477	1	9.1	12	1	FIF1_SARBU	P83349 sarcophaga
405	1	9.1	10	1	TKOF_AEGAE	P19425 aedes aegypt	478	1	9.1	12	1	GRAP_RANRU	P40754 rana rugosa
406	1	9.1	10	1	TRP5_LEUMA	P81747 leucophaea	479	1	9.1	12	1	HCY1_CARMA	P83176 carcinus ma
407	1	9.1	10	1	TRP6_LEUMA	P81748 leucophaea	480	1	9.1	12	1	HCY8_MEGCR	Q10584 megathura c
408	1	9.1	10	1	TRP7_LEUMA	P81749 leucophaea	481	1	9.1	12	1	HSYA_RAT	P82995 rattus norv
409	1	9.1	10	1	TRP8_LEUMA	P81746 leucophaea	482	1	9.1	12	1	LICH_BACLI	P82907 bacillus li
410	1	9.1	10	1	TRP9_LEUMA	P81741 leucophaea	483	1	9.1	12	1	LOSC_LOCM1	P47733 locusta mig
411	1	9.1	10	1	UHU5_RAT	P56573 rattus norv	484	1	9.1	12	1	NO40_LOTJA	O22426 lotus japon
412	1	9.1	10	1	UHA3_HUMAN	P40939 homo sapien	485	1	9.1	12	1	NO40_SESRO	O24369 sesbania ro
413	1	9.1	10	1	UPA2_HUMAN	P50088 homo sapien	486	1	9.1	12	1	NO40_SOYBN	P55960 glycine max
414	1	9.1	10	1	UPA4_HUMAN	P40936 homo sapien	487	1	9.1	12	1	NUDM_CANFA	P54713 canis famli
415	1	9.1	10	1	UPA8_HUMAN	P40934 homo sapien	488	1	9.1	12	1	OPS3_DROVI	P17645 drosophila
416	1	9.1	10	1	UPA9_HUMAN	P40945 homo sapien	489	1	9.1	12	1	PA21_MICFM	P25072 micurus fu
417	1	9.1	10	1	URAI_HUMAN	P32118 homo sapien	490	1	9.1	12	1	PA28_VIPBO	P31859 vipera beru
418	1	9.1	10	1	URAT_HUMAN	P34930 homo sapien	491	1	9.1	12	1	PPK4_PERAM	P82619 peripianeta
419	1	9.1	10	1	URE3_MORMO	P12339 morganella	492	1	9.1	12	1	PPK4_PERFU	P82690 peripianeta
420	1	9.1	10	1	UXA2_CHLIR	P16033 chlamydia t	493	1	9.1	12	1	PVK2_PERAM	P81555 peripianeta
421	1	9.1	10	1	UXA6_CHLIR	P38007 chlamydia t	494	1	9.1	12	1	RPI1_CONSP	P58805 conus spuri
422	1	9.1	10	1	YXH3_YEAST	P59012 saccharomyc	495	1	9.1	12	1	RI16_GINB1	P36207 ginkgo bilo
423	1	9.1	10	1	VEG3_BASU	P86699 bacillus su	496	1	9.1	12	1	RS19_TOBBP	Q56251 tomato big
424	1	9.1	11	1	ANG1_CRIGE	P09037 crinia geor	497	1	9.1	12	1	TA10_TREME	P01371 tremella me
425	1	9.1	11	1	ASL1_BACE	P81146 bacteroides	498	1	9.1	12	1	TIN2_HOPTI	P82652 hoplobatrac
426	1	9.1	11	1	ASL2_BACE	P81147 bacteroides	499	1	9.1	12	1	TIN3_HOPTI	P84653 hoplobatrac
427	1	9.1	11	1	BPF3_BOTIN	P30426 bothrops in	500	1	9.1	12	1	TKN2_KASMA	P08614 kassina mac
428	1	9.1	11	1	BPF4_BOTIN	P30424 bothrops in							
429	1	9.1	11	1	BEP_AGRHP	P45424 bothrops in							
430	1	9.1	11	1	BEK_ME3FL	P04562 agkistiodon							
431	1	9.1	11	1	CAL1_HITCI	P12797 megalocolla							
432	1	9.1	11	1	CAS2_HITCI	P82089 litoria cit							
433	1	9.1	11	1	CAL1_HITCI	P82090 litoria cit							
434	1	9.1	11	1	CAL2_HITCI	P82092 litoria cit							
435	1	9.1	11	1	CEPI_A_HFC	P22790 achelonia lu							
436	1	9.1	11	1	GOR2_PERAM	P11496 peripianeta							
437	1	9.1	11	1	GUXA_CANFA	P59501 canis famli							
438	1	9.1	11	1	CXSA_CONAL	P58846 conus aulic							
439	1	9.1	11	1	CX5R_CONAL	P58849 conus aulic							
440	1	9.1	11	1	CXLI_CONMR	P58807 conus marmo							
441	1	9.1	11	1	EFGL_CALVO	P81350 elostriadum							
442	1	9.1	11	1	FAR4_CALVO	P41864 calliphora							
443	1	9.1	11	1	HS72_FINES	P81672 pinus pinus							
444	1	9.1	11	1	CADU_CONY	P81016 cancoriyncha							
445	1	9.1	11	1	LSK1_LEUMA	P41328 leucophaea							
446	1	9.1	11	1	LSK2_PERAM	P86855 peripianeta							
447	1	9.1	11	1	MLG3_HETS	P41489 thermomyzon							
448	1	9.1	11	1	MCRN_HUMAN	P01763 homo sapien							
449	1	9.1	11	1	NXSN_PSETE	P59072 pseudonaja							
450	1	9.1	11	1	PKCI_CARMO	P82684 caradiscus m							
451	1	9.1	11	1	PUGC_PSEFL	P55373 pseudomoras							
452	1	9.1	11	1	PUCG_RANP1	P08051 rana pipien							
453	1	9.1	11	1	REA1_LLIRG	P82074 litoria rib							
454	1	9.1	11	1	REP2_CONAM	P42241 comopholis							
455	1	9.1	11	1	T2P1_PROVO	P31031 proteus vti							
456	1	9.1	11	1	TINI_HOPTI	P82651 heplotrach							
457	1	9.1	11	1	TINI_HOPTI	P82654 hoplobatrac							
458	1	9.1	11	1	TKC2_CALVO	P41518 calliphora							
459	1	9.1	11	1	TKN1_PSEGN	P42906 pseudophryn							
460	1	9.1	11	1	TKN1_UPEIN	P82026 upeoleia i							
461	1	9.1	11	1	TKN1_UPEIN	P08612 upeoleia r							
462	1	9.1	11	1	TKN2_PSEGN	P42907 pseudophryn							
463	1	9.1	11	1	TKN1_PSEGN	P42988 pseudophryn							
464	1	9.1	11	1	TKN1_PSEGN	P42989 pseudophryn							
465	1	9.1	11	1	TKN5_PSEGN	P42990 pseudophryn							
466	1	9.1	11	1	TKNA_CHLIR	P19580 gallus gal							
467	1	9.1	11	1	TKN_ELEMO	P01293 eleodone mos							
468	1	9.1	11	1	TKN_PHYBI	P05815 physalaema							
469	1	9.1	11	1	UE05_MOUSE	P48641 mus musculu							
470	1	9.1	12	1	CALM_TETIT	G05555 tetrahymena							
471	1	9.1	12	1	CD14_LITXA	P56246 litoria xan							

ALIGNMENTS

RESULT 1
 CH60_CANFA STANDARD: PRT: 13 AA.
 ID CH60_CANFA
 AC P49818;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 60 kDa heat shock protein, mitochondrial (Hsp60) (60 kDa chaperonin)
 DE (CPN60) (Heat shock protein 60) (HSP-60) (Mitochondrial matrix protein
 DE P1) (Fragment).
 GN HSP60 OR HSP60.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 CX NCBI_TaxID=9615;
 RN [1]
 PP TISSUE=Heart;
 RP MEDLINE=98163440; PubMed=9504812;
 RX Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -!- FUNCTION: IMPLICATED IN MITOCHONDRIAL PROTEIN IMPORT AND
 MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF
 IMPORTED PROTEINS. MAY ALSO PREVENT MISFOLDING AND PROMOTE THE
 REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED
 UNDER STRESS CONDITIONS IN THE MITOCHONDRIAL MATRIX.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
 DR HSC-2DPAGE: P49818; DOG.
 DR InterPro: IPR001844; Chaperin_Cpn60.
 DR PROSITE: PS00296; CHAPERONIN_CPN60; PARTIAL.
 KW Chaperone; ATP-binding; Mitochondrion.
 FT NON_TER 13
 SQ SEQUENCE 13 AA: 1363 MW: C6571E012DBFE879 CRC64:

Query Match 94.4% Score 4; DR 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ARAL 4
1111
10 ARAL 13

Db

RESULT 2

COXQ-SHEEP STANDARD: PRL 10 AA.

AC P80347

DT 01-OCT-1994 (Rel. 30, Created)

DI 01-OCT-1994 (Rel. 30, Last sequence update)

DE 28-FEB-2003 (Rel. 41, Last annotation update)

DE Cytochrome c oxidase polypeptide V:II-liver/heart (P01994.1)

DE (Fragment)

OS Ovis aries (Sheep)

OC Eukaryota: Metazoa: Chordata: Mammalia: Artiodactyla: Bovidae: Bovinae

OC Mammalia: Eutheria: Cetartiodactyla: Mammalia: Bovidae

OC Bovidae: Caprinae: Ovis

OX NCBI_TaxID=9940

RN 11

RK SEQUENCE

RP TISSUE=Heart, and Liver

RA Freund R., Kadenbach B.

RL Submitted (MAR-1994) to the SWISS-PROT data bank

CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NON-FERROUS POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.

CC -!- CATALYTIC ACTIVITY: 4 ferricytochrome c + (1/2) O₂ + 2 H⁺ → 4 ferricytochrome c + 2 H₂O.

CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VII: FAMILY.

AK Oxidoreductase; Mitochondria

FI NON TER 10

SQ SEQUENCE 10 AA: 1027 MW: 64595aa (a446349) (P 64)

Query Match: 27.3%: Score 3; DB 1; Length 10;
Best Local Similarity 100.0%: Pred. No. 1.2e+03;

Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 AKP 10
111
3 AKP 5

Db

RESULT 3

HTFL-ROMMI STANDARD: PRL 10 AA.

AC P81170

DT 01-NOV-1992 (Rel. 16, Created)

DI 01-FEB-1994 (Rel. 28, Last sequence update)

DE 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ro 1 (Hypertrehalosaemic factor)

OS Romalea microptera (Lubber grasshopper)

OC Eukaryota: Metazoa: Arthropoda: Hexapoda: Insecta: Pterygota: Neoptera: Orthopteroidea: Orthoptera: Caelifera: Acridoidea: Acrididae: Romaleidae; Romalea

OX NCBI_TaxID=7907

RN 11

RK SEQUENCE

RP TISSUE=Corpora cardiaca

RA MEDLINE=89145002; PubMed=3225948;

RA Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.

RT "Sequence analyses of two neuropeptides of the AKH/RPCH family from the lubber grasshopper, Romalea microptera."

RL Peptides 9:681-688(1988).

CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYPH (TREHALOSE IS THE MAJOR CARBOHYDRATE IN THE HEMOLYPH OF INSECTS).

CC -!- SIMILARITY: BELONGS TO THE AKH / RPCH FAMILY.

DR PIR: JCI416; JCI416.

DR PIR: S09138; S09138.

DR InterPro: IPR002047; AKH.

DR PROSITE: PS00256; AKH; 1.

KW Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT CARBOHYD 8 8 C-LINKED (MAN) (PROBABLE).

FT MOD_RES 10 10 AMIDATION.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA: 1164 MW: 989036745771A9D1 CRC64;

Query Match: 27.3%: Score 3; DB 1; Length 10;
Best Local Similarity 100.0%: Pred. No. 1.2e+03;

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA: 1164 MW: 056236745771A9C4 CRC64;

Query Match: 27.3%: Score 3; DB 1; Length 10;
Best Local Similarity 100.0%: Pred. No. 1.2e+03;

Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 NMG 7
111
7 NMG 9

Db

RESULT 4

HTF2-CARMO STANDARD: PRL 10 AA.

AC P11485

DT 01-JUL-1989 (Rel. 12, Created)

DI 01-FEB-1994 (Rel. 28, Last sequence update)

DI 28-FEB-2003 (Rel. 41, Last annotation update)

DE Hypertrehalosaemic factor II (HTF-II) (HRTII-II) (Hypertrehalosaemic neuropeptide II).

DE Carausius morosus (Indian stick insect), and

OS Extatosoma tiaratum (Stick insect)

OC Eukaryota: Metazoa: Arthropoda: Hexapoda: Insecta: Pterygota: Neoptera: Orthopteroidea: Phasmatodea: Euphasmida: Phasmatodea: Heteronemidae; Carausius

OX NCBI_TaxID=7022, 7024

RN 11

RK SEQUENCE

RP SPECIES=C. MOROSUS; TISSUE=Corpora cardiaca

RX MEDLINE=87157103; PubMed=3828078;

RA Gaede G., Rinehart K.L. Jr.

RT "Primary structure of the hypertrehalosaemic factor II from the corpora cardiaca of the Indian stick insect, Carausius morosus, determined by fast atom bombardment mass spectrometry."

RL Biol. Chem. Hoppe-Seyler 368:67-75(1987).

RN 12

RK SEQUENCE

RP SPECIES=Extatosoma tiaratum; TISSUE=Corpora cardiaca

RX MEDLINE=90253659; PubMed=2346112;

RA Gaede G., Rinehart K.L. Jr.

RT "Primary structures of hypertrehalosaemic neuropeptides isolated from the corpora cardiaca of the cockroaches Leucophaea maderae, Gryllotalpa orientalis, Blattella germanica and Blattella orientalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombardment mass spectrometry."

RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).

RN 13

RK CARBOHYDRATE LINKAGE SITE.

RP SPECIES=C. morosus; TISSUE=Corpora cardiaca

RX MEDLINE=93129788; PubMed=1482345;

RA Gaede G., Keilner K., Rinehart K.L. Jr., Proefke M.L.

RT "A tryptophan-substituted member of the AKH/RPCH family isolated from a stick insect corpora cardiaca."

RL Biochem. Biophys. Res. Commun. 189:1303-1309(1992).

CC -!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYPH (TREHALOSE IS THE MAJOR CARBOHYDRATE IN THE HEMOLYPH OF INSECTS).

CC -!- MASS SPECTROMETRY: MW=1308.61; METHOD=FAH.

CC -!- SIMILARITY: BELONGS TO THE AKH / RPCH FAMILY.

DR PIR: JCI416; JCI416.

DR PIR: S09138; S09138.

DR InterPro: IPR002047; AKH.

DR PROSITE: PS00256; AKH; 1.

KW Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.

FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

FT CARBOHYD 8 8 C-LINKED (MAN) (PROBABLE).

FT MOD_RES 10 10 AMIDATION.

FT MOD_RES 10 10 AMIDATION.

SQ SEQUENCE 10 AA: 1164 MW: 989036745771A9D1 CRC64;

Query Match: 27.3%: Score 3; DB 1; Length 10;
Best Local Similarity 100.0%: Pred. No. 1.2e+03;

Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 NWG 7
DB 7 NWG 9

RESULT 5
RS30_ONCMY
ID RS30_ONCMY STANDARD: PRI: 1: AA.
AC P83328
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 40S ribosomal protein S30 (Fragment).
CN FAU.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
CX NCBI_TaxID=8022;
RN 11
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE: Skin mucus;
RX MEDLINE: 22142142; PubMed:12147245;
FA Fernandes J.M.O., Smith V.C.
RT "A novel antimicrobial function for a ribosomal peptide from rainbow trout skin".
RL Biochem. Biophys. Res. Commun. 296:167-171(2002).
CC 1: FUNCTION: Has antibacterial activity against Gram-positive bacteria.
CC 1: MASS SPECTROMETRY: MW=5576 Da; METHOD: MALDI
CC 1: SIMILARITY: BELONGS TO THE SAME FAMILY OF RIBOSOMAL PROTEINS.
KW Ribosomal protein; Antibiotic.
FT N-TER 11
SQ SEQUENCE 11 AA: 1123 MW: 231246.6 Da; 1587 aa; 6964;

Query Match 27.3%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 ARA 3
DB 7 ARA 9

RESULT 6
RGE1_CANEA

ID RGE1_CANEA STANDARD: PRI: 1: AA.
AC P18651;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Heparin-binding growth factor 1 (HBGF-1) (HBGF-1) (Fibroblast growth factor) (AFGF) (Alpha-endothelial cell growth factor) (Fragment).
DE RGF1 OR FGF-1.
GN Canis familiaris (Dog).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
CX NCBI_TaxID=9615;
RN 11
RP SEQUENCE.
RX MEDLINE: 9321734; PubMed:2734282;
FA Quinkler W., Maasberg M., Bernotat G., Lohmann S., Lohner N., Sharma H.S., Schaper W.
RT "Isolation of heparin-binding growth factors from bovine, porcine and canine hearts".
RL Biochem. Biophys. Res. Commun. 181:67-73(1991).
CC 1: FUNCTION: THE HEPARIN-BINDING GROWTH FACTORS ARE ANGIOGENIC AGENTS IN VIVO AND ARE POTENT MITOGENS FOR A VARIETY OF CELL TYPES IN VITRO. THERE ARE DIFFERENCES IN THE TISSUE DISTRIBUTION AND CONCENTRATION OF THESE 2 GROWTH FACTORS.
CC 1: SUBUNIT: Monomer.

CC 1: MISCELLANEOUS: THIS PROTEIN BINDS HEPARIN, ALTHOUGH LESS STRONGLY THAN DOES BFGF.
CC 1: SIMILARITY: BELONGS TO THE HEPARIN-BINDING GROWTH FACTORS FAMILY.
DR PIR: SC3955; S03955.
DR InterPro: IPR002348; I1, HBGF.
DR PROSITE: PS00247; HBGF_FGF; PARTIAL.
KW Growth factor; Mitogen; Angiogenesis; Heparin-binding.
FT NON-TER 15 15
SQ SEQUENCE 15 AA: 1712 MW: 53093.33 Da; 1712 aa; 6964;

Query Match 27.3%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 9 KPK 11
DB 4 KPK 6

RESULT 7
ACL_THUAI

ID ACL_THUAI STANDARD: PRI: 8 AA.
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
CX NCBI_TaxID=8236;
RN 11
RP SEQUENCE.
RC TISSUE: Muscle;
RX MEDLINE: 88326322; PubMed:3415688;
FA Kohama Y., Matsumoto S., Oka H., Teramoto T., Okabe M., Mimura T.
RT "Isolation of angiotensin-converting enzyme inhibitor from tuna muscle".
RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
DR PIR: A31570; A31570.
SQ SEQUENCE 8 AA: 95; MW: 6448.633 Da; 1051 aa; 6964;

Query Match 19.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 6 WG 7
DB 6 WG 7

RESULT 8
AKH_MELML

ID AKH_MELML STANDARD: PRI: 8 AA.
AC P25423;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Adipokine hormone (AKH).
OS Melolontha melolontha (Cockchafer).
OS Geotrupes stercorarius (Dor beetle), and Pachnoda marginata (Flower beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Scarabaeiformia;
OC Scarabaeidae; Melolonthinae; Melolontha.
CX NCBI_TaxID=7061; 7087, 7058;
RN 11
RP SEQUENCE.
RC SPECIES: M. melolontha, and Geotrupes stercorarius; TISSUE: Corpora cardiaca;
RX MEDLINE: 91249100; PubMed:2019445;
FA Gaede G.

RT *A unique charged tyrosine-containing member of the adipokinetic
 RT hormone/red-pigment-concentrating hormone peptide family isolated and
 RL sequenced from two beetle species.*;
 RN Biochem. J. 275:671-677(1991).
 RP [2]

RP SPECIES-P. marginata; TISSUE=Corpora cardiaca;
 RX MEDLINE=92265187; PubMed=1586453;
 RA Gaede G., Lopata A., Kellner K., Rinehart K.L. Jiro.
 RI "Primary structures of neuropeptides isolated from the corpora
 RI cardiaca of various cetonid beetle species determined by
 RT pulsed liquid phase sequencing and tandem fast atom bombardment mass
 RT spectrometry.*;
 RL Biol. Chem. Hoppe-Seyler 373:133-142(1992).

CC -!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
 CC CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
 CC DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
 CC MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
 CC -!- SIMILARITY: BELONGS TO THE AKH / HETH / RPCH FAMILY.

DR PIR, A58641; A58641.
 DR PIR, S15422; S15422.
 DR InterPro: IPR002047; AKH.
 DR PROSITE: PS00256; AKH; 1.
 KW Neuropeptide; Amidation; Flight; Pyroglutamate carboxylic acid.
 FT MOD_RES 8 1 PYROGLUTAMINE CARBOXYLIC ACID.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 1022 MW: 867AB775AB54736 CRC64:

Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
 I,
 DB 2 LN 3

RESULT 9

ALL4_CVDPO STANDARD: PRT: # AA.
 AC P82155;
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Cydiastatin 4.
 OS Cydia pomonella (Codling moth).
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Davey M., East P.D., Thorpe A., Scott A.G., Winstanley D.,
 RA *Lepidopteran peptides of the allatostatin superfamily.*;
 RT "Lepidopteran peptides of the allatostatin superfamily.*;
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 910 MW: 92287905AB47740D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2
 I,
 DB 1 AR 2

RESULT 10

ALL5_CVDPO STANDARD: PRT: 8 AA.
 AC P82156;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE Cydiastatin 5.
 OS Cydia pomonella (Codling moth).
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 CC Tortricidae; Tortricidae; Olethreutinae; Cydia.
 OX NCBI_TaxID=82600;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Larva;
 RX MEDLINE=98054539; PubMed=9392829;
 RA Davey M., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
 RA *Lepidopteran peptides of the allatostatin superfamily.*;
 RT "Lepidopteran peptides of the allatostatin superfamily.*;
 RL Peptides 18:1301-1309(1997).
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 898 MW: 922879CABB58640D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2
 I,
 DB 1 AR 2

RESULT 11

FAR4_MACRS STANDARD: PRT: 8 AA.
 AC P83277;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE FMRamide-like neuropeptide FLP4 (APALRLF-amide).
 OS Macrobrachium rosenbergii (Giant freshwater prawn).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
 CC Palaemonoidea; Palaemonidae; Macrobrachium.
 OX NCBI_TaxID=79674;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Eyestalk;
 RA Sithigorngul P., Sarathongkum W., Jaidechoey S., Longyant S.,
 RA Sithigorngul W.;
 RT "Novel FMRamide-like neuropeptides from the eyestalk of the giant
 RT freshwater prawn Macrobrachium rosenbergii.*;
 RL Comp. Biochem. Physiol. 120B:587-595(1998).
 CC -!- MASS SPECTROMETRY: MW-943; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR GO: GO:0007218; P:neuropeptide signaling pathway; TAS.
 KW Neuropeptide; Amidation.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 943 MW: 9CD40734072DC76D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AL 4
 I,
 DB 3 AL 4

RESULT 12

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FARB_CALVO
ID FARB_CALVO STANDARD: PRT: 5 AA.
AC P41863;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE Calliphramide 8.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Musciformia; Tsetseididae;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN 1;
RP SEQUENCE.
RC TISSUE: Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Dave B., Johnson A.H., Sewell J.C., Scott A.G., Orchard L.,
RA Rehfeld J.F., Thorpe A.;
RT "Isolation, structure, and activity of the Met Arg-Pho-NH2
RT neuropeptides (designated calliphramides) from the blowfly
RT Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -1 SIMILARITY: BELONGS TO THE FARB (FMKFAIMIDE RELATED PEPTIDE)
CC FAMILY.
CC PIR: H41978;
DR Neuropeptide; Amidation.
KW MOD_RES 8 8 AMIDATION
FT MOD_RES 8 8 AMIDATION
SQ SEQUENCE 8 AA: 957 MW: 7224.6990/AA444048 CRK64;

Query Match. 18.2% Score 2: DB 1: Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GA 8
QB 1 GA 2

RESULT 13
GLUR_HUMAN
ID GLUR_HUMAN STANDARD: PRT: 8 AA.
AC P02729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Urine glycopeptide.
DE Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1;
RP SEQUENCE.
RX MEDLINE=72062338; PubMed=5126885;
RA Lohr C.J., Weiss J.B.;
RT "Identification in urine of a low molecular weight highly polar
RT glycopeptide containing cysteinyl-galactose."
RL Biochem. J. 123:25P-25P(1971).
CC -1 FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
CC IS DERIVED IS UNKNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
CC ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPROTEIN HAVING A
CC SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
CC PIR: A03188; XGHUEU.
DR GO: G03005576; C:extracellular; NAS.
DR GO: G03005576; C:extracellular; NAS.
KW Glycoprotein.
FT CARBOHYD 1 1 S-LINKED (GLUCOSE)
SQ SEQUENCE 8 AA: 855 MW: 8203.7441/PS1818 CRK64.

Query Match. 18.2% Score 2: DB 1: Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GA 8
QB 1 GA 2

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Db 7 GA 8

RESULT 14
HTFL_PERAM
ID HTFL_PERAM STANDARD: PRT: 8 AA.
AC P04548;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypertrahaloasemic factor I (Neuropeptide M-I) (Periplanetin CC-I)
DE (PeA-CAH-I) (LeD CC-I) (Hypertrahaloasemic neuropeptide I).
OS Periplaneta americana (American cockroach).
OS Leptinotarsa decemlineata (Colorado potato beetle), and
OS Blatta orientalis (Oriental cockroach).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattellidae; Periplaneta.
OX NCBI_TaxID=6978; 7539; 6976;
RN 1;
RP SEQUENCE.
RC SPECIES-P.americana;
RX MEDLINE=85046530; PubMed=6548628;
RA Witten J.L., Schafer M.H., O'Shea M., Cook J.C., Hemling M.E.,
RA Rinehart K.L. Jr.;
RT "Structures of two cockroach neuropeptides assigned by fast atom
RT bombardment mass spectrometry."
RL Biochem. Biophys. Res. Commun. 124:350-358(1984).
RN 12;
RP SEQUENCE.
RC SPECIES-P.americana;
RX MEDLINE=84298179; PubMed=6591205;
RA Scarborough R.M., Jamieson G.C., Kallish F., Kramer S.J., McEnroe G.A.,
RA Willer C.A., Schooley D.A.;
RT "Isolation and primary structure of two peptides with
RT cardioacceleratory and hyperglycemic activity from the corpora
RT cardiaca of Periplaneta americana."
RL Proc. Natl. Acad. Sci. U.S.A. 81:5575-5579(1984).
RN 13;
RP SEQUENCE.
RC SPECIES-L.decemlineata; TISSUE-Corpora cardiaca;
RX MEDLINE=90160053; PubMed=2576128;
RA Gaede G., Kellner R.;
RT "The metabolic neuropeptides of the corpus cardiaca from the potato
RT beetle and the American cockroach are identical."
RL Peptides 10:1287-1289(1989).
RN 14;
RP SEQUENCE.
RC SPECIES-B.orientalis; TISSUE-Corpora cardiaca;
RX MEDLINE=90253659; PubMed=2340112;
RA Gaede G., Rinehart K.L. Jr.;
RT "Primary structures of hypertrahaloasemic neuropeptides isolated from
RT the corpora cardiaca of the cockroaches Leucophaea maderae,
RT Gromphodrhina portentosa, Blattella germanica and Blatta orientalis
RT and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT atom bombardment mass spectrometry."
RL Biol. Chem. Hoppe-Seyler 371:345-354(1990).
CC -1 FUNCTION: HYPERTRHALOASEMIC FACTORS ARE NEUROPEPTIDES THAT
CC ELEVATE THE LEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS
CC THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH OF INSECTS).
CC -1 SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
CC PIR: A44960; A44960.
DR PIR: A49823; A49823.
DR PIR: S08995; S08995.
DR InterPro: IPR002047; AKH.
DR PROSITE: PS00256; AKH; 1.
KW Neuropeptide; Amidation; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 8 8 AMIDATION.
SQ SEQUENCE 8 AA: 991 MW: 86745775B9C452D6 CRK64;

Query Match. 18.2% Score 2: DB 1: Length 8;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;

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RI "Isolation, primary structure and synthesis of two neuropeptides
 RI from Leucophaea maderae: members of a new family of
 RI Cephalomyotropins."

RI Comp. Biochem. Physiol. 84C:205-211(1986).

CC 1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE

CC ACTIVITY OF COCKROACH PROTEIN (HINDGUT).

CC 1- SIMILARITY: TO THE OTHER LEUCOKININS.

KW Neuropeptide; Amidation.

FT MOD_RES 8 8 AMIDATION.

SV SEQUENCE 8 AA: 893 MW: 106365844906076A CRC64:

Query Match 18.2%, Score 2, DR 1, Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WS 7

DB 11

DB 7 WS 8

RESULT 18

LOC4_LEUMA

ID LOC4_LEUMA STANDARD: PRI: 8 AA.

AC P21142

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 01-MAY-1991 (Rel. 18, Last annotation update)

LE Leucokinin II (L-II).

OS Leucophaea maderae (Madeira cockroach).

CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;

CC Blaberidae; Leucophaea.

CX NCBI_TaxID=6988;

RN 11

RP TISSUE: Head.

SA Holman G.M., Cook H.J., Nachman R.J.

RI "Isolation, primary structure and synthesis of two neuropeptides
 RI from Leucophaea maderae: members of a new family of
 RI Cephalomyotropins."

RI Comp. Biochem. Physiol. 84C:205-211(1986).

CC 1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE

CC ACTIVITY OF COCKROACH PROTEIN (HINDGUT).

CC 1- SIMILARITY: TO THE OTHER LEUCOKININS.

KW Neuropeptide; Amidation.

FT MOD_RES 8 8 AMIDATION.

SV SEQUENCE 8 AA: 852 MW: 106365844906076A CRC64:

Query Match 18.2%, Score 2, DR 1, Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WS 7

DB 11

DB 7 WS 8

RESULT 19

LOC4_LEUMA

ID LOC4_LEUMA STANDARD: PRI: 8 AA.

AC P21142

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 01-MAY-1991 (Rel. 18, Last annotation update)

LE Leucokinin II (L-II)

OS Leucophaea maderae (Madeira cockroach)

CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;

CC Blaberidae; Leucophaea.

CX NCBI_TaxID=6988;

RN 11

RP TISSUE: Head.

SA Holman G.M., Cook H.J., Nachman R.J.

RI "Isolation, primary structure and synthesis of two neuropeptides
 RI from Leucophaea maderae: members of a new family of
 RI Cephalomyotropins."

RI Comp. Biochem. Physiol. 84C:205-211(1986).

CC 1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE

CC ACTIVITY OF COCKROACH PROTEIN (HINDGUT).

CC 1- SIMILARITY: TO THE OTHER LEUCOKININS.

KW Neuropeptide; Amidation.

FT MOD_RES 8 8 AMIDATION.

SV SEQUENCE 8 AA: 852 MW: 106365844906076A CRC64:

Query Match 18.2%, Score 2, DR 1, Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WS 7

DB 11

DB 7 WS 8

RESULT 20

LOC4_LEUMA

ID LOC4_LEUMA STANDARD: PRI: 8 AA.

AC P21142

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 01-MAY-1991 (Rel. 18, Last annotation update)

DE Leucokinin IV (L-IV).

OS Leucophaea maderae (Madeira cockroach).

CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;

CC Blaberidae; Leucophaea.

CX NCBI_TaxID=6988;

RN 11

RP TISSUE: Head.

SA Holman G.M., Cook H.J., Nachman R.J.

RI "Isolation, primary structure and synthesis of two additional neuropeptides
 RI from Leucophaea maderae: members of a new family of
 RI Cephalomyotropins."

RI Comp. Biochem. Physiol. 84C:271-276(1986).

CC 1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE

CC ACTIVITY OF COCKROACH PROTEIN (HINDGUT).

CC 1- SIMILARITY: TO THE OTHER LEUCOKININS.

KW Neuropeptide; Amidation.

FT MOD_RES 8 8 AMIDATION.

SV SEQUENCE 8 AA: 936 MW: 106365844906076A CRC64:

Query Match 18.2%, Score 2, DR 1, Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WS 7

DB 11

DB 7 WS 8

RESULT 21

LOC5_LEUMA

ID LOC5_LEUMA STANDARD: PRI: 8 AA.

AC P19887

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 30-MAY-2000 (Rel. 19, Last annotation update)

DE Leucokinin V (L-V).

OS Leucophaea maderae (Madeira cockroach).

CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;

CC Blaberidae; Leucophaea.

CX NCBI_TaxID=6988;

RN 11

RP TISSUE: Head.

SA Holman G.M., Cook H.J., Nachman R.J.

RI "Isolation, primary structure and synthesis of two additional neuropeptides
 RI from Leucophaea maderae: members of a new family of
 RI Cephalomyotropins."

RI Comp. Biochem. Physiol. 84C:271-276(1986).

CC 1- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE

CC ACTIVITY OF COCKROACH PROTEIN (HINDGUT).

CC 1- SIMILARITY: TO THE OTHER LEUCOKININS.

KW Neuropeptide; Amidation.

FT MOD_RES 8 8 AMIDATION.

SV SEQUENCE 8 AA: 936 MW: 106365844906076A CRC64:

Query Match 18.2%, Score 2, DR 1, Length 8;

Best Local Similarity 100.0%; Pred. No. 1.3e+05;

Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WS 7

DB 11

DB 7 WS 8

CC entities requires a license agreement. (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch.)

DR EMBL: L08171; AAA25376.1; -;
 DR PIR: S35538;
 DR HAMAP: MF_00480; -; 1;
 DR InterPro: IPR00235; Ribosomal_S7;
 DR PROSITE: PS00052; RIBOSOMAL_S7; PARTIAL;
 KW Ribosomal protein; RNA-binding; tRNA binding; tRNA binding;
 FT INITMET 0 0 BY SIM:LABITY;
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 850 MW; 632760768742417 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 PK 11
 II
 DB 7 PK 8

RESULT 29
 RI34_BOVIN
 ID RI34_BOVIN STANDARD; PRT; 8 AA.
 AC P82929;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitochondrial 28S ribosomal protein S14 (S14nt) (MRP-S14) (Fragment).
 GN MRPS14.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 RN (1)
 RP SEQUENCE
 RC TISSUE: Liver;
 RX MEDLINE-21276436; PubMed-11279123;
 RA Koe E.C., Burkart W., Blackburn K., Mosely A., Spremull L.L.;
 RT "The small subunit of the mammalian mitochondrial ribosome:
 RT identification of the full complement of ribosomal proteins present";
 RC J. Biol. Chem. 276:19363-19374(2001).
 CC -!- SUBUNIT: Component of the mitochondria; ribosome small subunit.
 CC (28S) which comprises a 12S rRNA and about 30 distinct proteins.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 KW Ribosomal protein; Mitochondrial.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 935 MW; 963901A7C058470 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WG 7
 II
 DB 2 WG 3

RESULT 30
 UF06_MOUSE
 ID UF06_MOUSE STANDARD; PRT; 8 AA.
 AC P18644;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Mus.
 CC NCBI_TaxID=10090;

RI SEQUENCE.
 RC TISSUE=Fibroblast;
 RX MEDLINE-9500907; PubMed-7523108;
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 RT using preparative two-dimensional gel electrophoresis";
 RL Electrophoresis 15:745-745(1994).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.2, ITS MW IS: 50 kDa.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 817 MW; A35DD878676805B1 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GA 8
 II
 DB 6 GA 7

RESULT 31
 WPL_PERAT
 ID WPL_PERAT STANDARD; PRT; 8 AA.
 AC P83195;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Wall protein-2 (Wp-1) (Fragment).
 OS Perkinsus atlanticus.
 CC Eukaryota; Alveolata; Perkinsa; Perkinsida; Perkinsidae; Perkinsus.
 CC NCBI_TaxID=106964;
 RN (1)
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RX MEDLINE-22044350; PubMed-12049410;
 RA Montes J.F., Burford M., Llado A., Garcia-Valero J.;
 RT "Characterization and immunolocalization of a main proteinaceous
 RT component of the cell wall of the protozoan parasite Perkinsus
 RT atlanticus";
 RL Parasitology 124:477-484(2002).
 CC -!- FUNCTION: Is a major protein component of the cell wall. May play
 CC a key role in the organization of the cell wall and in promoting
 CC the survival of this parasite.
 CC -!- SUBCELLULAR LOCATION: Cell wall. Disulfide-linked to other cell
 CC wall components.
 CC -!- DEVELOPMENTAL STAGE: Expressed throughout all walled developmental
 CC stages.
 KW Cell wall.
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 765 MW; F1787D87B1AAB16 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GA 8
 II
 DB 5 GA 6

RESULT 32
 CONO_CONGE
 ID CONO_CONGE STANDARD; PRT; 9 AA.
 AC P05486;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Lys-conopressin G.
 OS Conus geographus (Geography cone).
 CC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 CC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypogastropoda;
 CC Neogastropoda; Conoidea; Conidae; Conus.


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OX NCBI_TaxID:6491;
RN
RP
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Kamito J.A., Zeikus R.D.,
RA Gray W.R., Oliveira B.M.;
RT "Invertebrate vasopressin/oxytocin homologs: characterization of
KT peptides from Conus geographus and Conus striatus venoms";
RL J. Biol. Chem. 262:15821-15824 (1987);
RN
RP REVIEW
RX MEDLINE=59024586; PubMed=4652286;
RA Gray W.R., Oliveira B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails";
RL Annu. Rev. Biochem. 57:665-700 (1988);
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
DR InterPro: IPR000981; Neurohyp-form.
DR Pfam: PF00220; hormone4; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1037 MW; D4FC276FB4540659 Cys64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KP 11
DB 7 KP 8

RESULT 34
CONV CONVE STANDARD; PRT; 9 AA.
AC P83047;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Contryphan-Vn.
OS Conus ventricosus (Mollusca: Mollusca)
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Artibeostreptoda;
OC Apogastropoda; Caenogastropoda; Sorbeopoda; Artibeostreptoda;
OC Neogastropoda; Conidae; Conidae; Conus;
OX NCBI_TaxID:117492;
RN
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY
RX MEDLINE=21547785; PubMed=11688995;
RA Massilia G.R., Schinina M.E., Ascaris P., Bellavalli F.;
RT "Contryphan-Vn: a novel peptide from the venom of the Mediterranean
RL snail Conus ventricosus";
RL Biochem. Biophys. Res. Commun. 288:908-914 (2001)
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=1388.6; METHOD MALDI.
CC -1- SIMILARITY: BELONGS TO THE CONTRYPHAN FAMILY.
KW TISSUE: Amidation; D-amino acid.
FT DISULFID 3 9
FT MOD_RES 5 5
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1091 MW; 8D3867632167658A Cys64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KP 10
DB 6 KP 7

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RESULT 34
FAR4 CALVO STANDARD; PRT; 9 AA.
AC P41859;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CalliFMRamide 4.
OS Calliphora vomitoria (Insecta: Diptera).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
RN
RP SEQUENCE.
RX TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Duve H., Johnson A.H., Swell J.C., Scott A.G., Orchard I.,
RA Renfield J.F., Thorpe A.;
RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
RT neuropeptides (designated calliFMRamides) from the blowfly
RT Calliphora vomitoria";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330 (1992).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: D41978; D41978.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1162 MW; 31730699CAB6D457 Cys64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KP 10
DB 1 KP 2

RESULT 35
FAR5 ASCSU STANDARD; PRT; 9 AA.
AC P43170;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRamide-like neuropeptide AF5.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
RT Ascaris suum";
RL Peptides 16:491-500 (1995).
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1052 MW; 340B0059D1B76338 Cys64;

Query Match 18.2%; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KP 10
DB 3 KP 4

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RT Identification of a prothoracicostatic peptide in the larva, brain of
 the silkworm, *Bombyx mori*.
 J. Biol. Chem. 274:31169-31173(1999).

NCBI TaxID-9823;
 [1]
 RN SEQUENCE
 RX MEDLINE-74026571; PubMed-914862;
 RA Plein J.-M., Gaidano N., Wautlet Y., Bach J.-F.,
 RL J. Biol. Chem. 275:9892-9892(2000).
 CC FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic
 gland.
 CC SUBCELLULAR LOCATION: Secreted.
 CC DEVELOPMENTAL STAGE: EARLY FETAL INSULAR
 KW Hormone; Amidation.
 FT MOD_RES 9
 SEQUENCE 9 AA: 1090 MW: 487805447228600 CRC64;

Query Match 18.2% Score 2; DB 1; Length 9;
 Best local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
 DB 5 LN 6

RESULT 40
 ID RT130AVIN STANDARD; PRT; 9 AA
 AC P62926;
 DT 26-FEB-2003 (Rel. 41, Created)
 DI 28-FEB-2003 (Rel. 41, Last sequence update)
 DI 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mitochondrial 28S ribosomal protein, S16 (S16mt) (M6851) (Fragment).
 OS M6851.
 GN Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Bovidae; Bovidae;
 CC Bovidae; Bovidae; Bos.
 DX NCBI_TaxID-9913;
 RN [1]
 RP SEQUENCE
 RC TISSUE-Liver;
 RX MEDLINE-21276446; PubMed-11279420;
 RA Koe E.C., Burkhardt W., Blackburn K., Moscovici A., Sprafkin J.L.,
 RT The small subunit of the mammalian cytochrome P-450 CYP1A1.
 RT Identification of the full complement of ribosomal proteins present.
 RL J. Biol. Chem. 276:19363-19374(2001)
 CC SUBUNIT: Component of the cytochrome P-450 CYP1A1 subunit.
 CC WHICH COMPRISES A 125 KDA AND A 100 KDA SUBUNIT PROTEINS.
 CC SUBCELLULAR LOCATION: Mitochondrial.
 KW Ribosomal protein; Mitochondrion.
 FT NON_TER 1
 FT NON_TER 1
 SEQUENCE 9 AA: 1032 MW: 10410707068058176663

Query Match 18.2% Score 2; DB 1; Length 9;
 Best local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AK 9
 DB 8 AK 9

RESULT 41
 ID THYF_PIG STANDARD; PRT; 9 AA
 AC P31255;
 DT 21-JUL-1986 (Rel. 01, Created)
 DI 21-JUL-1986 (Rel. 01, Last sequence update)
 DI 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Thymic factor.
 OS Sus scrofa (Pig).

Query Match 18.2% Score 2; DB 1; Length 9;
 Best local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AK 9
 DB 8 AK 9

RESULT 42
 ID UPAB_HUMAN STANDARD; PRT; 9 AA
 AC P30092;
 DT 01-APR-1993 (Rel. 25, Created)
 DI 01-APR-1993 (Rel. 25, Last sequence update)
 DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2B Page of plasma (Spot 14) (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 DX NCBI_TaxID-9606;
 RN [1]
 RP SEQUENCE
 RC TISSUE-Plasma;
 RX MEDLINE-93092947; PubMed-1459597;
 RA Hughes G.J., Fraliger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., Camus R., Tissot J.-D., Bjellqvist B.,
 RA Hochstrasser D.F.
 RT Plasma protein map: an update by microsequencing.
 RL Electrophoresis 13:707-714(1992).
 CC MISCELLANEOUS: ON THE 2D GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5. ITS MW IS: 48 KDa.
 DB SWISS-2DPAGE; P30092; HUMAN.
 FT NON_TER 1
 FT NON_TER 9
 SEQUENCE 9 AA: 935 MW: 528242CAA8676447 CRC64;

Query Match 18.2% Score 2; DB 1; Length 9;
 Best local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
 DB 2 LN 3

CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 DX NCBI_TaxID-9823;
 RN [1]
 RN SEQUENCE
 RX MEDLINE-74026571; PubMed-914862;
 RA Plein J.-M., Gaidano N., Wautlet Y., Bach J.-F.,
 RL J. Biol. Chem. 275:9892-9892(2000).
 CC FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic
 gland.
 CC SUBCELLULAR LOCATION: Secreted.
 CC DEVELOPMENTAL STAGE: EARLY FETAL INSULAR
 KW Hormone; Amidation.
 FT MOD_RES 9
 SEQUENCE 9 AA: 1090 MW: 487805447228600 CRC64;

Query Match 18.2% Score 2; DB 1; Length 9;
 Best local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AK 9
 DB 2 AK 3

RESULT 43
 ID BPP2_BOTIN STANDARD; PRT; 10 AA
 AC P30422;
 DT 01-APR-1993 (Rel. 25, Created)
 DI 01-FEB-1994 (Rel. 28, Last sequence update)
 DI 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S4,3,1 (10C) (Angiotensin-converting
 enzyme inhibitor).
 OS Bothrops insularis (Island Jararaca) (Queimada Jararaca).

Query Match 18.2% Score 2; DB 1; Length 9;
 Best local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
 DB 2 LN 3

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 peptides from Bothrops insularis snake venom.*"
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR: H37196; H37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA: 1213 MW: 3053546076;F773 CRC64;
 Query Match 18.2% Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 NW 6
 DB 2 NW 3
 RESULT 44
 ID BPP2_BOTIN STANDARD; PRT; 10 AA.
 AC P31022;
 DT 21-JUL-1984 (Rel. 01, Created)
 DT 21-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide 105 (Angiotensin-converting enzyme
 DE inhibitor V-6-11).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Venom;
 RX MEDLINE=72118525; PubMed 433462.
 RA Oudet M.A., Williams N.J., Sato T., Kawanishi S., Watanabe E.K.;
 RA Kocy O.;
 RT "Angiotensin-converting enzyme inhibitors from the venom of Bothrops
 RT jararaca. Isolation, elucidation of structure, and synthesis.*"
 RL Biochemistry 10:4033-4039(1971).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR: A01255; XAV16B.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA: 1232 MW: 3053546074;F773 CRC64;
 Query Match 18.2% Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 NW 6
 DB 2 NW 3
 RESULT 45
 ID BPP2_BOTIN STANDARD; PRT; 10 AA.
 AC P31022;
 DT 21-JUL-1984 (Rel. 01, Created)
 DT 21-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide 105 (Angiotensin-converting enzyme
 DE inhibitor V-6-11).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8724;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 peptides from Bothrops insularis snake venom.*"
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR: A01255; XAV16B.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA: 1232 MW: 3053546074;F773 CRC64;
 Query Match 18.2% Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ID BPP2_BOTIN STANDARD; PRT; 10 AA.
 AC P30426;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide S5,1 (Angiotensin-converting
 DE enzyme inhibitor)
 OS Bothrops insularis (Island Jararaca) (Queimada Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 OX NCBI_TaxID=8723;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Venom;
 RX MEDLINE=90351557; PubMed=2386615;
 RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
 RT "Primary structure and biological activity of bradykinin potentiating
 peptides from Bothrops insularis snake venom.*"
 RL J. Protein Chem. 9:221-227(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR: H37196; H37196.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA: 1173 MW: 2FF835545761F6D8 CRC64;
 Query Match 18.2% Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 NW 7
 DB 2 NW 3
 RESULT 45
 ID BPP2_VIPAS STANDARD; PRT; 10 AA.
 AC P31351;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Bradykinin-potentiating peptide (Angiotensin-converting
 DE enzyme inhibitor).
 OS Vipera aspis (Aspis Viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Viperinae; Vipera.
 OX NCBI_TaxID=8705;
 RN [1]
 RP SEQUENCE.
 RC TISSUE-Venom;
 RX MEDLINE=90382616; PubMed=2169439;
 RA Komori Y., Sugihara H.;
 RT "Characterization of a new inhibitor for angiotensin converting
 RT enzyme from the venom of Vipera aspis aspis.*"
 RL Int. J. Biochem. 22:767-771(1990).
 CC -!- FUNCTION: This peptide both inhibits the activity of the
 CC angiotensin-converting enzyme and enhances the action of
 CC bradykinin by inhibiting the kinases that inactivate it.
 CC It acts as an indirect hypotensive agent.
 DR PIR: A60377; XASNPC.
 KW Hypotensive agent; Pyrrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 10 AA: 1062 MW: 3BA827C327686773 CRC64;
 Query Match 18.2% Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      10 PK 11
DB      6 PK 7

RESULT 47
CAVR_SHEEP
ID CATH_SHEEP STANDARD: PRT: 10 AA.
AC P81205:
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Cathepsin B (EC 3.4.22.1) (Cathepsin B) (Fragment).
GN CTSB
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN [1]
RV SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE-22394055; PubMed-12506352;
RA El Aniri B., Remy B., Sousa N.M., Joris B., Ottens N.G., Perenyi Z.,
RA Muko H.B., Beckers J.-F.M.P.;
RT Isolation and partial characterization of three pregnancy-associated
RT glycoproteins from the ewe placenta.;
RL Mol. Reprod. Dev. 64:199-206(2003).
CC -!- FUNCTION: Thiol protease which is believed to participate in
CC intracellular degradation and turnover of proteins. Has also been
CC implicated in tumor invasion and metastasis.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of proteins with broad specificity
CC for peptide bonds. Preferentially cleaves -Arg-Arg- and Xaa bonds in
CC small molecule substrates (thus differing from cathepsin L). In
CC addition to being an endopeptidase, shows peptidyl-dipeptidase
CC activity, liberating C-terminal dipeptides.
CC -!- SUBUNIT: Dimer of a heavy chain and a light chain cross-linked
CC by a disulfide bond (By similarity).
CC -!- SUBCELLULAR LOCATION: Lysosomal (by similarity).
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
DR InterPro: IPR001019; SHProl_acsite.
DR PROSITE: PS00640; THIOL_PROTEASE_ASN; PAM1A1.
DR PROSITE: PS00139; THIOL_PROTEASE_CYS; PAM1A1.
DR PROSITE: PS00639; THIOL_PROTEASE_HIS; PAM1A1.
KW Hydrolase; Thiol protease; Lysosome.
ST NON_TER 10 10
SQ SEQUENCE 10 AA: 1177 MW: 9795;PGLDAA-GLDPA-GLDPA-
Query Match 19.2%; Score 2: 10; DB 1: Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AR 2
DB      7 AR 8

RESULT 48
COXA_OMCY
ID COXA_OMCY STANDARD: PRT: 10 AA.
AC P80428:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome c oxidase polypeptide Va (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OC NCBI_TaxID=8022;
RN [1]
RV SEQUENCE.
RC TISSUE=Liver;

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RX MEDLINE-94237150; PubMed-8181469;
RA Freund R., Kadenbach B.;
RT Identification of tissue-specific isoforms for subunits Vb and Vila
RT of cytochrome c oxidase isolated from rainbow trout.;
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -!- FUNCTION: THIS IS THE HEME A-CONTAINING CHAIN OF CYTOCHROME C
CC OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) -> 4 ferrocycytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VA FAMILY.
DR PIR: S43625; S43625.
KW Oxidoreductase; Heme; Mitochondrion; Inner membrane.
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1144 MW: 5355;SBIAR02C33D CRC64;

Query Match 18.2%; Score 2: DB 1: Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 AK 9
DB      3 AK 4

RESULT 49
COXQ_RABIT
ID COXQ_RABIT STANDARD: PRT: 10 AA.
AC P80336:
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIII-liver/heart (EC 1.9.3.1)
DE (Fragment).
GN COX8b.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RV SEQUENCE.
RC TISSUE=Heart, and liver;
RA Freund R., Kadenbach B.;
RT Submitted (MAR-1994) to the SWISS-PROT data bank.
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocycytochrome c + O(2) -> 4 ferrocycytochrome
CC c + 2 H(2)O.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIII FAMILY.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 10 10
SQ SEQUENCE 10 AA: 1027 MW: 2325;CB40DC76338 CRC64;

Query Match 18.2%; Score 2: DB 1: Length 10;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AR 2
DB      6 AR 7

RESULT 50
FAR2_PENMO
ID FAR2_PENMO STANDARD: PRT: 10 AA.
AC P83317:
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE FMRFamide-like neuropeptide FLP2 (AYSNLYLRF-amide).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

```

OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_taxid:6687;
RN {}
RP SEQUENCE AND MASS SPECTROMETRY.
RC TISSUE: Eyestalk;
RX MEDLINE:21956277; PubMed:11959019;
RA Sittigornqui P.; Pupem J.; Kruangkarn C.; Lamyant S.;
RA Chavitsuthangkura P.; Sittigornqui W.; Pongsak A.;
RT "Seven novel FMRFamide-like neuropeptide sequences from the eyestalk
RI of the giant tiger prawn *Penaeus monodon*.";
RL Comp. Biochem. Physiol. 131B:325-337(2002).
OC -1 SUBCELLULAR LOCATION: Secreted.
OC -1 MASS SPECTROMETRY: MW:1260.67; METHOD: MALDI
OC -1 SIMILARITY: BELONGS TO THE FAPF (FMRFAMIDE RELATED PEPTIDE)
OC FAMILY.
KW Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1260 MW; 8BF902B954472455 CRC64;

Query Match 18.2% Score 2; 10B 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1;36+64;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
DB 5 LN 6

Search completed: September 30, 2003, 19:26:09
Job time : 8.25 secs

SeqWare version 5.1.1.6
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CM protein protein search, using SW model

Run on: September 30, 2003, 10:37:04 Search time: 11:45:55 Seconds
(without subparameters)
33 343 Million full updates/sec

Title: US-09-787-443-3
Perfect score: 11
Sequence: 1 ARALNWCAR 11

Scoring table: GCIGD
Gapop 60.0, Gapext 50.0

Searched: 283308 seqs, 56166682 residues

Word size: 0

Total number of hits satisfying chosen parameters 2094

Maximum DB seq length: 8
Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database: PIR 76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	13	2	protein 17 - home
2	3	27.3	8	2	hypothetical prote
3	3	27.3	8	4	hypothetical hist
4	3	27.3	9	2	hypothetical hist
5	3	27.3	10	2	hypothetical hist
6	3	27.3	10	2	hypothetical hist
7	3	27.3	10	2	hypothetical hist
8	3	27.3	10	2	hypothetical hist
9	3	27.3	10	2	hypothetical hist
10	3	27.3	10	2	hypothetical hist
11	3	27.3	10	2	hypothetical hist
12	3	27.3	10	2	hypothetical hist
13	3	27.3	10	2	hypothetical hist
14	3	27.3	10	2	hypothetical hist
15	3	27.3	10	2	hypothetical hist
16	3	27.3	10	2	hypothetical hist
17	3	27.3	10	2	hypothetical hist
18	3	27.3	10	2	hypothetical hist
19	3	27.3	10	2	hypothetical hist
20	3	27.3	10	2	hypothetical hist
21	3	27.3	10	2	hypothetical hist
22	3	27.3	10	2	hypothetical hist
23	3	27.3	10	2	hypothetical hist
24	3	27.3	10	2	hypothetical hist
25	3	27.3	10	2	hypothetical hist
26	3	27.3	10	2	hypothetical hist
27	3	27.3	10	2	hypothetical hist
28	3	27.3	10	2	hypothetical hist
29	3	27.3	10	2	hypothetical hist

T-cell receptor al
mixed lymphocyte r
red pigment-concen
hypertrehalosemic
hypertrehalosemic
hypertrehalosemic
adipokinetic hormo
adipokinetic hormo
neuropeptide Led-C
neuropeptide Led-C
adipokinetic hormo
hypertrehalosemic
hypertrehalosemic
adipokinetic hormo
lg heavy chain V r
sperm-activating p
sperm-activating p
sperm-activating p
urine glycopeptide
angiotensin-conver
rpsA protein - Brw
glycine reductase
endoglycosylcerami
R-phycoerythrin ga
unidentified 6.5/3
neuropeptide M-1 -
leucokinin V - Mad
leucokinin VII - M
leucokinin VIII -
neuropeptide - flo
p element, P cytot
calliphramide 8 -
acetylcholinestera
aspartate transami
serum albumin - do
thymic humoral fac
apolipoprotein A-1
lg H chain V-D-J r
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
T-cell receptor be
apolipoprotein A-1
thymic factor - pi
locustamoinhibiti
dihydrolipoamide S
conopressin G - co
thymocyte growth p
adipokinetic hormo
ribosomal protein
calsequestrin, car
xenopsin-related p
xenopsin-related p
vitamin B3 26-mono
sperm-activating p
photosystem II pro
alpha/beta-gliadin
neuropeptide Grb-A
neuropeptide Grb-A
calliphramide 4 -
c-rel protein - ch
118K stomach cance
gene NF2 protein -
lg heavy chain CRD
macrophage cytotox
zymogen granule me
alpha-2-macroglobu
alpha-2-macroglobu
ribosomal protein
lg H chain V-D-J r
lg heavy chain V r

[illegible]

395	2	18.2	13	2	PH0783	T-cell receptor al	468	2	18.2	14	2	PH1768	T cell receptor al
396	2	18.2	13	2	PH0805	T-cell receptor al	469	2	18.2	14	2	PH1769	T cell receptor al
397	2	18.2	13	2	PH0348	unidentified QM32	470	2	18.2	14	2	S57572	insulin-like grow
398	2	18.2	13	2	PH0728	T-cell receptor be	471	2	18.2	14	2	JH0516	leukotriene B-4 12
399	2	18.2	13	2	C47510	Iq kappa chain J r	472	2	18.2	14	2	A47421	glycoprotein compo
400	2	18.2	13	2	H47530	Iq kappa chain J r	473	2	18.2	14	2	F48394	thrombospondin 2 -
401	2	18.2	13	2	F51905	collecting duct wa	474	2	18.2	14	2	D45474	tubulin beta-3 cha
402	2	18.2	13	2	G81988	hypothetical prote	475	2	18.2	14	2	A39703	hypothetical 1.5K
403	2	18.2	13	2	S61558	serine proteinase	476	2	18.2	14	2	JS0272	Ig H chain V-D-J r
404	2	18.2	13	2	H85575	hypothetical prote	477	2	18.2	14	2	PH1626	Ig H chain V-D-J r
405	2	18.2	13	2	S54144	glyceroldehyde-3-p	478	2	18.2	14	2	PH1628	Ig H chain V-D-J r
406	2	18.2	13	4	F70076	glycophorin B/alyc	479	2	18.2	14	2	PH1639	Ig H chain V-D-J r
407	2	18.2	14	1	NYPC14	hypothalamic tetra	480	2	18.2	14	2	PH1617	Ig H chain V-D-J r
408	2	18.2	14	1	QMWAVV	mastoparan - yello	481	2	18.2	14	2	PH1623	Ig H chain V-D-J r
409	2	18.2	14	1	QMWVHM	mastoparan M - hor	482	2	18.2	14	2	PH1586	Ig H chain V-D-J r
410	2	18.2	14	1	QMWVHM	mastoparan X - hor	483	2	18.2	14	2	PH1594	Ig H chain V-D-J r
411	2	18.2	14	1	QMWVHX	mastoparan C - Eur	484	2	18.2	14	2	PH1597	Ig H chain V-D-J r
412	2	18.2	14	1	LFEBWI	trp operon leader	485	2	18.2	14	2	PH1598	Ig H chain V-D-J r
413	2	18.2	14	2	A33798	D-amino-acid oxida	486	2	18.2	14	2	PH1608	Ig H chain V-D-J r
414	2	18.2	14	2	JN0389	histamine-releasin	487	2	18.2	14	2	PH1448	T-cell receptor al
415	2	18.2	14	2	PH1677	Iq heavy chain V r	488	2	18.2	14	2	PH0800	T-cell receptor al
416	2	18.2	14	2	F51430	hemoglobin beta ch	489	2	18.2	14	2	PH0795	T-cell receptor al
417	2	18.2	14	2	F51432	histone H4-1 precu	490	2	18.2	14	2	PH0776	T-cell receptor al
418	2	18.2	14	2	A35377	GIP-binding protei	491	2	18.2	14	2	PH1450	T-cell receptor al
419	2	18.2	14	2	A42473	ermk leader peptid	492	2	18.2	14	2	PT0210	T-cell receptor al
420	2	18.2	14	2	A44515	trp EG leader pept	493	2	18.2	14	2	PH0765	T-cell receptor be
421	2	18.2	14	2	S27140	hypothetical prote	494	2	18.2	14	2	PH0747	T-cell receptor be
422	2	18.2	14	2	JH0328	probrusin tetradec	495	2	18.2	14	2	E35141	T-cell receptor de
423	2	18.2	14	2	S29532	xylar: 1,4-beta-xy	496	2	18.2	14	2	F49037	T-cell receptor de
424	2	18.2	14	2	F39753	nitrogenase (EC 1.	497	2	18.2	14	2	S65392	T-cell receptor de
425	2	18.2	14	2	F10142	carbon-monoxide de	498	2	18.2	14	2	C48394	T-cell receptor de
426	2	18.2	14	2	S07768	soluble hydrogenas	499	2	18.2	14	2	H83778	T-cell receptor de
427	2	18.2	14	2	S14864	methyl coenzyme M	500	2	18.2	14	2	E81280	T-cell receptor de
428	2	18.2	14	2	S29789	hypothetical prote							
429	2	18.2	14	2	H56319	PS-1 complex subu							
430	2	18.2	14	2	PA0111	protein GAI00054							
431	2	18.2	14	2	S09721	2S albumin small c							
432	2	18.2	14	2	PT0326	calotropin D1 - m2							
433	2	18.2	14	2	G44957	photosystem II oxy							
434	2	18.2	14	2	S34801	chaperone, TBP1-re							
435	2	18.2	14	2	S34802	chaperone, TBP1-re							
436	2	18.2	14	2	S34803	chaperone, TBP1-re							
437	2	18.2	14	2	S34804	16K protein 5404 -							
438	2	18.2	14	2	PS-258	48K protein 3228 -							
439	2	18.2	14	2	PS-258	unidentified 6.0/k							
440	2	18.2	14	2	PS-258	malate dehydrogena							
441	2	18.2	14	2	PS-258	lysine - karate							
442	2	18.2	14	2	PA0094	lysine (6S)-di							
443	2	18.2	14	2	PA0103	protein QF20020 -							
444	2	18.2	14	2	B34135	DNA-binding protei							
445	2	18.2	14	2	S14336	mastoparan B - hor							
446	2	18.2	14	2	S04530	Iq heavy chain J r							
447	2	18.2	14	2	S62374	alpha-1-antichymot							
448	2	18.2	14	2	F54815	carbonic anhydrase							
449	2	18.2	14	2	B61235	fibroblast-activat							
450	2	18.2	14	2	PT0223	Iq heavy chain CDR							
451	2	18.2	14	2	PT0223	Iq heavy chain CDR							
452	2	18.2	14	2	PH1347	Iq heavy chain DJ							
453	2	18.2	14	2	PH1348	Iq heavy chain DJ							
454	2	18.2	14	2	PH1327	Iq heavy chain DJ							
455	2	18.2	14	2	PH1356	Iq heavy chain DJ							
456	2	18.2	14	2	PH1332	Iq heavy chain DJ							
457	2	18.2	14	2	PH1322	Iq heavy chain DJ							
458	2	18.2	14	2	PH1313	Iq heavy chain DJ							
459	2	18.2	14	2	PH1321	Iq heavy chain DJ							
460	2	18.2	14	2	PH1405	Iq heavy chain DJ							
461	2	18.2	14	2	PH1306	Iq heavy chain DJ							
462	2	18.2	14	2	S41601	interferon alpha 1							
463	2	18.2	14	2	PH1757	T cell receptor al							
464	2	18.2	14	2	PH1758	T cell receptor al							
465	2	18.2	14	2	PH1759	T cell receptor al							
466	2	18.2	14	2	PH1766	T cell receptor al							
467	2	18.2	14	2	PH1767	T cell receptor al							

ALIGNMENTS

RESULT 1

B44957 protein I7 - common tobacco (cv. Samsun NN) (fragment)

C:Species: Nicotiana glauca (common tobacco)

C:Date: 01-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 30-Sep-1993

C:Accession: B44957

R:Takeda, S.; Sato, F.; Ida, K.; Yamada, Y.

Plant Cell Physiol. 31, 215-221, 1990

A:Title: Characterization of polypeptides that accumulate in cultured Nicotiana tab

A:Reference number: A44957

A:Accession: B44957

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <TAK>

Query Match 36.4% Score 4; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAKP 10

Db 7 GAKP 10

RESULT 2

T48890

hypothetical protein ORF-B [imported] - Streptomyces coelicolor (fragment)

C:Species: Streptomyces coelicolor

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 20-Jan-2003

C:Accession: T48890

R:Matsumoto, A.; Honq, S.; Ishizuka, H.; Horinouchi, S.; Beppu, T.

Gene 146, 47-56, 1994

A:Title: Phosphorylation of the AfsR protein involved in secondary metabolism in St

A:Reference number: 224852; MUID:94341568; PMID:8063104

A:Accession: T48890

```

A:Status: Preliminary; translated from GB/EMBL/GenBank;
A:Molecule type: DNA
A:Residues: 18 <MAT>
A:Cross-references: EMBL:DJ1502; PDB:1BA54695; 1
A:Experimental source: strain M10

Query Match: 27.3%; Score 3; 18 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RAL 4
Ds 11
6 RAL 8

RESULT:
155411
hypothetical: histone H2A.X (untranslated) human (transmem)
C:Species: Homo sapiens (man)
C:Date: 28-Jan-2000 #sequence_revision 28 Jan-2000 #text_change 28 Jan-2000
C:Accession: I55411
R:Yanovsky, V. S.; Hatch, C. L.; Bonner, W. M.
J. Biol. Chem. 267, 24189-24194, 1994
A:Title: Characterization of the human histone H2A.X gene. Comparison of its promoter w
A:Reference number: I55411; MUID:95014156; PMID:7929675
A:Accession: I55411
A:Status: translation not shown; translated from GB/EMBL/GenBank
A:Molecule type: DNA
A:Residues: 18 <IVA>
A:Cross-references: GB:S74863; NID:q765495; PDB:1AAB14141; PIR:q4261841
A:Note: this is a hypothetical translation of a sequence from the promoter region precede
C:Genetics:
A:Gene: H2A.X

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Query Match      27.3%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2, 4e-06;
Matches      3; Conservative      0; Mismatches      0; Gaps      0;

QY      1 ARA 3
      III
DB      5 ARA 7

RESULT 4
PT0562
I Cell receptor: beta chain V-D-1 region (126-1AK) mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 1-30 1992 #text_change 40-May-1997
C:Accession: PT0562
R:Feeney, A.J.
J:Exp. Med. 174, 115-124, 1991
A:Title: Functional sequences of beta-1 cell receptor beta chains have few N regions.
A:Reference number: PT0569; MUID:912776a1; PMID:171158
A:Accession: PT0562
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 159 <FE>
A:Experimental source: day 18 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match      27.3%; Score 3; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 2, 4e-06;
Matches      3; Conservative      0; Mismatches      0; Gaps      0;

QY      5 NWC 7
      III
DB      6 NWC 8

RESULT 5
CC1416
Hypothalamic hormone 1 - stick insect (Griensberg)
Alternate names: neuropeptide Cam-III 1

```

N:Contains: hypertrehalosemic factor II
C:Species: Carausius morosus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: JCI1416; S07157
R:Gaede, G.; Kellner, R.; Kinehart, K.L.; Proefke, M.L.
Biochem. Biophys. Res. Commun.: 189, 1303-1309, 1992
A:Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick insect
A:Reference number: JCI1416; MUID:93129:88; PMID:1482345
A:Accession: JCI1416
A:Molecule type: protein
A:Residues: 1-10 <GAE1>
R:Gaede, G.; Kinehart Jr., K.L.
Biol. Chem. Hoppe-Seyler 368, 67-75, 1987
A:Title: Primary structure of the hypertrehalosaemic factor II from the corpus card
A:Reference number: S07157; MUID:87157103; PMID:3828078
A:Accession: S07157
A:Molecule type: protein
A:Residues: 27,2-10 <GAE2>
C:Comment: Hypertrehalosemic factor II lacks the tryptophan modification.
C:Comment: This peptide raises hemolymph levels of trehalose in the cockroach Pe-
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutami
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:8/Binding site: carbohydrate (Trp) (covalent) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 27.3%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NWG 7
III
DB 7 NWG 9

RESULT 6
S09138
hypertrehalosemic hormone II - stick insect (Extatosoma tiaratum)
N:Alternate names: Cam-Hrth II;
C:Species: Extatosoma tiaratum
C:Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C:Accession: S09138
R:Gaede, G.; Kinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A:Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the c
entails and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bo
A:Reference number: S08995; MUID:90253659; PMID:2340112
A:Accession: S09138
A:Molecule type: protein
A:Residues: 1-10 <GAE>
A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we
C:Superfamily: adipokinetic hormone
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10/Modified site: amidated carboxyl end (Thr) #status experimental

Query Match 27.4%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NWG 7
III
DB 7 NWG 9

RESULT 7
Jp0072
ribosomal protein l32 - Lactobacillus plantarum (fragment)
C:Species: Lactobacillus plantarum
C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 28-Oct-1994
C:Accession: Jp0072
R:Ochi, K.
Submitted to JPIB, February 1994

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A:Status: Preliminary; translated from GH/EMBL/CDDB;
A:Molecule type: DNA
A:Residues: 1-8 <MAT>
A:Cross-references: EMBL:DJ5062; PDB:BA540955, 1
A:Experimental source: strain M19

Query Match: 27.3%; Score 3; BB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2, Dec-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAL 4
DB 6 RAL 8

RESULT 3
155411
hypothetical histone H2A.X (mistranslated) human (treatment)
C:Species: Homo sapiens (man)
C:Date: 28-Jan-2000 #sequence_revision 28 Jan 2000 #text_change 28 Jan 2000
C:Accession: 155411
R: Ivanova, V.S.; Hatch, C.L.; Bonner, W.M.
J. Biol. Chem. 269, 24189-24194, 1994
A:Title: Characterization of the human histone H2A.X gene. Comparison of its promoter with
A:Reference number: 155411; MUID:95C14156; PMID:792975
A:Accession: 155411
A:Status: translation not shown; translated from GH/EMBL/CDDB
A:Molecule type: DNA
A:Residues: 1-8 <IVA>
A:Cross-references: GB:S74863; NCBI:9765795; PDB:AA041411; EMBL:Q426184
A:Note: This is a hypothetical translation of a sequence from the promoter region precede
C:Genetics:
A:Gene: H2A.X

Query Match: 27.3%; Score 3; BB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2, Dec-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARA 3
DB 5 ARA 7

RESULT 4
PT0562
T cell receptor: beta chain V-D-J region (126 AA) mouse (treatment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul 1992 #text_change 30-May-1997
C:Accession: PT0562
R: Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Functional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0569; MUID:91277601; PMID:1711558
A:Accession: PT0562
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-9 <FEE>
A:Experimental source: day 18 fetal thymus; strain BALB/c
C:Keywords: T-cell receptor

Query Match: 27.3%; Score 3; BB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2, Dec-05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NWC 7
DB 6 NWC 8

RESULT 5
CC1416
hypothetical gonadotropin hormone 1 - stuck insert (Gonadotropin hormone)
A:Alternate names: neuropeptide Cam-Br11

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Accession: JP0042
 A:Reference number: JP0042
 A:Accession: JP0072
 A:Molecule type: protein
 A:Residues: 110 <OCH>
 C:Keywords: protein biosynthesis; ribosome

Query Match 27.4% Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKP 10
 III
 DB 4 AKP 6

RESULT 8

A40753
 aldehyde ferredoxin oxidoreductase (EC 1.2.1.7) Pyrococcus furiosus (fragment)
 S:Alternate names: glyceraldehyde:ferredoxin oxidoreductase; red toadstool protein (RTP)
 C:Species: Pyrococcus furiosus
 C:Date: 21-Apr-1992 #sequence_revision 21 Apr-1992 #text_change 13-Sep-1996

R:Muhammad, S.; Adams, M.W.W.
 J. Biol. Chem. 255, 14208-14216, 1991
 A:Title: The novel, tungsten iron-sulfur protein of the hyperthermophilic archaeobacterium
 colytic pathway.
 A:Reference number: A40753; MUID:91017769; PMID:1907274

A:Accession: A40753
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 110 <MK>
 C:Keywords: iron-sulfur protein; oxidoreductase; tungsten

Query Match 27.3% Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 LNW 7
 III
 DB 4 LNW 6

RESULT 9

P0289
 Ig heavy chain C3H region (Chain C190-91) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 10-Aug-1996

R:Yamada, M.; Wasserman, K.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 174, 495-507, 1991

A:Title: Preferential utilization of specific IgG antibodies in heavy chain diversity and

A:Reference number: P0289; MUID:91108107; PMID:1879712

A:Accession: P0289

A:Molecule type: DNA

A:Residues: 110 <YAM>

A:Experimental source: B lymphocyte

C:Keywords: heterotetramer; immunoglobulin

Query Match 27.3% Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LNW 6
 I
 DB 2 LNW 4

RESULT 10

P49164
 chromogranin B, rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 19-Feb-1994 #sequence_revision 14-Nov-1994 #text_change 6-Jun-1995

C:Accession: B49164
 R:Nielsen, E.; Wellinder, K.S.; Madsen, O.D.
 Endocrinology 129, 3247-3156, 1991
 A:Title: Chromogranin B, a putative precursor of eight novel rat glucagonoma peptid

A:Reference number: A49164; MUID:92063871; PMID:1954895

A:Accession: B49164

A:Status: preliminary

A:Molecule type: protein

A:Residues: 111 <NIE>

A:Note: sequence extracted from NBL backbone (NCBIP:66370)

C:Superfamily: chromogranin B precursor

Query Match 27.4% Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NMG 7
 III
 DB 7 NMG 9

RESULT 11

S71304
 amine oxidase (copper-containing) (EC 1.4.3.6) 11 - Aspergillus niger (fragment)
 C:Species: Aspergillus niger
 C:Date: 12-Feb-1998 #sequence_revision 01-May-1998 #text_change 07-May-1999

R:Reibort, L.; Tanaki, H.; Ishida, H.; Pec, P.; Luhova, L.; Tsuno, H.; Halata, M.; /
 Eur. J. Biochem. 237, 255-265, 1996

A:Title: Two distinct quinoprotein amine oxidases are induced by n-butylamine in the

A:Reference number: S71304; MUID:96204933; PMID:8620882

A:Accession: S71304

A:Molecule type: protein

A:Residues: 111 <PRE>

C:Keywords: copper binding; monomer; oxidoreductase; quinoprotein; topaquirone

Query Match 27.4% Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALN 5
 I
 DB 5 ALN 7

RESULT 12

PH1343
 Ig heavy chain L3 region (Chain C190-91) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

A:Accession: PH1343

R:Wasserman, K.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DJH joining in young children with B precursor

A:Reference number: PH1343; MUID:93094761; PMID:1460419

A:Accession: PH1343

A:Molecule type: DNA

A:Residues: 111 <WAS>

C:Keywords: heterotetramer; immunoglobulin

Query Match 27.4% Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NMG 7
 III
 DB 6 NMG 8

RESULT 13

S49044
 Ig heavy chain C3H region (Chain C190-91) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 26-May 1995 #text_change 17-Mar-1999
 C:Accession: S23164
 R:Pluschke, G.; Ricken, G.; Taube, H.; Kronenberg, S.; Melchers, J.; Peter, H.H.; Eichman, E.R.; Immunol., 21, 2749-2754, 1991
 A:Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheumatoid arthritis
 A:Reference number: S23364; MUID:92037420; PMID:1657615
 C:Accession: S23364
 A:Status: preliminary; translation: not shown
 A:Molecule type: mRNA
 A:Residues: 1-11 <PLD>
 A:Cross references: EMBL:X58164
 C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ALN 5
 DB 8 ALN 10

RESULT 14
 A29169
 phospholipase A2 (EC 3.1.1.4) precursor, sheep (fragment)
 C:Species: ovis orientalis aries, ovis aries (domestic sheep)
 C>Date: 22-Jun-1988 #sequence_revision 02-Jun-1998 #text_change 31-Oct-1997
 C:Accession: A29169
 R:Butlin, C.E.; Van Doren, P.J.; Verheij, F.E.A.M.; Le Baus, G.H.; Eur. J. Biochem., 53, 91-97, 1975
 A:Title: Isolation and properties of phospholipase A2 from ox and sheep pancreas.
 A:Reference number: A94661
 A:Accession: A29169
 A:Molecule type: protein
 A:Residues: 1-12 <BD>
 C:Superfamily: phospholipase A2
 C:Keywords: carboxylic ester hydrolase; pyroglutamate and
 F1/Modified site: pyrrolidone carboxylic acid (Gln) #status: experimental

Query Match 27.3% Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ALN 4
 DB 7 ALN 9

RESULT 15
 E58502
 44-2K bile stone protein - unidentified bacterium (fragment)
 C:Species: unidentified bacterium
 C>Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
 C:Accession: E58502
 R:Binette, C.P.; Binette, M.B.
 Submitted to the Protein Sequence Database, October 1997
 A:Description: The proteins of kidney and gallbladder stones.
 A:Reference number: A58501
 A:Accession: E58502
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <BIN>
 A:Experimental source: human bile with stones
 A:Note: a secondary sequence DVIQGVANS was also found

Query Match 27.3% Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ALN 5
 DB 4 ALN 6

RESULT 16
 A60336
 outer membrane protein ompA homolog - Actinobacillus actinomycetemcomitans (fragment)
 C:Species: Actinobacillus actinomycetemcomitans
 C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 18-Jun-1993
 C:Accession: A60336
 R:Wilson, M.E.; Infect. Immun., 59, 2505-2507, 1991
 A:Title: The heat-modifiable outer membrane protein of Actinobacillus actinomycetemcomitans
 A:Reference number: A60336; MUID:91257635; PMID:2050416
 A:Accession: A60336
 A:Molecule type: protein
 A:Residues: 1-13 <WIL>
 C:Superfamily: outer membrane protein A
 C:Keywords: membrane protein

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9
 DB 15 GAK 12

RESULT 17
 A60458
 protocatechuate 3,4-dioxygenase (EC 1.13.11.3) alpha chain - Moraxella sp. (strain N)
 A:Alternate names: protocatechuate oxygenase
 C:Species: Moraxella sp.
 C>Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 07-May-1999
 C:Accession: A60458
 R:Storjohanes, R.; Peimant, J.; Appl. Environ. Microbiol., 55, 140-147, 1989
 A:Title: Occurrence of two different forms of protocatechuate 3,4-dioxygenase in a
 A:Reference number: A60458; MUID:89245845; PMID:2541659
 A:Accession: A60458
 A:Molecule type: protein
 A:Residues: 1-13 <STE>
 A:Note: two forms P and G of the alpha subunit yielded identical amino terminal seq
 C:Keywords: iron; oxidoreductase

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKP 10
 DB 5 AKP 7

RESULT 18
 A39836
 aggrecan - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 24-Jun-1993
 C:Accession: A39836
 R:Sandy, J.D.; Neame, P.J.; Boynton, R.E.; Flannery, C.R.; J. Biol. Chem., 265, 8683-8685, 1991
 A:Title: Catabolism of aggrecan in cartilage explants. Identification of a major cleavage site
 A:Reference number: A39836; MUID:91224956; PMID:2026585
 A:Accession: A39836
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-13 <SAN>

Query Match 27.3% Score 3; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKP 10
 DB 5 AKP 7

A:Accession: PH0804

A:Molecule type: mRNA

A:Residues: 1-14 <CAS>

A:Cross-references: EMBL:X60913

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAL 4

DB 9 RAL 11

RESULT 25

C48401

ribosomal protein L1 - Thermus aquaticus (fragment)

C:Species: Thermus aquaticus

C>Date: 01-Dec-1993 #sequence_revision 18 Nov-1994 #text_change 18-Nov-1994

C:Accession: C48401

R:Garber, M.B.; Agalarov, S.C.; Eliseikina, I.A.; Fomenkova, N.P.; Nikonov, S.V.; Sedold

Biochimie 74, 327-336, 1992

A:Title: Ribosomal proteins from Thermus thermophilus for structural investigations.

A:Reference number: A48401; MUID:9234525; PMID:151986

A:Accession: C48401

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <GAR>

A:Note: sequence extracted from NCBI backbone (N5518:19994)

Query Match 27.3% Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RAL 4

DB 3 RAL 10

RESULT 26

PT0082

protein G460023 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse cell lines)

C>Date: 07-Feb-1996 #sequence_revision 14 Apr-1996 #text_change 06-Jun-1997

C:Accession: PT0082

R:Tsuigita, A.; Kamo, M.; Kawakami, M.; Otsu, Y.

submitted to JIBID, December 1995

A:Description: Two dimensional electrophoresis of plant proteins and standardization of

A:Reference number: PN0173

A:Accession: PT0082

A:Molecule type: protein

A:Residues: 1-15 <TSU>

A:Experimental source: leaf

Query Match 27.3% Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11

DB 4 KPK 6

RESULT 27

S41956

Ig mu chain V region (clone 17) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999

C:Accession: S41956

R:Waeber, S.D.; Williams, G.T.; Larsen, L.; Neutonen, M.S.; Kitamura, D.; Rajewsky, K.

Nucleic Acids Res. 22, 1389-1393, 1994

A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice

A:Reference number: S43956; MUID:94248036; PMID:8190629

A:Accession: S43956

A:Molecule type: DNA

A:Residues: 1-15 <WAG>

C:Keywords: immunoglobulin

Query Match 27.3% Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AKP 10

DB 3 AKP 5

RESULT 28

PH0136

T-cell receptor beta chain V-D-J region MS18 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-May-1997

C:Accession: PH0136

R:Martin, R.; Howell, M.D.; Jaraquemada, D.; Flierlage, M.; Richert, J.; Brostoff, S

J. Exp. Med. 173, 19-24, 1991

A:Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the c

A:Reference number: PH0135; MUID:91086843; PMID:1702137

A:Accession: PH0136

A:Molecule type: mRNA

A:Residues: 1-15 <MAR>

C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ALN 5

DB 10 ALN 12

RESULT 29

S03955

acidic fibroblast growth factor - dog (fragment)

N:Alternate names: alpha-endothelial cell growth factor

C:Species: Canis lupus familiaris (dog)

C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993

C:Accession: S03955

R:Quinkler, W.; Maasberg, M.; Bernotas-Danielowski, S.; Luethe, N.; Sharma, H.S.; S

Eur. J. Biochem. 181, 67-73, 1989

A:Title: Isolation of heparin-binding growth factors from bovine, porcine and canin

A:Reference number: S03953; MUID:89231704; PMID:2714282

A:Accession: S03955

A:Molecule type: protein

A:Residues: 1-15 <QUI>

C:Keywords: growth factor

Query Match 27.3% Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11

DB 4 KPK 6

RESULT 30

PH0779

T-cell receptor alpha chain (H83) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PH0779

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 137-1483, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex allelic exclusion and antigen-specific repertoire
 A:Reference number: PH0746; MUID:92078846; PMID:184416
 A:Accession: PH0779
 A:Molecule type: mRNA
 A:Residues: 1-15 <CAS>
 A:Cross references: EMBL:X60677
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 27.2% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ALN 5
 II
 II

DB 2 ALN 4

RESULT 31
 PH0031
 mixed lymphocyte reaction inhibitor - rat (Hagedoorn)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31 Dec-1990 #sequence_revision 31; Dec-1990 #text_change 24-Feb-1995
 C:Accession: PH0031
 R:Shizomiya, T.; Ohara, T.; Wada, N.; Ohnishi, A.; Kanada, N.
 J. Biochem. 127, 435-439, 1990
 A:Title: Rat liver arylase suppresses mixed lymphocyte reaction.
 A:Reference number: PH0031; MUID:90256726; PMID:2146356
 A:Accession: PH0031
 A:Molecule type: protein
 A:Residues: 1-15 <SR1>
 A:Experimental source: liver
 C:Keywords: lymphocyte

Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 KFK 11
 III

DB 10 KFK 12

RESULT 32
 A61348
 red pigment-concentrating hormone - northern shrew
 N:Alternate names: blanching hormone
 C:Species: Pandulus borealis (northern shrew)
 C:Date: 02-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
 C:Accession: A61348; S07139
 R:Perlund, P.; Josefsson, L.
 Science 177, 173-175, 1972
 A:Title: Crustacean color-change hormone: amino acid sequence and chemical synthesis.
 A:Reference number: A61348; MUID:7228758; PMID:564164
 A:Accession: A61348
 A:Molecule type: protein
 A:Residues: 1-8 <PER1>
 R:Perlund, P.
 Biochim. Biophys. Acta 371, 304-311, 1974

A:Title: Structure of the red-pigment concentrating hormone of the shrimp, *Pandalus borealis*
 A:Reference number: S07139; MUID:75054965; PMID:446643
 A:Accession: S07139
 A:Molecule type: protein
 A:Residues: 'E', 2-8 <PER2>

A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
 C:Comment: This neuropeptide, isolated from the eyestalks of the shrimp and active in pig-
 ment containing cells.
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; blocked amino end; hormone; neuropeptide; pyrrolidone
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental;
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental;

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
 II
 II

DB 2 LN 3

RESULT 33
 S08995
 hypertrehalosemic hormone I - oriental cockroach
 N:Alternate names: Pta-GAH I
 C:Species: Blatta orientalis (oriental cockroach)
 C:Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
 C:Accession: S08995
 R:Gaede, G.; Rinehart, K.L.
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
 A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the or-
 entalis and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bon
 A:Reference number: S08995; MUID:90253659; PMID:2340112
 A:Accession: S08995
 A:Molecule type: protein
 A:Residues: 1-8 <GAE>
 A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyrrolidone carboxylic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NW 5
 II
 II

DB 7 NW 8

RESULT 34
 S08996
 hypertrehalosemic hormone II - oriental cockroach
 N:Alternate names: Pta-GAH II
 C:Species: Blatta orientalis (oriental cockroach)
 C:Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
 C:Accession: S08996
 R:Gaede, G.; Rinehart, K.L.
 Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
 A:Title: Primary structures of hypertrehalosemic neuropeptides isolated from the or-
 entalis and of the stick insect *Extatosoma tiaratum* assigned by tandem fast atom bon
 A:Reference number: S08995; MUID:90253659; PMID:2340112
 A:Accession: S08996
 A:Molecule type: protein
 A:Residues: 1-8 <GAE>
 A:Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyrrolidone carboxylic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2% Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NW 6
 II
 II

DB 7 NW 8

RESULT 35
 A49823
 adipokinetic hormone I - American cockroach
 N:Alternate names: periplanetic CC-1

C:Species: *Pteroplaneta americana* (American cockroach)
 C:Date: 03-May-1994 #sequence_revision 03-May 1994 #text_change 07-May 1999
 C:Accession: A49623
 R:Scarthrough, R.M.; Jamieson, G.C.; Kallish, J.F.; Kramer, S.J.; McEntee, J.A.; Miller, C.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
 A:Title: Isolation and primary structure of two peptides with cardioacceleratory and hyp
 A:Reference number: A49823; MUID:84298179; PMID:6591205
 A:Accession: A49823
 A:Molecule type: protein
 A:Residues: 1-8 <SCA>
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglut
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2% Score 2: DB 2: Length 8;
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NW 6
 II
 DB 7 NW 8

RESULT 36
 B49823
 adipokinetic hormone II - American cockroach
 N:Alternate names: neuropeptide M-II; periplanetin IV 1
 C:Species: *Pteroplaneta americana* (American cockroach)
 C:Date: 03-May 1994 #sequence_revision 03-May 1994 #text_change 07-May 1999
 C:Accession: B49823; A05170
 R:Scarthrough, R.M.; Jamieson, G.C.; Kallish, J.F.; Kramer, S.J.; McEntee, J.A.; Miller, C.
 Proc. Natl. Acad. Sci. U.S.A. 81, 5575-5579, 1984
 A:Title: Isolation and primary structure of two peptides with cardioacceleratory and hyp
 A:Reference number: A49823; MUID:84298179; PMID:6591205
 A:Accession: B49823
 A:Molecule type: protein
 A:Residues: 1-8 <SCA>
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglut
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2% Score 2: DB 2: Length 8;
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NW 6
 II
 DB 7 NW 8

RESULT 37
 A44960
 neuropeptide Leu-QC-11 Colorado potato beetle
 C:Species: *Leptinotarsa decemlineata* (Colorado potato beetle)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep 1993 #text_change 07-May-1999
 C:Accession: A44960
 R:Gaede, G.; Kellner, R.
 Peptides 10, 1287-1289, 1989
 A:Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle
 A:Reference number: A44960; MUID:90160053; PMID:2576128
 A:Accession: A44960
 A:Molecule type: protein
 A:Residues: 1-8 <GAE>
 C:Superfamily: adipokinetic hormone
 C:Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglut
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimen

Query Match 18.2% Score 2: DB 2: Length 8;
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NW 6
 II
 DB 7 NW 8

RESULT 39
 S15422
 adipokinetic hormone - cockchafer
 C:Species: *Melolontha melolontha* (cockchafer)
 C:Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
 C:Accession: S15422
 R:Gaede, G.
 Biochem. J. 275, 671-677, 1991
 A:Title: A unique charged tyrosine containing member of the adipokinetic hormone/ r
 A:Reference number: S15422; MUID:91248100; PMID:2039445
 A:Accession: S15422
 A:Molecule type: protein
 A:Residues: 1-8 <HIO>
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2% Score 2: DB 2: Length 8;
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
 I
 DB 2 LN 3

RESULT 40
 A43976
 hypotrehalose hormone - yellow mealworm
 C:Species: *Tenebrio molitor* (yellow mealworm)
 C:Date: 03-Feb-1999 #sequence_revision 03-Feb 1999 #text_change 07-May 1999
 C:Accession: A43976
 A:Molecule type: protein
 A:Residues: 1-8 <GAE>
 C:Superfamily: adipokinetic hormone

C:Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglut
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimen

Query Match 18.2% Score 2: DB 2: Length 8;
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NW 6
 II
 DB 7 NW 8

RESULT 38
 B44960
 neuropeptide Leu-QC-11 Colorado potato beetle
 C:Species: *Leptinotarsa decemlineata* (Colorado potato beetle)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep 1993 #text_change 07-May-1999
 C:Accession: B44960
 R:Gaede, G.; Kellner, R.
 Peptides 10, 1287-1289, 1989
 A:Title: The metabolic neuropeptides of the corpus cardiacum from the potato beetle
 A:Reference number: A44960; MUID:90160053; PMID:2576128
 A:Accession: B44960
 A:Molecule type: protein
 A:Residues: 1-8 <GAE>
 C:Superfamily: adipokinetic hormone
 C:Keywords: blocked carboxyl end; corpora cardiaca; hormone; neuropeptide; pyroglut
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: blocked carboxyl end (Trp) (probably amidated) #status experimen

Query Match 18.2% Score 2: DB 2: Length 8;
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NW 6
 II
 DB 7 NW 8

RESULT 39
 S15422
 adipokinetic hormone - cockchafer
 C:Species: *Melolontha melolontha* (cockchafer)
 C:Date: 19-Mar-1997 #sequence_revision 31-Oct-1997 #text_change 31-Oct-1997
 C:Accession: S15422
 R:Gaede, G.
 Biochem. J. 275, 671-677, 1991
 A:Title: A unique charged tyrosine containing member of the adipokinetic hormone/ r
 A:Reference number: S15422; MUID:91248100; PMID:2039445
 A:Accession: S15422
 A:Molecule type: protein
 A:Residues: 1-8 <HIO>
 C:Superfamily: adipokinetic hormone
 C:Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
 F:8/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 18.2% Score 2: DB 2: Length 8;
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LN 5
 I
 DB 2 LN 3

RESULT 40
 A43976
 hypotrehalose hormone - yellow mealworm
 C:Species: *Tenebrio molitor* (yellow mealworm)
 C:Date: 03-Feb-1999 #sequence_revision 03-Feb 1999 #text_change 07-May 1999
 C:Accession: A43976
 A:Molecule type: protein
 A:Residues: 1-8 <GAE>
 C:Superfamily: adipokinetic hormone

[illegible]

Query Match:
Best local Similarity
0.000; P-adj. No. 2, Be-05;
P-28; Score 2; DB 2; Length 8;

Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
 QY 3 AL 4
 DB 3 AL 4

Query Match 18.2% Score 2: DB 2: Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

RESULT 46
 XGRUEU
 A:Title: sperm activating peptide c - sea urchin (Pseudotriton cristatus)
 A:Superfamily: speract homolog
 C:Species: pseudoboletia maculata
 C:Date: 17-Apr-1993 #sequence_revision 17 Apr-1993 #text_change 18 Aug-2000
 C:Accession: G60588
 R:Yoshino, K.; Kajiyama, H.; Nomura, K.; Takao, I.; Shigenishi, Y.; Kurita, M.; Yamaoka, Comp. Biochem. Physiol. B 94, 739-751, 1989
 A:Title: A halogenated amino acid-containing sperm activating peptide and its related peptides nodus, Echinometra mathaei and heterocentrotus mamillatus.
 A:Reference number: A60527
 A:Accession: G60588
 A:Molecule type: protein
 A:Residues: 1-8 <YOS>
 C:Superfamily: unassigned animal peptides

Query Match 18.2% Score 2: DB 2: Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 AL 4
 DB 3 AL 4

RESULT 47
 XGRUEU
 A:Title: urine glycopeptide - human
 C:Species: homo sapiens (man)
 C:Date: 29-Jun-2000 #sequence_revision 20 Jun-2000 #text_change 29-Jun-2000
 C:Accession: A01188
 R:Rote, C.J.; Weiss, J.B. Biochem. J. 123, 25P, 1971
 A:Title: Identification in urine of a low-molecular-weight polar glycopeptide containing
 A:Reference number: A01188; MUI:7206238; PMID:5126865
 A:Accession: A01188
 A:Molecule type: protein
 A:Residues: 1-8 <GEP>
 C:Comment: The identity of the glycopeptide in human urine as peptide is derived is unknown
 C:Superfamily: unassigned animal peptides
 C:Keywords: glycoprotein
 F1/Binding site: carbohydrate (Cys) (oxidized) oxidizes experimental

Query Match 18.2% Score 2: DB 2: Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 CA 8
 DB 7 CA 5

RESULT 48
 A11570
 A:Title: angiotensin-converting enzyme inhibitor yellowfin tuna
 C:Species: Thunnus albacares (yellowfin tuna)
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Aug-2000
 C:Accession: A11570
 R:Kohama, Y.; Matsumoto, S.; Oka, H.; Teramachi, T.; Okabe, M.; Mitsuura, T. Biochem. Biophys. Res. Commun. 155, 342-347, 1988
 A:Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.
 A:Reference number: A11570; MUI:88426322; PMID:3415638
 A:Accession: A11570
 A:Molecule type: protein

A:Residues: 1-8 <KCH>
 A:Note: the source is designated as Neothunnus macropterus
 C:Superfamily: unassigned animal peptides
 C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 18.2% Score 2: DB 2: Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 6 WG 7
 DB 6 WG 7

RESULT 49
 S37141
 A:Title: rpsA protein - Erwinia chrysanthemi
 C:Species: Erwinia chrysanthemi
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1999
 C:Accession: S37141
 R:Douillie, A.; Toussaint, A.; Paelen, M. submitted to the EMBL Data Library, August 1993
 A:Description: Identification of the integration host factor genes of E. chrysanthemi
 A:Reference number: S37139
 A:Accession: S37141
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-8 <CGG>
 A:Cross-references: EMBL:X74750; NID:q399669; PID:CAA52769.1; PID:q581108

Query Match 18.2% Score 2: DB 2: Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 8 AK 9
 DB 5 AK 6

RESULT 50
 A39308
 A:Title: glycine reductase (EC 1.4.99.-) sulphydryl protein C, alpha chain - Clostridium sticklandii
 C:Species: Clostridium sticklandii
 C:Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 15-Aug-1997
 C:Accession: A39308
 R:Stadman, T.C.; Davis, J.N. J. Biol. Chem. 266, 22147-22153, 1991
 A:Title: Glycine reductase protein C. Properties and characterization of its role in
 A:Reference number: A39308; MUI:92042141; PMID:1919235
 A:Accession: A39308
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <STA>
 C:Function:
 A:Description: glycine reductase complex catalyzes the reductive deamination of glycine
 C:Keywords: ATP; oxidoreductase

Query Match 18.2% Score 2: DB 2: Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 9 KP 10
 DB 2 KP 3

Search completed: September 30, 2003, 10:09:43
 Job time : 13.4167 secs

101	3	27.3	8	2	US-08-687-219B-16	Sequence 15, Appl	174	3	27.3	9	1	US-08-468-543-5	Sequence 5, Appl1
102	3	27.3	8	2	US-08-687-219B-17	Sequence 17, Appl	175	3	27.3	9	1	US-08-156-552A-14	Sequence 14, Appl
103	3	27.3	8	2	US-08-687-219B-18	Sequence 18, Appl	176	3	27.3	9	1	US-08-445-042-11	Sequence 11, Appl
104	3	27.3	8	2	US-08-687-219B-19	Sequence 19, Appl	177	3	27.3	9	1	US-08-633-772-16	Sequence 16, Appl
105	3	27.3	8	3	US-08-350-215-19	Sequence 39, Appl	178	3	27.3	9	1	US-08-464-318-5	Sequence 5, Appl1
106	3	27.3	8	3	US-08-350-215-19	Sequence 40, Appl	179	3	27.3	9	1	US-08-146-145-1	Sequence 1, Appl1
107	3	27.3	8	3	US-08-871-455A-260	Sequence 260, App	180	3	27.3	9	1	US-08-465-167A-5	Sequence 5, Appl1
108	3	27.3	8	3	US-08-945-002-43	Sequence 43, Appl	181	3	27.3	9	1	US-08-465-167A-25	Sequence 25, Appl
109	3	27.3	8	3	US-09-011-1-1	Sequence 3, Appl1	182	3	27.3	9	1	US-08-465-167A-28	Sequence 28, Appl
110	3	27.3	8	3	US-08-862-865-24	Sequence 24, Appl	183	3	27.3	9	1	US-08-465-167A-38	Sequence 38, Appl
111	3	27.3	8	3	US-09-287-145A-19	Sequence 19, Appl	184	3	27.3	9	1	US-08-615-181-42	Sequence 42, Appl
112	3	27.3	8	3	US-09-287-145A-48	Sequence 48, Appl	185	3	27.3	9	1	US-08-615-181-78	Sequence 78, Appl
113	3	27.3	8	3	US-09-092-636-11	Sequence 11, Appl	186	3	27.3	9	1	US-08-615-181-102	Sequence 102, App
114	3	27.3	8	3	US-09-296-284-14	Sequence 14, Appl	187	3	27.3	9	1	US-08-428-733A-14	Sequence 14, Appl
115	3	27.3	8	3	US-09-053-604-43	Sequence 43, Appl	188	3	27.3	9	1	US-08-642-255-106	Sequence 106, App
116	3	27.3	8	3	US-08-160-604-11	Sequence 31, Appl	189	3	27.3	9	1	US-08-808-641-12	Sequence 12, Appl
117	3	27.3	8	3	US-08-160-604-12	Sequence 32, Appl	190	3	27.3	9	1	US-08-397-633A-6	Sequence 6, Appl1
118	3	27.3	8	3	US-08-160-604-33	Sequence 33, Appl	191	3	27.3	9	1	US-08-397-633A-13	Sequence 13, Appl
119	3	27.3	8	3	US-08-160-604-34	Sequence 34, Appl	192	3	27.3	9	1	US-08-468-975-5	Sequence 5, Appl1
120	3	27.3	8	3	US-09-226-985-24	Sequence 24, Appl	193	3	27.3	9	1	US-08-703-988A-2	Sequence 2, Appl1
121	3	27.3	8	4	US-09-227-906-24	Sequence 24, Appl	194	3	27.3	9	1	US-08-470-152-8	Sequence 8, Appl1
122	3	27.3	8	4	US-09-014-598-44	Sequence 44, Appl	195	3	27.3	9	1	US-08-191-866D-43	Sequence 43, Appl
123	3	27.3	8	4	US-09-556-111-39	Sequence 39, Appl	196	3	27.3	9	1	US-08-191-866D-51	Sequence 51, Appl
124	3	27.3	8	4	US-09-556-111-48	Sequence 48, Appl	197	3	27.3	9	1	US-08-191-866D-56	Sequence 56, Appl
125	3	27.3	8	4	US-09-573-497-3	Sequence 3, Appl1	198	3	27.3	9	1	US-08-787-547-47	Sequence 47, Appl
126	3	27.3	8	4	US-09-241-945-260	Sequence 260, App	199	3	27.3	9	1	US-08-787-547-52	Sequence 52, Appl
127	3	27.3	8	4	US-09-415-643-4	Sequence 4, Appl1	200	3	27.3	9	1	US-08-463-052-1	Sequence 1, Appl1
128	3	27.3	8	4	US-09-510-422A-6	Sequence 6, Appl1	201	3	27.3	9	1	US-08-414-417B-17	Sequence 17, Appl
129	3	27.3	8	4	US-08-437-673-2	Sequence 2, Appl1	202	3	27.3	9	2	US-08-480-551-1	Sequence 1, Appl1
130	3	27.3	8	4	US-08-187-447-17	Sequence 17, Appl	203	3	27.3	9	2	US-08-472-659-5	Sequence 5, Appl1
131	3	27.3	8	4	US-09-588-414-7	Sequence 7, Appl1	204	3	27.3	9	2	US-08-700-035A-13	Sequence 13, Appl
132	3	27.3	8	4	US-09-670-076A-1	Sequence 1, Appl1	205	3	27.3	9	2	US-08-486-348A-17	Sequence 17, Appl
133	3	27.3	8	4	US-09-104-437A-453	Sequence 453, App	206	3	27.3	9	2	US-08-471-341-5	Sequence 5, Appl1
134	3	27.3	8	4	US-09-104-437A-453	Sequence 460, App	207	3	27.3	9	2	US-08-290-381A-6	Sequence 6, Appl1
135	3	27.3	8	4	US-09-104-437A-515	Sequence 515, App	208	3	27.3	9	2	US-08-461-566-5	Sequence 5, Appl1
136	3	27.3	8	4	US-09-104-437A-525	Sequence 520, App	209	3	27.3	9	2	US-08-751-965-10	Sequence 10, Appl
137	3	27.3	8	4	US-09-129-192-41	Sequence 41, Appl	210	3	27.3	9	2	US-08-474-661-5	Sequence 5, Appl1
138	3	27.3	8	4	US-09-569-834-12	Sequence 12, Appl	211	3	27.3	9	2	US-08-185-949B-43	Sequence 43, Appl
139	3	27.3	8	5	PGT-0593-1269-25	Sequence 25, Appl	212	3	27.3	9	2	US-08-185-949B-51	Sequence 51, Appl
140	3	27.3	8	5	PGT-0594-01319-43	Sequence 42, Appl	213	3	27.3	9	2	US-08-185-949B-56	Sequence 56, Appl
141	3	27.3	8	5	PGT-0595-04121-17	Sequence 17, Appl	214	3	27.3	9	2	US-08-468-545B-17	Sequence 17, Appl
142	3	27.3	8	6	5436138-8	Patent No. 5436138	215	3	27.3	9	2	US-08-389-360-3	Sequence 3, Appl1
143	3	27.3	8	6	5436138-9	Patent No. 5436138	216	3	27.3	9	2	US-08-389-360-4	Sequence 4, Appl1
144	3	27.3	9	1	US-08-127-211-42	Sequence 42, Appl	217	3	27.3	9	2	US-08-389-360-5	Sequence 5, Appl1
145	3	27.3	9	1	US-08-036-131-2	Sequence 6, Appl	218	3	27.3	9	2	US-08-738-975-10	Sequence 10, Appl
146	3	27.3	9	1	US-08-036-131-2	Sequence 7, Appl	219	3	27.3	9	2	US-08-902-516-24	Sequence 24, Appl
147	3	27.3	9	1	US-08-036-131-2	Sequence 8, Appl	220	3	27.3	9	2	US-08-902-516-25	Sequence 25, Appl
148	3	27.3	9	1	US-08-212-160A-1	Sequence 2, Appl1	221	3	27.3	9	2	US-08-728-626-10	Sequence 10, Appl
149	3	27.3	9	1	US-08-096-641-1	Sequence 1, Appl1	222	3	27.3	9	2	US-08-625-695A-6	Sequence 6, Appl1
150	3	27.3	9	1	US-08-217-189A-17	Sequence 17, Appl	223	3	27.3	9	2	US-08-968-676-13	Sequence 13, Appl
151	3	27.3	9	1	US-08-427-227A-22	Sequence 22, Appl	224	3	27.3	9	2	US-08-468-964B-6	Sequence 6, Appl1
152	3	27.3	9	1	US-08-215-456A-10	Sequence 56, Appl	225	3	27.3	9	2	US-08-993-738A-1	Sequence 1, Appl1
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155	3	27.3	9	1	US-08-407-446-14	Sequence 6, Appl	228	3	27.3	9	2	US-08-747-137-98	Sequence 98, Appl
156	3	27.3	9	1	US-08-217-189A-1	Sequence 6, Appl1	229	3	27.3	9	2	US-08-747-137-132	Sequence 132, App
157	3	27.3	9	1	US-08-241-160A-2	Sequence 2, Appl1	230	3	27.3	9	2	US-08-469-692-5	Sequence 5, Appl1
158	3	27.3	9	1	US-08-427-227A-22	Sequence 22, Appl	231	3	27.3	9	2	US-08-433-133-54	Sequence 54, Appl
159	3	27.3	9	1	US-08-517-522A-10	Sequence 23, Appl	232	3	27.3	9	2	US-08-433-133-102	Sequence 102, App
160	3	27.3	9	1	US-08-460-470-42	Sequence 20, Appl	233	3	27.3	9	2	US-07-871-282A-6	Sequence 6, Appl1
161	3	27.3	9	1	US-08-449-818A-10	Sequence 10, Appl	234	3	27.3	9	2	US-09-036-582-4	Sequence 4, Appl1
162	3	27.3	9	1	US-08-217-189A-1	Sequence 1, Appl1	235	3	27.3	9	2	US-09-036-582-6	Sequence 6, Appl1
163	3	27.3	9	1	US-08-217-189A-1	Sequence 2, Appl1	236	3	27.3	9	2	US-09-064-839-12	Sequence 12, Appl
164	3	27.3	9	1	US-08-446-446-17	Sequence 37, Appl	237	3	27.3	9	2	US-09-064-839-12	Sequence 14, Appl
165	3	27.3	9	1	US-08-446-446-17	Sequence 10, Appl	238	3	27.3	9	2	US-08-318-856A-19	Sequence 19, Appl
166	3	27.3	9	1	US-08-438-634-26	Sequence 26, Appl	239	3	27.3	9	2	US-08-318-856A-20	Sequence 20, Appl
167	3	27.3	9	1	US-08-464-456-1	Sequence 1, Appl1	240	3	27.3	9	2	US-08-318-856A-25	Sequence 25, Appl
168	3	27.3	9	1	US-08-196-60A-10	Sequence 10, Appl	241	3	27.3	9	2	US-08-318-856A-26	Sequence 26, Appl
169	3	27.3	9	1	US-08-687-226-47	Sequence 47, Appl	242	3	27.3	9	2	US-08-318-856A-27	Sequence 27, Appl
170	3	27.3	9	1	US-08-454-207A-35	Sequence 55, Appl	243	3	27.3	9	2	US-08-318-856A-28	Sequence 28, Appl
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173	3	27.3	9	1	US-08-487-083-17	Sequence 17, Appl	246	3	27.3	9	2	US-08-612-842-2	Sequence 2, Appl1

247	3	27.3	9	2	US-08-251-678A-6	Sequence 6, Appl	320	3	27.3	4	US-09-705-160-35	Sequence 35, Appl
248	3	27.3	9	3	US-07-792-600-43	Sequence 34, Appl	321	3	27.3	4	US-09-705-160-38	Sequence 38, Appl
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253	3	27.3	9	3	US-08-159-349A-131	Sequence 191, App	326	3	27.3	4	US-08-197-484-88	Sequence 88, Appl
254	3	27.3	9	3	US-08-159-349A-638	Sequence 608, App	327	3	27.3	4	US-08-197-484-94	Sequence 94, Appl
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258	3	27.3	9	3	US-08-159-349A-822	Sequence 822, App	331	3	27.3	4	US-09-697-884-48	Sequence 48, Appl
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262	3	27.3	9	3	US-08-426-680B-17	Sequence 17, Appl	335	3	27.3	4	US-08-469-260A-184	Sequence 184, App
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264	3	27.3	9	3	US-09-064-904-9	Sequence 9, Appl	337	3	27.3	4	US-08-627-820-5	Sequence 5, Appl
265	3	27.3	9	3	US-08-170-299-5	Sequence 6, Appl	338	3	27.3	4	US-09-435-524-3	Sequence 3, Appl
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267	3	27.3	9	3	US-09-152-021-34	Sequence 34, Appl	340	3	27.3	4	US-09-259-478A-5	Sequence 5, Appl
268	3	27.3	9	3	US-09-156-842-14	Sequence 14, App	341	3	27.3	4	US-09-023-905A-19	Sequence 19, Appl
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273	3	27.3	9	3	US-09-035-276-15	Sequence 15, Appl	346	3	27.3	4	US-09-861-966-134	Sequence 134, App
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276	3	27.3	9	3	US-09-139-804-182	Sequence 182, App	349	3	27.3	4	US-09-561-499-17	Sequence 17, Appl
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279	3	27.3	9	3	US-09-183-941-28	Sequence 28, Appl	352	3	27.3	4	US-09-311-784A-326	Sequence 326, App
280	3	27.3	9	3	US-09-183-941-35	Sequence 35, Appl	353	3	27.3	4	US-09-311-784A-463	Sequence 463, App
281	3	27.3	9	3	US-09-183-941-38	Sequence 38, Appl	354	3	27.3	4	US-09-574-749B-4	Sequence 4, Appl
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284	3	27.3	9	3	US-09-551-511-4	Sequence 4, Appl	357	3	27.3	4	US-09-341-982-92	Sequence 92, Appl
285	3	27.3	9	3	US-09-177-241-26-1	Sequence 260, App	358	3	27.3	4	US-08-446-184	Sequence 184, App
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288	3	27.3	9	3	US-08-960-944A-25	Sequence 26, Appl	361	3	27.3	4	US-09-534-943-1	Sequence 1, Appl
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290	3	27.3	9	3	US-08-713-454-1	Sequence 1, Appl	363	3	27.3	4	PCT-US91-07506-37	Sequence 37, Appl
291	3	27.3	9	3	US-08-657-496A-1	Sequence 184, App	364	3	27.3	4	PCT-US94-14920-5	Sequence 5, Appl
292	3	27.3	9	3	US-09-120-388A-14	Sequence 153, App	365	3	27.3	4	PCT-US95-02121-88	Sequence 88, Appl
293	3	27.3	9	3	US-09-510-388A-15	Sequence 169, App	366	3	27.3	4	PCT-US95-02121-94	Sequence 94, Appl
294	3	27.3	9	3	US-09-510-388A-16	Sequence 19, App	367	3	27.3	4	PCT-US95-02121-116	Sequence 116, App
295	3	27.3	9	3	US-09-061-554-3	Sequence 48, Appl	368	3	27.3	4	PCT-US95-02121-147	Sequence 147, App
296	3	27.3	9	3	US-09-100-428-48	Sequence 50, Appl	369	3	27.3	4	PCT-US95-02121-153	Sequence 153, App
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309	3	27.3	9	4	US-09-241-268-1	Sequence 1, Appl	382	3	27.3	10	US-07-890-422B-18	Sequence 18, App
310	3	27.3	9	4	US-08-457-648A-1	Sequence 10, Appl	383	3	27.3	10	US-08-453-924-16	Sequence 16, Appl
311	3	27.3	9	4	US-09-099-543B-14	Sequence 29, Appl	384	3	27.3	10	US-08-264-759-1	Sequence 1, Appl
312	3	27.3	9	4	US-08-292-492B-1	Sequence 5, Appl	385	3	27.3	10	US-08-300-386A-60	Sequence 60, Appl
313	3	27.3	9	4	US-08-959-496A-22	Sequence 22, Appl	386	3	27.3	10	US-08-338-634-11	Sequence 11, Appl
314	3	27.3	9	4	US-09-057-052-8	Sequence 9, Appl	387	3	27.3	10	US-08-338-634-27	Sequence 27, Appl
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317	3	27.3	9	4	US-09-412-928-19	Sequence 19, Appl	390	3	27.3	10	US-08-465-167A-47	Sequence 47, Appl
318	3	27.3	9	4	US-09-411-081-19	Sequence 19, Appl	391	3	27.3	10		
319	3	27.3	9	4	US-09-705-160-43	Sequence 26, Appl	392	3	27.3	10		

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-720-3500
 TELEFAX: 617-720-2441
 TEFLEX:
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-016-366A-44

Query Match 36.4%: Score 4; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
 Db 4 ARAL 7

RESULT 2
 US-09-256-194-13
 Sequence 13, Application US/09256194
 Patent No. 6395714
 GENERAL INFORMATION:
 APPLICANT: Sia, Charles D.Y.
 APPLICANT: Gao, Shi Xian
 APPLICANT: Persson, Roy
 APPLICANT: Kovinski, Benjamin
 TITLE OF INVENTION: EXPRESSING GP140 FRAGMENT OF PRIMARY HIV : ISOLATE
 FILE REFERENCE: 1038-920
 CURRENT APPLICATION NUMBER: US/09/256-194
 CURRENT FILING DATE: 1999-02-24
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 13
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Human immunodeficiency virus type 1
 US-09-256-194-13

Query Match 36.4%: Score 4; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
 Db 6 ARAL 9

RESULT 3
 US-09-387-715-10
 Sequence 10, Application US/09387715
 Patent No. 6551574
 GENERAL INFORMATION:
 APPLICANT: Sharma, Shubh
 TITLE OF INVENTION: Tuftsin Metallopeptides Analogs and Uses Thereof
 FILE REFERENCE: 1173/1D794US1
 CURRENT APPLICATION NUMBER: US/09/387-715
 CURRENT FILING DATE: 1999-08-30
 PRIOR APPLICATION NUMBER: PCT/US99/05654
 PRIOR FILING DATE: 1999-03-18
 NUMBER OF SEQ ID NOS: 55
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 10
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial: Sequence: Synthetic
 OTHER INFORMATION: peptide

NAME/KEY: modified residue
 LOCATION: 3,6,8
 OTHER INFORMATION: D-amino acid
 US-09-387-715-10

Query Match 36.4%: Score 4; DB 4; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
 Db 3 AKPK 6

RESULT 4
 US-08-166-195A-21
 Sequence 21, Application US/08166195A
 Patent No. 5480799
 GENERAL INFORMATION:
 APPLICANT: O'Rand, Michael G.
 APPLICANT: Widgren, Esther E.
 APPLICANT: Richardson, Richard T.
 APPLICANT: Lea, Isabel
 TITLE OF INVENTION: Sperm Antigen Corresponding to a
 TITLE OF INVENTION: Sperm Zona Binding Protein Autoantigenic Epitope
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kenneth D. Sibley
 STREET: P.O. Box 34009
 CITY: Charlotte
 STATE: No. 5480799th Carolina
 COUNTRY: USA
 ZIP: 28234
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/166,195A
 FILING DATE: 10 DEC 1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Sibley, Kenneth D.
 REGISTRATION NUMBER: 31,665
 REFERENCE/DOCKET NUMBER: 5470/73
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-881-3140
 TELEFAX: 919-881-3175
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-166-195A-21

Query Match 36.4%: Score 4; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WGAK 4
 Db 6 WGAK 9

RESULT 5
 US-08-166-195A-22
 Sequence 22, Application US/08166195A
 Patent No. 5480799
 GENERAL INFORMATION:
 APPLICANT: O'Rand, Michael G.


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1  APPLICANT:  Widdgren, Esther E.
2  APPLICANT:  Richardson, Richard E.
3  APPLICANT:  Lea, Isabel
4  TITLE OF INVENTION:  Sperm Antigen Corresponding To A
5  NUMBER OF SEQUENCES:  51
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE:  Kenneth D. Sibey
8  STREET:  P.O. Box 34009
9  CITY:  Charlotte
10 STATE:  No. 5480799th Carolina
11 COUNTRY:  USA
12 ZIP:  28234
13 COMPUTER READABLE FORM:
14 MEDIUM TYPE:  Floppy disk
15 OPERATING SYSTEM:  PC-DOS/MS DOS
16 SOFTWARE:  Patent In Release #1.0, Version #1.25
17 CURRENT APPLICATION DATA:
18 FILING DATE:  10 DEC 1994
19 CLASSIFICATION:  435
20 ATTORNEY/AGENT INFORMATION:
21 NAME:  Sibey, Kenneth E.
22 REGISTRATION NUMBER:  31,665
23 REFERENCE/DOCKET NUMBER:  547677
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE:  919-881-3140
26 TELEFAX:  919-881-3175
27 INFORMATION FOR SEQ ID NO:  22:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH:  10 amino acids
30 TYPE:  amino acid
31 STRANDEDNESS:  single
32 TOPOLOGY:  linear
33 MOLECULE TYPE:  peptide
34 US 08-166-195A-22
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37 Best Local Similarity 100.0%  Pred. No. 1.7e+02:
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41         1 1 1
42         1 WCAK 6

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1  RESULT 6
2  US-08-478-761A-52
3  Sequence 52, Application US/08478761A
4  Patent No. 5645384
5  GENERAL INFORMATION:
6  APPLICANT:  WALSH, TERENCE A
7  APPLICANT:  HEY, TIMOTHY D
8  APPLICANT:  MORGAN, ALICE ER
9  TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
10 TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
11 TITLE OF INVENTION:  USING
12 NUMBER OF SEQUENCES:  81
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE:  ANDREA T. BORUCKI
15 STREET:  9330 ZIONSVILLE ROAD
16 CITY:  INDIANAPOLIS
17 STATE:  IN
18 COUNTRY:  US
19 ZIP:  46268
20 COMPUTER READABLE FORM:
21 MEDIUM TYPE:  Floppy disk
22 OPERATING SYSTEM:  IBM PC compatible
23 SOFTWARE:  Patent In Release #1.0, Version #1.25
24 CURRENT APPLICATION DATA:
25 APPLICATION NUMBER:  US/08/378,761A

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1  FILING DATE:  26-JAN-1995
2  CLASSIFICATION:  435
3  ATTORNEY/AGENT INFORMATION:
4  NAME:  BORUCKI, ANDREA T
5  REGISTRATION NUMBER:  33651
6  REFERENCE/DOCKET NUMBER:  38272B
7  TELECOMMUNICATION INFORMATION:
8  TELEPHONE:  (317) 337-4846
9  INFORMATION FOR SEQ ID NO:  52:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH:  10 amino acids
12 TYPE:  amino acid
13 STRANDEDNESS:  single
14 TOPOLOGY:  linear
15 MOLECULE TYPE:  protein
16 US-08-378-761A-52
17
18 Query Match          36.4%  Score 4:  DB 1:  Length 10:
19 Best Local Similarity 100.0%  Pred. No. 1.7e+02:
20 Matches      4:  Conservative  0:  Mismatches  0:  Indels  0:  Gaps  0:
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22 QY      4 LNWG 7
23         1 1 1 1
24         2 LNWG 5
25
26 RESULT 7
27 US-08-485-286-52
28 Sequence 52, Application US/08485286
29 Patent No. 5646026
30 Patent No. 5646026 5646119
31 GENERAL INFORMATION:
32 APPLICANT:  WALSH, TERENCE A
33 APPLICANT:  HEY, TIMOTHY D
34 APPLICANT:  MORGAN, ALICE ER
35 TITLE OF INVENTION:  RIBOSOME-INACTIVATING PROTEINS, INACTIVE
36 TITLE OF INVENTION:  PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
37 TITLE OF INVENTION:  USING
38 NUMBER OF SEQUENCES:  81
39 CORRESPONDENCE ADDRESS:
40 ADDRESSEE:  ANDREA T. BORUCKI
41 STREET:  9330 ZIONSVILLE ROAD
42 CITY:  INDIANAPOLIS
43 STATE:  IN
44 COUNTRY:  US
45 ZIP:  46268
46 COMPUTER READABLE FORM:
47 MEDIUM TYPE:  Floppy disk
48 OPERATING SYSTEM:  IBM PC compatible
49 SOFTWARE:  Patent In Release #1.0, Version #1.25
50 CURRENT APPLICATION DATA:
51 APPLICATION NUMBER:  US/08/485,286
52 FILING DATE:
53 CLASSIFICATION:  435
54 PRIOR APPLICATION DATA:
55 APPLICATION NUMBER:  US 08/378761
56 FILING DATE:  26-JAN-1995
57 ATTORNEY/AGENT INFORMATION:
58 NAME:  BORUCKI, ANDREA T
59 REGISTRATION NUMBER:  33651
60 REFERENCE/DOCKET NUMBER:  38272B
61 TELECOMMUNICATION INFORMATION:
62 TELEPHONE:  (317) 337-4846
63 INFORMATION FOR SEQ ID NO:  52:
64 SEQUENCE CHARACTERISTICS:
65 LENGTH:  10 amino acids
66 TYPE:  amino acid
67 STRANDEDNESS:  single
68 TOPOLOGY:  linear
69 MOLECULE TYPE:  protein
70 US-08-485-286-52

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Query Match          36.4%, Score 4, DB 2, Length 10;
Best Local Similarity 100.0%, Pred. No. 1.7e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LNWG 7
Db 2 LNWG 5

RESULT 8
US-08-436-772-21
: Sequence 21, Application US/08436772
: Patent No. 5814456
: GENERAL INFORMATION:
: APPLICANT: O'Rand, Michael G.
: APPLICANT: Widgren, Esther E.
: APPLICANT: Richardson, Richard T.
: APPLICANT: Lea, Isabel
: TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
: TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
: NUMBER OF SEQUENCES: 60
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kenneth D. Sibley
: STREET: P.O. Box 34009
: CITY: Charlotte
: STATE: No. 5814456th Carolina
: COUNTRY: USA
: ZIP: 28234
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/436,772
: FILING DATE: 08-MAY-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Sibley, Kenneth D.
: REGISTRATION NUMBER: 31,665
: REFERENCE/DOCKET NUMBER: 5470-73B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-881-3140
: TELEFAX: 919-881-3175
: INFORMATION FOR SEQ ID NO: 21:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-436-772-21

Query Match          36.4%, Score 4, DB 2, Length 10;
Best Local Similarity 100.0%, Pred. No. 1.7e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WGAK 9
Db 6 WGAK 9

RESULT 9
US-08-436-772-22
: Sequence 22, Application US/08436772
: Patent No. 5814456
: GENERAL INFORMATION:
: APPLICANT: O'Rand, Michael G.
: APPLICANT: Widgren, Esther E.
: APPLICANT: Richardson, Richard T.
: APPLICANT: Lea, Isabel
: TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
: TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope

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: NUMBER OF SEQUENCES: 60
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kenneth D. Sibley
: STREET: P.O. Box 34009
: CITY: Charlotte
: STATE: No. 5814456th Carolina
: COUNTRY: USA
: ZIP: 28234
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/436,772
: FILING DATE: 08-MAY-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Sibley, Kenneth D.
: REGISTRATION NUMBER: 31,665
: REFERENCE/DOCKET NUMBER: 5470-73B
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 919-881-3140
: TELEFAX: 919-881-3175
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-436-772-22

Query Match          36.4%, Score 4, DB 2, Length 10;
Best Local Similarity 100.0%, Pred. No. 1.7e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WGAK 9
Db 3 WGAK 6

RESULT 10
US-08-436-883B-21
: Sequence 21, Application US/084368484
: Patent No. 5823861
: GENERAL INFORMATION:
: APPLICANT: O'Rand, Michael G.
: APPLICANT: Widgren, Esther E.
: APPLICANT: Richardson, Richard T.
: APPLICANT: Lea, Isabel
: TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
: TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
: NUMBER OF SEQUENCES: 60
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Kenneth D. Sibley
: STREET: P.O. Box 34009
: CITY: Charlotte
: STATE: No. 5820861th Carolina
: COUNTRY: USA
: ZIP: 28234
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/436,883B
: FILING DATE: 08-MAY-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Sibley, Kenneth D.
: REGISTRATION NUMBER: 31,665

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1 REFERENCE/LOCKET NUMBER: 5470-730
 2 TELECOMMUNICATION INFORMATION:
 3 TELEPHONE: 919-420-2200
 4 TELEFAX: 919-881-3175
 5 INFORMATION FOR SEQ ID NO: 2:
 6 SEQUENCE CHARACTERISTICS:
 7 LENGTH: 10 amino acids
 8 TYPE: amino acid
 9 STRANDEDNESS: single
 10 TOPOLOGY: linear
 11 MOLECULE TYPE: peptide
 12 US-08-436-883B-22

Query Match 36.4% Score 4 DB 2 Length 10
 Best Local Similarity 100.0% Pident No. 1.7e+02
 Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 6 WGAK 9
 DB 6 WGAK 9

1 RESULT 11
 2 US-08-436-883B-22
 3 Sequence 22, Application US/084068436
 4 Patent No. 5820861
 5 GENERAL INFORMATION:
 6 APPLICANT: O'Rand, Michael G.
 7 APPLICANT: Widgren, Esther E.
 8 APPLICANT: Richardson, Richard L.
 9 APPLICANT: Lea, Isabel
 10 TITLE OF INVENTION: Serum Antigen Corresponding to a Serum
 11 NUMBER OF SEQUENCES: 60
 12 CORRESPONDENCE ADDRESS:
 13 ADDRESSEE: Kenneth G. Sibbey
 14 STREET: P.O. Box 34009
 15 CITY: Charlotte
 16 STATE: NC 28208
 17 COUNTRY: USA
 18 ZIP: 28284

19 COMPUTER READABLE FORM:
 20 MEDIUM TYPE: Floppy disk
 21 COMPUTER: IBM PC Compatible
 22 OPERATING SYSTEM: PC-DOS/MS-DOS
 23 SOFTWARE: Patent In Release #1.0, Version #1.0
 24 CURRENT APPLICATION DATA:
 25 APPLICATION NUMBER: US/08/436-883B
 26 FILING DATE: 08-MAY-1995
 27 CLASSIFICATION: 435
 28 ATTORNEY/AGENT INFORMATION:
 29 NAME: Sibbey, Kenneth G.
 30 REGISTRATION NUMBER: 31,640
 31 REFERENCE/LOCKET NUMBER: 5470-730
 32 TELECOMMUNICATION INFORMATION:
 33 TELEPHONE: 919-420-2200
 34 TELEFAX: 919-881-3175
 35 INFORMATION FOR SEQ ID NO: 22:
 36 SEQUENCE CHARACTERISTICS:
 37 LENGTH: 10 amino acids
 38 TYPE: amino acid
 39 STRANDEDNESS: single
 40 TOPOLOGY: linear
 41 MOLECULE TYPE: peptide
 42 US-08-436-883B-22

Query Match 36.4% Score 4 DB 2 Length 10
 Best Local Similarity 100.0% Pident No. 1.7e+02
 Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 6 WGAK 9
 DB 6 WGAK 9

1 RESULT 12
 2 US-08-556-597-129
 3 Sequence 129, Application US/08556597
 4 Patent No. 5877155
 5 GENERAL INFORMATION:
 6 APPLICANT: Miller, Jonathan L.
 7 APPLICANT: Lytle, Vicki A.
 8 TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
 9 TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
 10 NUMBER OF SEQUENCES: 173
 11 CORRESPONDENCE ADDRESS:
 12 ADDRESSEE: Nixon, Hartlage, Levens & Doyle LLP
 13 STREET: Clinton Square, P.O. Box 1051
 14 CITY: Rochester
 15 STATE: New York
 16 COUNTRY: USA
 17 ZIP: 14604
 18 COMPUTER READABLE FORM:
 19 MEDIUM TYPE: Floppy disk
 20 COMPUTER: IBM PC Compatible
 21 OPERATING SYSTEM: PC-DOS/MS-DOS
 22 SOFTWARE: Patent In Release #1.0, Version #1.30
 23 CURRENT APPLICATION DATA:
 24 APPLICATION NUMBER: US/08/556,597
 25 FILING DATE:
 26 CLASSIFICATION: 530
 27 PRIOR APPLICATION DATA:
 28 APPLICATION NUMBER: US 08/406,430
 29 FILING DATE: 17-MAR-1995
 30 ATTORNEY/AGENT INFORMATION:
 31 NAME: Timlin, Susan J.
 32 REGISTRATION NUMBER: 34,193
 33 REFERENCE/LOCKET NUMBER: 20884/101
 34 TELECOMMUNICATION INFORMATION:
 35 TELEPHONE: (716) 263 1636
 36 TELEFAX: (716) 263 1600
 37 INFORMATION FOR SEQ ID NO: 129:
 38 SEQUENCE CHARACTERISTICS:
 39 LENGTH: 10 amino acids
 40 TYPE: amino acid
 41 STRANDEDNESS:
 42 TOPOLOGY: linear
 43 MOLECULE TYPE: peptide
 44 US-08-556-597-129

Query Match 36.4% Score 4 DB 2 Length 10
 Best Local Similarity 100.0% Pident No. 1.7e+02
 Matches 4 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 6 WGAK 9
 DB 2 WGAK 5

1 RESULT 13
 2 US-08-556-597-140
 3 Sequence 140, Application US/08556597
 4 Patent No. 5877155
 5 GENERAL INFORMATION:
 6 APPLICANT: Miller, Jonathan L.
 7 APPLICANT: Lytle, Vicki A.
 8 TITLE OF INVENTION: MIMOTOPES AND ANTI-MIMOTOPES OF
 9 TITLE OF INVENTION: HUMAN PLATELET GLYCOPROTEIN Ib/IX
 10 NUMBER OF SEQUENCES: 173
 11 CORRESPONDENCE ADDRESS:
 12 ADDRESSEE: Nixon, Hartlage, Levens & Doyle LLP
 13 STREET: Clinton Square, P.O. Box 1051
 14 CITY: Rochester
 15 STATE: New York
 16 COUNTRY: USA
 17 ZIP: 14604

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1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: Patent In Release #1.0, Version #1.00
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/08/456,997
8  FILING DATE:
9  CLASSIFICATION: 510
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US 08/406,140
12 FILING DATE: 17-MAR-1995
13 ATTORNEY/AGENT INFORMATION:
14 NAME: Tianan, Susan J.
15 REGISTRATION NUMBER: 34,103
16 REFERENCE/DOCKET NUMBER: 20884/101
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: (716) 263-1636
19 TELEFAX: (716) 263-1600
20 INFORMATION FOR SEQ ID NO: 140:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 10 amino acids
23 TYPE: amino acid
24 STRANDEDNESS:
25 POLARITY: linear
26 MOLECULE TYPE: peptide
27 US 08-556 597-140
28
29 Query Match 36.4%; Score 4; DB 2; Length 10;
30 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
31 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
32
33 QY 2 RALN 5
34 DB 4 RALN 7
35
36 RESULT 14
37 5248606 37
38 PATENT NO. 5248606
39 APPLICANT: WALSH, TERENCE A. (BY: TIMOTHY D. MURPHY)
40 TITLE: E.R.
41 TITLE OF INVENTION: DNA ENCODING NATIVE PEPTIDES R AND
42 NATIVE FORMS OF MAIZE RIBOSOME INACTIVATOR
43 NUMBER OF SEQUENCES: 49
44 CURRENT APPLICATION DATA:
45 APPLICATION NUMBER: US/01/45,100
46 FILING DATE: 11-JUN-1990
47 SEQ ID NO: 37
48 LENGTH: 10
49 5248606-47
50
51 Query Match 36.4%; Score 4; DB 2; Length 10;
52 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
53 Matches 4; Conservative 0; Mismatches 0; Indels 0;
54
55 QY 4 LNWG 7
56 DB 2 LNWG 5
57
58 RESULT 15
59 US 08-844 978-12
60 SEQUENCE 12, Application US/08844978
61 PATENT NO. 6075004
62 GENERAL INFORMATION:
63 APPLICANT: Benedict, Stephen
64 APPLICANT: Stahaa, Teruna
65 APPLICANT: Chan, Marcia
66 APPLICANT: Tibbets, Scott
67 TITLE OF INVENTION: Peptide Compositions Which Induce Immune
68 NUMBER OF SEQUENCES: 36
69 CORRESPONDENCE ADDRESS:

```

```

1  ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
2  STREET: 2405 Grand Boulevard, Suite 400
3  CITY: Kansas City
4  STATE: MO
5  COUNTRY: USA
6  ZIP: 64108
7  COMPUTER READABLE FORM:
8  MEDIUM TYPE: Floppy disk
9  COMPUTER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: Patent In Release #1.0, Version #1.25
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/844,978
14 FILING DATE:
15 CLASSIFICATION: 514
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Collins, John M.
18 REGISTRATION NUMBER: 26262
19 REFERENCE/DOCKET NUMBER: 24769-A
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: (816)474-9050
22 TELEFAX: (816)474-9057
23 TELEX: 434-363
24 INFORMATION FOR SEQ ID NO: 32:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 11 amino acids
27 TYPE: amino acid
28 TOPOLOGY: linear
29 MOLECULE TYPE: peptide
30 US-08-844-978-12
31
32 Query Match 36.4%; Score 4; DB 3; Length 11;
33 Best Local Similarity 100.0%; Pred. No. 1.9e-02;
34 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
35
36 QY 2 RALN 5
37 DB 6 RALN 9
38
39 RESULT 16
40 US-08-844-978-35
41 SEQUENCE 35, Application US/08844978
42 PATENT NO. 6075004
43 GENERAL INFORMATION:
44 APPLICANT: Benedict, Stephen
45 APPLICANT: Stahaa, Teruna
46 APPLICANT: Chan, Marcia
47 APPLICANT: Tibbets, Scott
48 TITLE OF INVENTION: Peptide Compositions Which Induce Immune
49 NUMBER OF SEQUENCES: 36
50 CORRESPONDENCE ADDRESS:
51 ADDRESSEE: HOVEY, WILLIAMS, TIMMONS & COLLINS
52 STREET: 2405 Grand Boulevard, Suite 400
53 CITY: Kansas City
54 STATE: MO
55 COUNTRY: USA
56 ZIP: 64108
57 COMPUTER READABLE FORM:
58 MEDIUM TYPE: Floppy disk
59 COMPUTER: IBM PC compatible
60 OPERATING SYSTEM: PC-DOS/MS-DOS
61 SOFTWARE: Patent In Release #1.0, Version #1.25
62 CURRENT APPLICATION DATA:
63 APPLICATION NUMBER: US/08/844,978
64 FILING DATE:
65 CLASSIFICATION: 514
66 ATTORNEY/AGENT INFORMATION:
67 NAME: Collins, John M.
68 REGISTRATION NUMBER: 26262
69 REFERENCE/DOCKET NUMBER: 24769-A
70 TELECOMMUNICATION INFORMATION:
71 TELEPHONE: (816)474-9050

```

TELEFAX: 8161474-9057
 TELEX: 434 363
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11 amino acids
 TYPE: amino acid
 TOPOLOGY: circular
 MOLECULE TYPE: peptide
 US-08 644-978-35

Query Match 36.4%, Score 4; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2;le-02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 2 ALNW 5
 II
 DL 6 ALNW 9

RESULT 17
 US-08-461 9908-27
 Sequence 27, Application US/084619908
 Patent No. 5851810

GENERAL INFORMATION:
 APPLICANT: JOHN S. BLANCHARD
 TITLE OF INVENTION: NUCLEIC ACID-ENCODED PEPTIDES
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: AMSTER, ROHSTEIN & EHRNSTEIN
 STREET: 90 PARK AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10016

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 INCH 1.44 MB SOFTWARE DISKETTE
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: ASCIT
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/461 9908
 FILING DATE: JUNE 5, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: CRAIG J. ARNOLD
 REGISTRATION NUMBER: 34,267
 REFERENCE/DOCKET NUMBER: 96767/2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 697-5995
 TELEFAX: (212) 286-0854 OF 286 6992
 TELEX: TWX 710-581-4766
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12
 TYPE: AMINO ACID
 TOPOLOGY: LINEAR
 MOLECULE TYPE: PEPTIDE
 DESCRIPTION: NO
 HYPOTHETICAL: NO
 ORGANISM: RHODOCOCCUS SP. M4
 INDIVIDUAL ISOLATE: PHENYLALANINE DEHYDROGENASE
 US-08-461-9908-27

Query Match 36.4%, Score 4; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 2;le-02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 3 ALNW 5
 II-1
 DL 5 ALNW 9

RESULT 18
 US-08-248-819A-44
 Sequence 44, Application US/08248819A
 Patent No. 5700638
 GENERAL INFORMATION:
 APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 60
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/248,819A
 FILING DATE: 25-NOV-1994
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/112,204
 FILING DATE: 26-AUG 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith, William M.
 REGISTRATION NUMBER: 30,224
 REFERENCE/DOCKET NUMBER: 15726A-000610
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 326-2400
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 44:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 STRANDEDNESS: Not relevant
 TOPOLOGY: Not relevant
 MOLECULE TYPE: peptide
 US-08-248 819A-44

Query Match 36.4%, Score 4; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 2;le-02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 5 NWGA 8
 II-1
 DL 7 NWGA 10

RESULT 19
 US-08-317-646A-62
 Sequence 62, Application US/08317646A
 Patent No. 5856171
 GENERAL INFORMATION:
 APPLICANT: KORSMEYER, Stanley J.
 TITLE OF INVENTION: CELL DEATH REGULATORS
 NUMBER OF SEQUENCES: 78
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend Kourie and Crew
 STREET: 379 Lytton Avenue
 CITY: Palo Alto
 STATE: California
 COUNTRY: US
 ZIP: 94301

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/337,646A
; FILING DATE: 10-NOV-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/248,819
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/112,408
; FILING DATE: 26-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A 0.03620
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-337-646A-62

Query Match 36.4%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NWGA 8
DB 7 NWGA 10

RESULT 26
US-09-041-889-37
; Sequence 37, Application US/09-041-889
; Patent No. 603864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Colavy, Ofer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Microbial DC PANCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 200
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/837,959
; FILING DATE: 11-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PH 3036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-337-646A-62

Query Match 36.4%; Score 4; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NWGA 8
DB 7 NWGA 10

RESULT 26
US-09-041-889-37
; Sequence 37, Application US/09-041-889
; Patent No. 603864
; GENERAL INFORMATION:
; APPLICANT: Braun, Jonathan
; APPLICANT: Colavy, Ofer
; TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
; TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
; TITLE OF INVENTION: Microbial DC PANCA antigens
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 200
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/041,889
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/837,959
; FILING DATE: 11-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-PH 3036
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-337-646A-62

Query Match 36.4%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 10 AKPK 13

RESULT 21
US-08-930-589A-20
; Sequence 20, Application US/08930589A
; Patent No. 6107087
; GENERAL INFORMATION:
; APPLICANT: MERCK FROSST CANADA & CO.
; APPLICANT: O'NEILL, GARY P.
; APPLICANT: MANCINI, JOSEPH A.
; TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
; TITLE OF INVENTION: CYCLOOXYGENASE-2
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/930,589A
; FILING DATE: 28-JUN-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coppola, Joseph A
; REGISTRATION NUMBER: 38,413
; REFERENCE/DOCKET NUMBER: 19029PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-6734
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-930-589A-20

Query Match 36.4%; Score 4; DB 3; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
DB 3 ARAL 6

RESULT 22
US-08-927-326-62
```

```

: Sequence 62, Application US/08927326
: Patent No. 6184202
: GENERAL INFORMATION:
: APPLICANT: KORSMEYER, Stanley J.
: TITLE OF INVENTION: CELL DEATH REGULATORS
: NUMBER OF SEQUENCES: 78
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend Bio-Phic and New
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/927,326
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/337,646
: FILING DATE: 10-NOV-1994
: APPLICATION NUMBER: US 08/248,614
: FILING DATE: 25-MAY-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/112,206
: FILING DATE: 26-AUG-1993
: ATTORNEY/AGENCY INFORMATION:
: NAME: Smith, William M
: REGISTRATION NUMBER: 30,224
: REFERENCE/DOCKET NUMBER: 157,246 US/09/20
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 62:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 13 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: not relevant
: MOLECULE TYPE: peptide
US 08-927-326-62

Query Match 46.4% Score 4: 1P 1S 1S 1S 1S 1S
Best Local Similarity 100.0% Pred No. 2.1e+02
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 5 NWGA 8
Db 7 NWGA 10

RESULT 23
US-09-599-781-20
: Sequence 20, Application US/09599781
: Patent No. 6362327
: GENERAL INFORMATION:
: APPLICANT: MERCK FROSST CANADA S 200
: O'NEILL, GARY P.
: MANCINI, JOSEPH A.
: TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
: CYCLOOXYGENASE-2
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merck & Co., Inc.
: STREET: P.O. Box 2000, 126 E. Lincoln Ave.
: CITY: Rahway
: STATE: NJ
: COUNTRY: USA
: ZIP: 07065-0900

```

```

: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM compatible
: OPERATING SYSTEM: Windows
: SOFTWARE: FastSeq for Windows Version 2.0b
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/599,781
: FILING DATE: 21 Jun-2000
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/084,033
: FILING DATE: 27-Sep-1993
: ATTORNEY/AGENCY INFORMATION:
: NAME: Coppola, Joseph A
: REGISTRATION NUMBER: 38,413
: REFERENCE/DOCKET NUMBER: 19029PC
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 732-594 6734
: TELEFAX: 732-594-4720
: TELEX: <Unknown>
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 13 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-599-781-20

Query Match 46.4% Score 4: DB 4: Length 13:
Best Local Similarity 100.0% Pred No. 2.1e+02;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ARAL 4
Db 3 ARAL 5

RESULT 24
US-09-417-264-37
: Sequence 37, Application US/09417264
: Patent No. 6537768
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: APPLICANT: Cohavy, Ofer
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
: Microbial UC PANCA antigens
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/417,264
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 09/041,889
: FILING DATE:
: ATTORNEY/AGENCY INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-PH 3006

```

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US 09-417-264 37

Query Match: 36.4%, Score 4, DB 1, Length 13

Best Local Similarity: 100.0%, Pred. No. 2, 3e-02

Matches: 4; Conservative 0; Mismatches 0; Gaps 0

QY 8 AKPK 11

ID 10 AKPK 13

RESULT 25

US-08-232-453A-23

Sequence 23, Application US/08242453A

Patent No. 5589568

GENERAL INFORMATION:

APPLICANT: HIGASHIJIMA, TSUTOMU

APPLICANT: ROSS, ELLIOTT M.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

MODULATING G PROTEIN ACTION

NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE & DUKKEE

STREET: P.O. BOX 4433

CITY: HOUSTON

STATE: TX

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232-453A

FILING DATE: APRIL 22, 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/748,319

FILING DATE: AUGUST 21, 1991

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: PARKER, DAVID L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: UTSD:253/PAR

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-232-453A-23

Query Match: 36.4%, Score 4, DB 1, Length 14

Best Local Similarity: 100.0%, Pred. No. 2, 3e-02

Matches: 4; Conservative 0; Mismatches 0; Gaps 0

QY 1 ARAL 4

ID 10 ARAL 13

RESULT 26

US-08-232-453A-28

Sequence 28, Application US/08212453A

Patent No. 5589568

GENERAL INFORMATION:

APPLICANT: HIGASHIJIMA, TSUTOMU

APPLICANT: ROSS, ELLIOTT M.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

MODULATING G PROTEIN ACTION

NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE & DUKKEE

STREET: P.O. BOX 4433

CITY: HOUSTON

STATE: TX

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/232-453A

FILING DATE: APRIL 22, 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/748,319

FILING DATE: AUGUST 21, 1991

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: PARKER, DAVID L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: UTSD:253/PAR

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 14 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-232-453A-28

Query Match: 36.4%, Score 4, DB 1, Length 14

Best Local Similarity: 100.0%, Pred. No. 2, 3e-02

Matches: 4; Conservative 0; Mismatches 0; Gaps 0

QY 1 ARAL 4

ID 10 ARAL 13

RESULT 27

US-08-232-453A-41

Sequence 41, Application US/08232453A

Patent No. 5589568

GENERAL INFORMATION:

APPLICANT: HIGASHIJIMA, TSUTOMU

APPLICANT: ROSS, ELLIOTT M.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

MODULATING G PROTEIN ACTION

NUMBER OF SEQUENCES: 71

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE & DUKKEE

STREET: P.O. BOX 4433

CITY: HOUSTON

STATE: TX

COUNTRY: USA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/242,456A
 FILING DATE: APRIL 22, 1994
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/748,414
 FILING DATE: AUGUST 23, 1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: PARKER, DAVID L.
 REGISTRATION NUMBER: 32,195
 REFERENCE/DOCKET NUMBER: DIS: 254/HAR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (512) 418-3000
 TELEFAX: (512) 474-7577
 INFORMATION FOR SEQ ID NO: 41:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-242-453A 41

Query Match: 36.4%; Score 4; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;
 QY 1 ARA 4
 DB 10 WGA 13
 RESULT 28
 US-09-482-528 13
 Sequence 13, Application US/08482528
 Patent No. 6017719
 GENERAL INFORMATION:
 APPLICANT: Tsenq-Law, Janet
 APPLICANT: Kobori, Joan A.
 APPLICANT: Al-Abdaly, Fahad A.
 APPLICANT: Guillermo, Roy
 APPLICANT: Helgerson, Sam L.
 APPLICANT: Deans, Robert J.
 TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL
 NUMBER OF SEQUENCES: 215
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Janice Guthrie, Ph.D.
 STREET: P.O. Box 15210
 CITY: Irvine
 STATE: California
 COUNTRY: USA
 ZIP: 92713-5210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,528
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Guthrie, Janice
 REGISTRATION NUMBER: 35,170
 REFERENCE/DOCKET NUMBER: IT 4630CIP4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (714) 440-5353
 TELEFAX: (714) 553-1952
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 Molecule Type: peptide
 US-09-482-528 13

Query Match: 36.4%; Score 4; DB 3; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 QY 6 WGA 9
 DB 10 WGA 13
 RESULT 29
 US-09-482-528 14

INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US 08 482-228 13
 Query Match: 36.4%; Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 WGA 9
 DB 10 WGA 13

RESULT 29
 US-08-482-528-13
 Sequence 13, Application US/08482528
 Patent No. 6017719
 GENERAL INFORMATION:
 APPLICANT: Tsenq-Law, Janet
 APPLICANT: Kobori, Joan A.
 APPLICANT: Al-Abdaly, Fahad A.
 APPLICANT: Guillermo, Roy
 APPLICANT: Helgerson, Sam L.
 APPLICANT: Deans, Robert J.
 TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
 NUMBER OF SEQUENCES: 215
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Janice Guthrie, Ph.D.
 STREET: P.O. Box 15210
 CITY: Irvine
 STATE: California
 COUNTRY: USA
 ZIP: 92713-5210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,528
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Guthrie, Janice
 REGISTRATION NUMBER: 35,170
 REFERENCE/DOCKET NUMBER: IT 4630CIP4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (714) 440-5353
 TELEFAX: (714) 553-1952
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 14 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-482-528-13

Query Match: 36.4%; Score 4; DB 3; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;
 QY 6 WGA 9
 DB 10 WGA 13

RESULT 30
 US-09-482-528 14

```

? Sequence 13, Application US/0940065A
? Patent No. 6348311
? GENERAL INFORMATION:
? APPLICANT: Kastan, Michael
? APPLICANT: Carman, Christine
? APPLICANT: Kim, Seong-Tae
? APPLICANT: Lim, Dae-Sik
? APPLICANT: St. Jude Children's Research Hospital
? TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
? FILE REFERENCE: 2427/0142
? CURRENT APPLICATION NUMBER: US/09/400,653A
? PRIOR FILING DATE: 1999-09-21
? PRIOR APPLICATION NUMBER: 09/248,061
? NUMBER OF SEQ ID NOS: 49
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 13
? LENGTH: 14
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-400-653A-13

Query Match 36.4%, Score 47, DB 41, Length 14,
Best Local Similarity 100.0%, Pred. No. 2.4e+02,
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
Db 2 ARAL 5

RESULT 31
US-09-248-061B-31
? Sequence 31, Application US/09248061b
? Patent No. 6387640
? GENERAL INFORMATION:
? APPLICANT: Kastan, M.
? APPLICANT: Carman, C.
? APPLICANT: Kim, S-T.
? APPLICANT: Lim, D-S.
? APPLICANT: St. Jude Children's Research Hospital
? TITLE OF INVENTION: ATM Kinase Modulation for Screening and Therapies
? FILE REFERENCE: 2427/0142
? CURRENT APPLICATION NUMBER: US/09/248,061b
? CURRENT FILING DATE: 1999-02-10
? NUMBER OF SEQ ID NOS: 32
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 31
? LENGTH: 14
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-09-248-061B-31

Query Match 36.4%, Score 47, DB 41, Length 14,
Best Local Similarity 100.0%, Pred. No. 2.4e+02,
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
Db 2 ARAL 5

RESULT 32
US-08-467-083-48
? Sequence 48, Application US/08467083
? Patent No. 5726023
? GENERAL INFORMATION:
? APPLICANT: Cheever, Martin A.
? APPLICANT: Disis, Mary L.
? TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
? TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
? TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
? NUMBER OF SEQUENCES: 68

```

```

? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Seed and Berry
? STREET: 6300 Columbia Center, 701 Fifth Avenue
? CITY: Seattle
? STATE: Washington
? COUNTRY: US
? ZIP: 98104-7092
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/467,083
? FILING DATE: 06-JUN-1995
? CLASSIFICATION: 424
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/414,417
? FILING DATE: 06-JUN-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: Sharkey, Richard G.
? REGISTRATION NUMBER: 32,629
? REFERENCE/DOCKET NUMBER: 920010.448C2
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 622 4900
? TELEFAX: (206) 682-6031
? TELEX: 3723836 SEELANDERRY
? INFORMATION FOR SEQ ID NO: 48:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 15 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? US-08-467-083-48

Query Match 36.4%, Score 47, DB 41, Length 15,
Best Local Similarity 100.0%, Pred. No. 2.4e+02,
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAKP 10
Db 9 GAKP 12

RESULT 33
US-08-414-417B-48
? Sequence 48, Application US/08414417B
? Patent No. 5801005
? GENERAL INFORMATION:
? APPLICANT: Cheever, Martin A.
? APPLICANT: Disis, Mary L.
? TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
? TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
? TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
? NUMBER OF SEQUENCES: 69
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Seed and Berry LLP
? STREET: 6300 Columbia Center, 701 Fifth Avenue
? CITY: Seattle
? STATE: Washington
? COUNTRY: US
? ZIP: 98104-7092
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/414,417B
? FILING DATE: 31-MAR-1995
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Sharkey, Richard G.
? REGISTRATION NUMBER: 32,629

```

```

: REFERENCE/DOCKET NUMBER: 920010.448C2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 48:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-414-417B-48

```

```

Query Match: 36.4%; Score 4; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 7 GAKP 10
    ||||
DL 9 GAKP 12

```

```

RESULT 14
US-08-486-348A-48
: Sequence 48, Application US/08486348A
: Patent No. 5846538
: GENERAL INFORMATION:
: APPLICANT: Cheever, Martin A.
: APPLICANT: Disis, Mary L.
: TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
: TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
: TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
: NUMBER OF SEQUENCES: 69
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seed and Berry LLP
: STREET: 6300 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: US
: ZIP: 98104-7092
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: IBM PC compatible
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/486,348A
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Sharkey, Richard G.
: REGISTRATION NUMBER: 32,629
: REFERENCE/DOCKET NUMBER: 920010.448C2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 48:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-486-348A-48

```

```

Query Match: 36.4%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 7 GAKP 10
    ||||
DL 9 GAKP 12

```

```

RESULT 15
US-08-710-249-18
: Sequence 18, Application US/98710249

```

```

: Patent No. 5858777
: GENERAL INFORMATION:
: APPLICANT: Villeponteau, Bryant
: APPLICANT: Feng, Junli
: APPLICANT: Adams, William H.
: APPLICANT: Adams, Robert R.
: TITLE OF INVENTION: Methods and Reagents for Regulating
: TITLE OF INVENTION: Telomere Length and Telomerase Activity
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/710,249
: FILING DATE: 13-SEP-1996
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/583,808
: FILING DATE: 05-JAN-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/003,492
: FILING DATE: 08-SEP-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Storella, John R.
: REGISTRATION NUMBER: 32,944
: REFERENCE/DOCKET NUMBER: 015389-0012200S
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 576-0200
: TELEFAX: (415) 576-0300
: INFORMATION FOR SEQ ID NO: 18:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-710-249-18

```

```

Query Match: 36.4%; Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 8 GAKP 11
    ||||
DL 12 GAKP 15

```

```

RESULT 36

```

```

US-08-468-545B-48
: Sequence 48, Application US/08468545B
: Patent No. 5876712
: GENERAL INFORMATION:
: APPLICANT: Cheever, Martin A.
: APPLICANT: Disis, Mary L.
: TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
: TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
: TITLE OF INVENTION: HER-2/neu ONCOGENE IS ASSOCIATED
: NUMBER OF SEQUENCES: 69
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seed and Berry LLP
: STREET: 6300 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: US

```

ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,545B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.44805
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4960
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-468-545B-48

Query Match 36.4% Score 4; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AKPK 10
DB 5 GAKP 12

RESULT 37
US-09-041-889-15
Sequence 15, Application US/09041889
Patent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
Ulcerative Colitis, and Clinical Subtypes Thereof, Using
Microbial UC PANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-041-889-16

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 2 AKPK 5

RESULT 39
US-09-041-889-22
Sequence 22, Application US/09041889
Patent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer

TYPE: amino acid
TOPOLOGY: linear
US-09-041-889-15

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 12 AKPK 15

RESULT 38
US-09-041-889-16
Sequence 16, Application US/09041889
Patent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
Ulcerative Colitis, and Clinical Subtypes Thereof, Using
Microbial UC PANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,889
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/837,058
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 3006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-041-889-16

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 2 AKPK 5

RESULT 39
US-09-041-889-22
Sequence 22, Application US/09041889
Patent No. 6033864
GENERAL INFORMATION:
APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer

```

1 TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
2 TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
3 TITLE OF INVENTION: Microbial UC PANCA antigens
4 NUMBER OF SEQUENCE ADDRESSES: 41
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: Campbell & Flores LLP
7 STREET: 4370 La Jolla Village Drive, Suite 700
8 CITY: San Diego
9 STATE: California
10 COUNTRY: USA
11 ZIP: 92122
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Patent in Release #1.0, Version #1.25
17 CURRENT APPLICATION NUMBER: US/09/041.889
18 FILING DATE:
19 CLASSIFICATION:
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US 08/837,058
22 FILING DATE: 11-APR-1997
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Campbell, Cathryn A.
25 REGISTRATION NUMBER: 31,815
26 REFERENCE/DOCKET NUMBER: P-PM 3006
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (619) 535-9001
29 TELEFAX: (619) 535-8949
30 INFORMATION FOR SEQ ID NO: 24:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 15 amino acids
33 TYPE: amino acid
34 TOPOLOGY: linear
35 US-09-041-889-22
36
37 Query Match 36.4% Score 4; DB 3; Length 15;
38 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
39 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
40
41 QY 8 AKPK 11
42 DB 111
43 6 AKPK 9
44
45 RESULT 43
46 US-09-041-889-24
47 Sequence 24, Application US/09041889
48 Patent No. 6033864
49 GENERAL INFORMATION:
50 APPLICANT: Braun, Jonathan
51 APPLICANT: Cohavy, Ofer
52 TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
53 TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
54 TITLE OF INVENTION: Microbial UC PANCA antigens
55 NUMBER OF SEQUENCES: 41
56 CORRESPONDENCE ADDRESS:
57 ADDRESSEE: Campbell & Flores LLP
58 STREET: 4370 La Jolla Village Drive, Suite 700
59 CITY: San Diego
60 STATE: California
61 COUNTRY: USA
62 ZIP: 92122
63 COMPUTER READABLE FORM:
64 MEDIUM TYPE: Floppy disk
65 COMPUTER: IBM PC compatible
66 OPERATING SYSTEM: PC-DOS/MS-DOS
67 SOFTWARE: Patent in Release #1.0, Version #1.25
68 CURRENT APPLICATION NUMBER: US/09/041.889
69 FILING DATE:
70 CLASSIFICATION:
71 PRIOR APPLICATION DATA:
72 APPLICATION NUMBER: US 08/837,058
73 FILING DATE: 11-APR-1997
74 ATTORNEY/AGENT INFORMATION:
75 NAME: Campbell, Cathryn A.
76 REGISTRATION NUMBER: 31,815
77 REFERENCE/DOCKET NUMBER: P-PM 3006
78 TELECOMMUNICATION INFORMATION:
79 TELEPHONE: (619) 535-9001
80 TELEFAX: (619) 535-8949
81 INFORMATION FOR SEQ ID NO: 25:
82 SEQUENCE CHARACTERISTICS:
83 LENGTH: 15 amino acids
84 TYPE: amino acid
85 TOPOLOGY: linear
86 MOLECULE TYPE: peptide
87 US-09-041-889-25
88
89 Query Match 36.4% Score 4; DB 3; Length 15;
90 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
91 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
92
93 QY 8 AKPK 11
94 DB 111
95 6 AKPK 9
96
97 RESULT 44
98 US-09-041-889-35
99 Sequence 35, Application US/09041889
100 Patent No. 6033864
101 GENERAL INFORMATION:
102 APPLICANT: Braun, Jonathan
103 APPLICANT: Cohavy, Ofer
104 TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
105 TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
106 TITLE OF INVENTION: Microbial UC PANCA antigens
107 NUMBER OF SEQUENCES: 41
108 CORRESPONDENCE ADDRESS:
109 ADDRESSEE: Campbell & Flores LLP
110 STREET: 4370 La Jolla Village Drive, Suite 700
111 CITY: San Diego
112 STATE: California
113 COUNTRY: USA
114 ZIP: 92122
115 COMPUTER READABLE FORM:
116 MEDIUM TYPE: Floppy disk
117 COMPUTER: IBM PC compatible
118 OPERATING SYSTEM: PC-DOS/MS-DOS
119 SOFTWARE: Patent in Release #1.0, Version #1.25
120 CURRENT APPLICATION NUMBER: US/09/041.889
121 FILING DATE:
122 CLASSIFICATION:
123 PRIOR APPLICATION DATA:
124 APPLICATION NUMBER: US 08/837,058
125 FILING DATE: 11-APR-1997
126 ATTORNEY/AGENT INFORMATION:
127 NAME: Campbell, Cathryn A.
128 REGISTRATION NUMBER: 31,815
129 REFERENCE/DOCKET NUMBER: P-PM 3006
130 TELECOMMUNICATION INFORMATION:
131 TELEPHONE: (619) 535-9001
132 TELEFAX: (619) 535-8949
133 INFORMATION FOR SEQ ID NO: 35:
134 SEQUENCE CHARACTERISTICS:
135 LENGTH: 15 amino acids
136 TYPE: amino acid
137 TOPOLOGY: linear
138 MOLECULE TYPE: peptide
139 US-09-041-889-35
140
141 Query Match 36.4% Score 4; DB 3; Length 15;
142 Best Local Similarity 100.0%; Pred. No. 2.4e+02;
143 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Matches      4:  Conservative      0:  Mismatches      6:  Indels      9:  Gaps      0:

QY      8 AKPK 11
DB      12 AKPK 15

RESULT 42
US-09-041-889-36
: Sequence 36, Application US/0904189
: Patent No. 6074835
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
: TITLE OF INVENTION: Microbial UC PANDA antigens
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/041-889
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/837-058
: FILING DATE: 11-APR-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-PM 2438
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 36:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-09-041-889-36

Query Match      36.4%      Score 4:  DB 3:  Length 15:
Best Local Similarity 100.0%      Pred. No. 2.4e-02:
Matches      4:  Conservative      0:  Mismatches      9:  Indels      9:  Gaps      0:

QY      8 AKPK 11
DB      2 AKPK 5

RESULT 43
US-09-837-058-15
: Sequence 15, Application US/09837058
: Patent No. 6074835
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: APPLICANT: Targan, Stephen R.
: APPLICANT: Egnen, Mark
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
: TITLE OF INVENTION: Histone H1
: NUMBER OF SEQUENCES: 26

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837-058
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 2438
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-837-058-15

Query Match      36.4%      Score 4:  DB 3:  Length 15:
Best Local Similarity 100.0%      Pred. No. 2.4e-02:
Matches      4:  Conservative      0:  Mismatches      0:  Indels      0:  Gaps      0:

QY      8 AKPK 11
DB      12 AKPK 15

RESULT 44
US-08-837-058-15
: Sequence 16, Application US/08837058
: Patent No. 6074835
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: APPLICANT: Targan, Stephen R.
: APPLICANT: Egnen, Mark
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
: TITLE OF INVENTION: Histone H1
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837-058
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM 2438
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

```

```

: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-837-058-16

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e-02;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 8 AKPK 11
DL 2 AKPK 5

RESULT 45
US-08-837-058-22
: Sequence 22, Application US/08847058
: Patent No. 6074835
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: APPLICANT: Targan, Stephan R.
: APPLICANT: Eggena, Mark
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/837-058
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-PM 2438
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-837-058-24

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e-02;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 8 AKPK 11
DL 4 AKPK 7

RESULT 47
US-08-466-6808-48
: Sequence 48, Application US/08466808
: Patent No. 6075122
: GENERAL INFORMATION:
: APPLICANT: Cheever, Mattie A.
: APPLICANT: Davis, Mary L.
: TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
: TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
: TITLE OF INVENTION: HER 2/neu ONCOGENE IS ASSOCIATED
: NUMBER OF SEQUENCES: 69
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seed and Berry LLP
: STREET: 6400 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: US
: ZIP: 98104-7092
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/466,6808
: FILING DATE: 06 JUN 1995
: CLASSIFICATION: 424

```

```

: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-837-058-16

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e-02;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 8 AKPK 11
DL 2 AKPK 5

RESULT 45
US-08-837-058-22
: Sequence 22, Application US/08847058
: Patent No. 6074835
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: APPLICANT: Targan, Stephan R.
: APPLICANT: Eggena, Mark
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/837-058
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-PM 2438
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
US-08-837-058-24

Query Match 36.4% Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e-02;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 8 AKPK 11
DL 6 AKPK 9

RESULT 46
US-08-837-058-24
: Sequence 24, Application US/08847058
: Patent No. 6074835
: GENERAL INFORMATION:

```

ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 92010.448C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US 08-466-680B-48

Query Match 36.4%; Score 4; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 7 GAKP 10
Db 9 GAKP 12

RESULT 48
US-08-602-999A-333
Sequence 333, Application US/0860299A
Patent No. 6184205
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: OJILLIAM, Lawrence A.
APPLICANT: DEK, Channing J.
APPLICANT: FOWLES, Dana M.
APPLICANT: RIDGER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1,001 262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 333:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-333

Query Match 36.4%; Score 4; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 4 ARAL 4
Db 4 ARAL 7
RESULT 49
US-09-220-157A-18
Sequence 18, Application US/09220157A
Patent No. 6300110
GENERAL INFORMATION:
APPLICANT: Villeponteau, Bryant
APPLICANT: Feng, Sunli
APPLICANT: Adams, William H.
APPLICANT: Adams, Robert R.
TITLE OF INVENTION: Methods and Reagents for Regulating
TITLE OF INVENTION: Telomere Length and Telomerase Activity
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/220,157A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/710,249
FILING DATE: 13-SEP-1996
APPLICATION NUMBER: US 08/583,808
FILING DATE: 05-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/003,492
FILING DATE: 08-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE/DOCKET NUMBER: 015189-00122005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-220-157A-18

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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 8 AKPK 11
Db 12 AKPK 15

RESULT 50
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Sequence 333, Application US/09500124
Patent No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.

APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,499
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-262
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9093
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 333:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-333

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10 4 ARAL 7

Search completed: September 30, 2003, 10:28:35
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CM protein - protein search, using sw model

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Title: US-09-787-443-3

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Searched: 566894 seqs, 15137095 residues

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Fired No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	4	36.4	10	11	US-09-572-404B-1156 Sequence 1136, Ap
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9	7	US-08-344-824-273	Sequence 273, App
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ALIGNMENTS

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 : Sequence 10, Application US/09487715
 : Publication NO. US20030059422A1
 : GENERAL INFORMATION:
 : APPLICANT: Sharma, Shubh
 : TITLE OF INVENTION: Tuftsin Metallopeptides Analogs and Uses Thereof
 : FILE REFERENCE: 1173/107940S1
 : CURRENT APPLICATION NUMBER: US/09/387.715
 : CURRENT FILING DATE: 1999-08-30
 : PRIOR APPLICATION NUMBER: PCT/US99/05693
 : PRIOR FILING DATE: 1999-03-18
 : NUMBER OF SEQ ID NOS: 55
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 10
 : LENGTH: 9
 : TYPE: PPT
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: Description of Artificial Sequence: synthetic
 : OTHER INFORMATION: peptide

NAME/KEY: modified residue
LOCATION: 3,6,8
OTHER INFORMATION: D-amino acid
US-09-787-715-20

Query Match 36.4%: Score 4: DB 11: Length 9:
Best Local Similarity 100.0%: Pred. No. 5.1e+05:
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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III
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US-10-364-842-10
Sequence 10, Application US/10364842
Publication No. US20030165427A1
GENERAL INFORMATION:
APPLICANT: Sharma, Shubh
TITLE OF INVENTION: Tuftsin Metallopeptides Analogs and Uses Thereof
FILE REFERENCE: 1173/1D794US1
CURRENT APPLICATION NUMBER: US/0/364,842
CURRENT FILING DATE: 2003-02-11
PRIOR APPLICATION NUMBER: PCT/US99/05694
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 10

LENGTH: 9

TYPE: PPT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: synthetic

OTHER INFORMATION: peptide

FEATURE:

NAME/KEY: modified residue

LOCATION: 3,6,8

OTHER INFORMATION: D-amino acid

US-10-364-842-10

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RESULT 3

US-08-344-824-179
Sequence 179, Application US/08344824
Publication No. US20030152580A1
GENERAL INFORMATION:

APPLICANT: SEITE, Alessandro

APPLICANT: SIDNEY, John

TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES

NUMBER OF SEQUENCES: 399

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kleinfelder and Frew

STREET: One Market Plaza, Stewart Street Tower, 20th

FLOOR: Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/344,824
FILING DATE: 23-NOV-1994
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/278,634

FILING DATE: 21-JUL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Rastlaur, Kevin L.

REGISTRATION NUMBER: 34,774

REFERENCE/DOCKET NUMBER: 14137 80-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 543 9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 179:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-344-824-179

Query Match 36.4%: Score 4: DB 7: Length 10:

Best Local Similarity 100.0%: Pred. No. 3.7e+02:

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ARAL 4

III

7 ARAL 10

RESULT 4

US-09-572-404B-1880

Sequence 1880, Application US/09572404B

Publication No. US20030078374A1

GENERAL INFORMATION:

APPLICANT: Proteom Ltd

TITLE OF INVENTION: Complementary peptide ligands from the human genome

FILE REFERENCE: Human patent

CURRENT APPLICATION NUMBER: US/09/572,404B

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 4203

SOFTWARE: ProtPatent version 1.0

SEQ ID NO 1880

LENGTH: 10

TYPE: PPT

ORGANISM: Homo Sapiens

FEATURE:

OTHER INFORMATION: sequence located in PCD17 at 230-239 and may interact with S

US-09-572-404B-1880

Query Match 36.4%: Score 4: DB 11: Length 10:

Best Local Similarity 100.0%: Pred. No. 3.7e+02:

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 ARAL 4

III

5 ARAL 8

RESULT 5

US-09-572-404B-1882

Sequence 1882, Application US/09572404B

Publication No. US20030078374A1

GENERAL INFORMATION:

APPLICANT: Proteom Ltd

TITLE OF INVENTION: Complementary peptide ligands from the human genome

FILE REFERENCE: Human patent

CURRENT APPLICATION NUMBER: US/09/572,404B

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 4203

SOFTWARE: ProtPatent version 1.0

```

; SEQ ID NO 1882
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
;
; FEATURE:
;
; OTHER INFORMATION: sequence located in p0117 at 229-248 and may interact with Sequed
; OTHER INFORMATION: in this patent.
US-09-572-404B-1882

Query Match 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
   1 11
Db 6 ARAL 9

RESULT 6
US-09-572-404B-3136
; Sequence 3136, Application US/095724043
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide variants from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,4043
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 4136
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
;
; FEATURE:
;
; OTHER INFORMATION: sequence located in TP11 at 84-93 and may interact with Sequence
US-09-572-404B-3136

Query Match 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. 3 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AKPK 11
   1 11
Db 6 AKPK 9

RESULT 7
US-09-572-270A-891
; Sequence 891, Application US/09572270A
; Publication No. US20030148366A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572,270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 891
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
;
; OTHER INFORMATION: Sequence located in LTP11 at 79-88 and may interact with
US-09-572-270A-891

Query Match 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 4 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
   1 11
Db 1 ARAL 4

us-09-572-270A-893
; Sequence 893, Application US/09572270A
; Publication No. US20030148366A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Inter- complementary peptide listing
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/572,270A
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 1144
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 893
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Arabidopsis Thaliana
;
; OTHER INFORMATION: Sequence located in LTP11 at 78-87 and may interact with
US-09-572-270A-893

Query Match 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
   1 11
Db 4 ARAL 7

RESULT 9
US-10-239-313A-480
; Sequence 480, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Lilliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 480
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-239-313A-480

Query Match 36.4%; Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 3 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
   1 11
Db 3 ARAL 6

RESULT 10
US-09-810-385-26
; Sequence 26, Application US/09810385
; Patent No. US20020137662A1
; GENERAL INFORMATION:
; APPLICANT: Laughon, Allen
```

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: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR NEGATIVE REGULATION OF TGF-BETA PATH
: FILE REFERENCE: WARF-0002
: CURRENT APPLICATION NUMBER: US/09/810,385
: CURRENT FILING DATE: 2001-03-16
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 26
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Shr. peptide.
: US-09-810,385:26

Query Match          36.4%  Score 4: 10 10: Length 12;
Best Local Similarity 100.0%  Prod. No. 4.4e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 9 AKPK 12

RESULT 1:
US-10-050,200:59
: Sequence 59, Application US/1005,200
: Publication No. US20030166037A1
: GENERAL INFORMATION:
: APPLICANT: Colles, Fawn
: APPLICANT: Karlsson, Lars
: TITLE OF INVENTION: Aggrecaasone-1 and 2 Peptide Substrates and Methods
: FILE REFERENCE: ORT-1417
: CURRENT APPLICATION NUMBER: US/10/950,200
: CURRENT FILING DATE: 2002-01-16
: NUMBER OF SEQ ID NOS: 60
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 59
: LENGTH: 12
: TYPE: PRT
: ORGANISM: artificial sequence
: FEATURE:
: OTHER INFORMATION: peptide substrate
: US-10-050,200:59

Query Match          36.4%  Score 4: 05 05: Length 12;
Best Local Similarity 100.0%  Prod. No. 4.4e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KALN 5
DB 8 KALN 11

RESULT 2:
US-09-753-126:85
: Sequence 85, Application US/0975,126
: Patent No. US26020127219A1
: GENERAL INFORMATION:
: APPLICANT: OKRELS, JENS SIGURD
: APPLICANT: JENSEN, ANNE DAM
: APPLICANT: BALKIER, TORBEN
: APPLICANT: JENSEN, RIKKE BOLDING
: TITLE OF INVENTION: IMPROVED LYSOSOMAL ENZYMS AND LYSOSOMAL ENZYME
: FILE REFERENCE: 31-00060005
: CURRENT APPLICATION NUMBER: US/09/75,126
: CURRENT FILING DATE: 2001-06-11
: PRIOR APPLICATION NUMBER: PA 1999 01899
: PRIOR FILING DATE: 1999-12-30
: PRIOR APPLICATION NUMBER: 60/174,562
: PRIOR FILING DATE: 2000-01-06
: PRIOR APPLICATION NUMBER: PA 200 003005

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: PRIOR FILING DATE: 2000-06-02
: PRIOR APPLICATION NUMBER: 60/210,984
: PRIOR FILING DATE: 2000-06-12
: PRIOR APPLICATION NUMBER: 60/211,124
: PRIOR FILING DATE: 2000-06-12
: PRIOR APPLICATION NUMBER: PA 2000 01027
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: 60/217,497
: PRIOR FILING DATE: 2000-07-11
: NUMBER OF SEQ ID NOS: 147
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 85
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: US-09-753-126:85

Query Match          36.4%  Score 4: DB 10: Length 13;
Best Local Similarity 100.0%  Prod. No. 4.6e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ALNW 6
DB 1 ALNW 4

RESULT 13
US-09-896,896A:49
: Sequence 49, Application US/09896896A
: Publication No. US20030046181A1
: GENERAL INFORMATION:
: APPLICANT: MAXGEN APS
: TITLE OF INVENTION: PEPTIDE EXTENDED GLYCOSYLATED POLYPEPTIDES
: FILE REFERENCE: 0217us210
: CURRENT APPLICATION NUMBER: US/09/896,896A
: CURRENT FILING DATE: 2001-06-29
: PRIOR APPLICATION NUMBER: US 60/217,497
: PRIOR FILING DATE: 2000-07-11
: PRIOR APPLICATION NUMBER: US 60/225,558
: PRIOR FILING DATE: 2000-08-16
: PRIOR APPLICATION NUMBER: DK PA 2000 01027
: PRIOR FILING DATE: 2000-06-30
: PRIOR APPLICATION NUMBER: DK PA 2000 01092
: PRIOR FILING DATE: 2000-07-14
: PRIOR APPLICATION NUMBER: PCT/DK00/00743
: PRIOR FILING DATE: 2000-12-29
: PRIOR APPLICATION NUMBER: PCT/DK01/00090
: PRIOR FILING DATE: 2001-02-09
: NUMBER OF SEQ ID NOS: 123
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 49
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
: US-09-896-896A:49

Query Match          36.4%  Score 4: DB 11: Length 13;
Best Local Similarity 100.0%  Prod. No. 4.6e+02;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ALNW 6
DB 1 ALNW 4

RESULT 14
US-10-027,661A:29

```


Sequence 20, Application US/10027961A
 Publication No. US2003032799A1
 GENERAL INFORMATION:
 APPLICANT: G'NEILL, GARY P.
 APPLICANT: MANCINI, JOSEPH A.
 TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF HUMAN
 TITLE OF INVENTION: CYCLOOXYGENASE 2
 FILE REFERENCE: 19029PCADA
 CURRENT APPLICATION NUMBER: US/10027961A
 CURRENT FILING DATE: 2001-10-25
 PRIOR APPLICATION NUMBER: 09/599,781
 PRIOR FILING DATE: 2000-06-21
 PRIOR APPLICATION NUMBER: 08/930,589
 PRIOR FILING DATE: 1996-02-22
 PRIOR APPLICATION NUMBER: PCT/CA94/00501
 PRIOR FILING DATE: 1994-09-13
 PRIOR APPLICATION NUMBER: 08/084,039
 PRIOR FILING DATE: 1993-09-27
 PRIOR APPLICATION NUMBER: 08/064,271
 PRIOR FILING DATE: 1993-05-06
 PRIOR APPLICATION NUMBER: 07/994,750
 PRIOR FILING DATE: 1992-12-22
 NUMBER OF SEQ ID NOS: 23
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 20
 LENGTH: 13
 TYPE: PRI
 ORGANISM: Human
 US-10-027 961A-20

Query Match 36.4% Score 41 DB 100.0% Length 13
 Best Local Similarity 100.0% Pred. No. 4.6e+02
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 1 AKPK 4
 DB 3 AKAL 6

RESULT 15
 US-10-229 567 47
 Sequence 47, Application US/10027961A
 Publication No. US20030092080A1
 GENERAL INFORMATION:
 APPLICANT: Braden, Jonathan
 TITLE OF INVENTION: Diagonosis, Prevention and Treatment of
 Address: 4370 La Jolla Village Drive, Suite 200
 City: San Diego
 State: California
 Country: USA
 Zip: 92122
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent Release #17, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10027961A
 FILING DATE: 27-Aug-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/417,294
 FILING DATE: <Unknown>
 APPLICATION NUMBER: US 09/541,889
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 41.815
 REFERENCE/DOCKET NUMBER: P-PM 3006
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (619) 535-9001
 TELEFAX: (619) 535-8949
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 37:
 US-10-229-567-37

Query Match 36.4% Score 41 DB 100.0% Length 13
 Best Local Similarity 100.0% Pred. No. 4.6e+02
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 8 AKPK 11
 DB 10 AKPK 13

RESULT 16
 US-10-024-123-13
 Sequence 13, Application US/00024123
 Publication No. US2003022263A1
 GENERAL INFORMATION:
 APPLICANT: Kastan, Michael
 APPLICANT: Canman, Christine
 APPLICANT: Kim, Seong-fae
 APPLICANT: Lim, Dao-Suk
 APPLICANT: St. Jude Children's Research Hospital
 TITLE OF INVENTION: ATM Kinase Modulation for Screening and
 TITLE OF INVENTION: Therapies
 FILE REFERENCE: 2427/1F142
 CURRENT APPLICATION NUMBER: US/10024123
 CURRENT FILING DATE: 2001-12-17
 PRIOR APPLICATION NUMBER: 09/400,653
 PRIOR FILING DATE: 1999-09-21
 PRIOR APPLICATION NUMBER: 09/448,061
 PRIOR FILING DATE: 1999-02-10
 NUMBER OF SEQ ID NOS: 49
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 13
 LENGTH: 14
 TYPE: PRI
 ORGANISM: Homo sapiens
 US-10-024-123-13

Query Match 36.4% Score 41 DB 100.0% Length 14
 Best Local Similarity 100.0% Pred. No. 4.9e+02
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 1 AKAL 4
 DB 2 AKAL 5

RESULT 17
 US-09-873-409-17
 Sequence 17, Application US/09873409
 Patent No. US20020037522A1
 GENERAL INFORMATION:
 APPLICANT: Frank, Markus
 APPLICANT: Sayegh, Mohamed
 TITLE OF INVENTION: A Gene Encoding a Multidrug Resistance Human P-Glycoprotein
 TITLE OF INVENTION: Homologue on Chromosome 7p13-21 and Uses Thereof
 FILE REFERENCE: 81994/268611
 CURRENT APPLICATION NUMBER: US/09/873,409
 CURRENT FILING DATE: 2001-06-05
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: FASTSEQ Version 3.0

SEQ ID NO 17
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-873-439-17

Query Match 36.4% Score 4; DB 12; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5, 2e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 ARAL 4
 1111
 1b 12 ARAL 15

US-10-268-561-16
 Sequence 16, Application US/10268561
 Publication No. US20030148333A1

GENERAL INFORMATION:
 APPLICANT: Ortho-Clinical Diagnostics, Inc.
 TITLE OF INVENTION: HCV Anti-Core Monoclonal Antibodies
 FILE REFERENCE: CDS0286
 CURRENT APPLICATION NUMBER: US/10/268,561
 CURRENT FILING DATE: 2002-10-10
 PRIOR APPLICATION NUMBER: US 60/337453
 PRIOR FILING DATE: 2001-11-05
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 16
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Hepatitis C virus
 US-10-268-561-16

Query Match 36.4% Score 4; DB 12; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5, 2e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 ARAL 4
 1111
 1b 3 ARAL 5

US-10-268-569-16
 Sequence 16, Application US/10268569
 Publication No. US20030152965A1

GENERAL INFORMATION:
 APPLICANT: Ortho-Clinical Diagnostics, Inc.
 TITLE OF INVENTION: HCV Core Protein Sequences
 FILE REFERENCE: CDS-0288
 CURRENT APPLICATION NUMBER: US/10/268,569
 CURRENT FILING DATE: 2002-10-10
 PRIOR APPLICATION NUMBER: 60/347,303
 PRIOR FILING DATE: 2001-11-11
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 16
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Hepatitis C virus
 US-10-268-569-16

Query Match 36.4% Score 4; DB 12; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5, 2e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 ARAL 4
 1111
 1b 3 ARAL 5

RESULT 20

US-10-014-322A-11
 Sequence 11, Application US/10014322A
 Publication No. US20030167129A1
 GENERAL INFORMATION:
 APPLICANT: Nestor, Jr., John
 APPLICANT: Wilson, Carol
 APPLICANT: Tan Behr, Christina
 APPLICANT: Kates, Steven
 APPLICANT: Krstenansky, John
 TITLE OF INVENTION: Binding Compounds and Methods for Identifying Binding Compou
 FILE REFERENCE: CNS-008
 CURRENT APPLICATION NUMBER: US/10/014,322A
 CURRENT FILING DATE: 2002-07-08
 PRIOR APPLICATION NUMBER: US 60/243,587
 PRIOR FILING DATE: 2000-10-27
 PRIOR APPLICATION NUMBER: US 09/813,651
 PRIOR FILING DATE: 2001-03-20
 PRIOR APPLICATION NUMBER: US 09/813,653
 PRIOR FILING DATE: 2001-03-20
 PRIOR APPLICATION NUMBER: US 09/813,448
 PRIOR FILING DATE: 2001-03-20
 NUMBER OF SEQ ID NOS: 126
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 11
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: CXCK4 binding peptide
 US-10-014-322A-11

Query Match 36.4% Score 4; DB 12; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5, 2e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 1 ARAL 4
 1111
 1b 2 ARAL 5

RESULT 21

US-10-174-105A-94
 Sequence 94, Application US/10174105A
 Publication No. US2003008652A1
 GENERAL INFORMATION:
 APPLICANT: Cell Signaling Technology, Inc.
 APPLICANT: ZHANG, Hui
 APPLICANT: COMB, Michael, Jr.
 APPLICANT: TAN, Yi
 TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PHOSPHO-PROTEINS USING MOTIF-SPBC
 FILE REFERENCE: CSI 138 CIP3
 CURRENT APPLICATION NUMBER: US/10/174,105A
 CURRENT FILING DATE: 2002-06-18
 PRIOR APPLICATION NUMBER: US 09/148,712
 PRIOR FILING DATE: 1998-09-04
 PRIOR APPLICATION NUMBER: US 09/535,364
 PRIOR FILING DATE: 2000-03-24
 NUMBER OF SEQ ID NOS: 193
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 94
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic Peptide
 NAME/KEY: MOD-RES
 LOCATION: (8)..(8)
 OTHER INFORMATION: PHOSPHORYLATION: threonine at position 8 is phosphorylated
 US-10-174-105A-94

```

Query Match          36.4% Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WQAK 9
      1111
Db      10 WQAK 13

RESULT 22
US-10-174-105A-95
: Sequence 95, Application US/10174.105A
: Publication No. US2003006852A1
: GENERAL INFORMATION:
: APPLICANT: Cell Signaling Technology, Inc.
: APPLICANT: ZHANG, Hui
: APPLICANT: COMB, Michael J.
: APPLICANT: TAN, Yi
: TITLE OF INVENTION: POSITIVE IDENTIFICATION OF PROSPECTED PROTEINS USING MOTIF-SPECIFIC
: TITLE OF INVENTION: CONTEXT-INDEPENDENT ANTIBODIES COUPLED WITH DATABASE SEARCHING
: FILE REFERENCE: CST-138 CIP3
: CURRENT APPLICATION NUMBER: US/10/174.105A
: CURRENT FILING DATE: 2002-06-18
: PRIOR APPLICATION NUMBER: US 09/148.712
: PRIOR FILING DATE: 1998-09-04
: PRIOR APPLICATION NUMBER: US 09/535.564
: PRIOR FILING DATE: 2000-03-24
: NUMBER OF SEQ ID NOS: 193
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 95
: LENGTH: 15
: TYPE: PRI
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Synthetic Peptide
US-10-174-105A-95

Query Match          36.4% Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WQAK 9
      1111
Db      10 WQAK 13

RESULT 24
US-10-229-567-16
: Sequence 15, Application US/10229.567
: Publication No. US2003009280A1
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: APPLICANT: Cohavy, Ofer
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
: Microbial UC PANCA antigens
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION NUMBER: US/10/229.567
: FILING DATE: 27-Aug-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/417.264
: FILING DATE: <Unknown>
: APPLICATION NUMBER: US 09/041.889
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31.815
: REFERENCE/DOCKET NUMBER: P-PM 3006
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear

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: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/417.264
: FILING DATE: <Unknown>
: APPLICATION NUMBER: US 09/041.889
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31.815
: REFERENCE/DOCKET NUMBER: P-PM 3006
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 15:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-229-567-15

Query Match          36.4% Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 AKPK 11
      1111
Db      12 AKPK 15

RESULT 24
US-10-229-567-16
: Sequence 16, Application US/10229.567
: Publication No. US2003009280A1
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: APPLICANT: Cohavy, Ofer
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
: Microbial UC PANCA antigens
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION NUMBER: US/10/229.567
: FILING DATE: 27-Aug-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/417.264
: FILING DATE: <Unknown>
: APPLICATION NUMBER: US 09/041.889
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31.815
: REFERENCE/DOCKET NUMBER: P-PM 3006
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear

```

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: SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-229-567-16
Query Match 36.4%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 2 AKPK 5

RESULT 25
US-10-229-567-22
: Sequence 22, Application US/10229567
: Publication No. US20030092080A1
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: Cohavy, Offer
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
: Microbial UC PANCA antigens
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/417,264
: FILING DATE: <Unknown>
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US/10/229,567
: FILING DATE: 27-Aug-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/417,264
: FILING DATE: <Unknown>
: APPLICATION NUMBER: US/09/041,889
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-PM 3006
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-229-567-24
Query Match 36.4%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 4 AKPK 7

RESULT 27
US-10-229-567-35
: Sequence 35, Application US/10229567
: Publication No. US20030092080A1
: GENERAL INFORMATION:
: APPLICANT: Braun, Jonathan
: Cohavy, Offer
: TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
: Ulcerative Colitis, and Clinical Subtypes Thereof, Using
: Microbial UC PANCA antigens
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/229,567
: FILING DATE: 27-Aug-2002
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/09/417,264
: FILING DATE: <Unknown>
: APPLICATION NUMBER: US/09/041,889
: FILING DATE: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-PM 3006
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-10-229-567-22
Query Match 36.4%; Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 6 AKPK 9

RESULT 26
US-10-229-567-24
: Sequence 24, Application US/10229567
: Publication No. US20030092080A1
: GENERAL INFORMATION:

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,567
FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
FILING DATE: <Unknown>
APPLICATION NUMBER: US/09/417,264
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-28 4006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
US 10-229-567-35

Query Match 36.4%: Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 12 AKPK 15

RESULT 24
US 10-229-567-35

Sequence 16, Application US/10/229,567
Publication No. US20030092880A1
GENERAL INFORMATION:
APPLICANT: Braum, Jonathan
Cohavy, Ofer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
Glucagonoma, Insulinoma and Clinical Subtypes Thereof Using
Microbial or Pancreatic Antigen

NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Edwards LLP
STREET: 4470 La Jolla Village Drive Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/229,567
FILING DATE: 27-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/417,264
FILING DATE: <Unknown>
APPLICATION NUMBER: US/09/417,264
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-28 4006
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949

TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US 10-229-567-36

Query Match 36.4%: Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AKPK 11
DB 2 AKPK 5

RESULT 29
US 10-103-327-2

Sequence 2, Application US/10103327
Publication No. US20030106095A1
GENERAL INFORMATION:
APPLICANT: GARGER, Stephen A.
APPLICANT: TURPEN, Thomas H.
TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
PLANTS BY TRANSIENT EXPRESSION
FILE REFERENCE: 008010087CPS06
CURRENT APPLICATION NUMBER: US/10/103,327
CURRENT FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: US/09/993,059
PRIOR FILING DATE: 2001-11-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US 10-103-327-2

Query Match 36.4%: Score 4; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.2e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARAL 4
DB 5 ARAL 8

RESULT 30

US 09-756-283A 51
Sequence 51, Application US/09756283A
Patent No. US20020151478A1
GENERAL INFORMATION:
APPLICANT: Chernajovsky, Yuri
APPLICANT: Dreja, Hanna Stina
APPLICANT: Adams, Gillian
TITLE OF INVENTION: Latent Fusion Protein
FILE REFERENCE: 0623.100000
CURRENT APPLICATION NUMBER: US/09/756,283A
CURRENT FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
SEQ ID NO 51
LENGTH: 8
TYPE: PRT
ORGANISM: Rattus sp.
US 09-756-283A-51

Query Match 27.4%: Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;

```
Matches 3: Conservative 27 Mismatches 0 Indels 0 Gaps 0
QY 7 GAK 9
   III
DB 1 GAK 3

RESULT 31
US-09-778-200-3
: Sequence 3, Application US/09/778200
: Patent No. US20020160471A1
: GENERAL INFORMATION:
: APPLICANT: Kisiday, John
: APPLICANT: Grodzinsky, Alan
: APPLICANT: Zhang, Shuquan
: TITLE OF INVENTION: Peptide Scaffold Encapsulation of Tissue
: FILE REFERENCE: 01997/537001
: CURRENT APPLICATION NUMBER: US/09/778,200
: CURRENT FILING DATE: 2000-02-06
: NUMBER OF SEQ ID NOS: 43
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 3
: TYPE: PRI
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Designed Peptide
US-09-778-200-9

Query Match 27.3% Score 3: DB 10: Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 3: Conservative 0 Mismatches 0 Indels 0 Gaps 0;

QY 1 ARA 3
   III
DB 4 ARA 6

RESULT 34
US-09-910-552-43
: Sequence 43, Application US/09/910552
: Publication No. US20020197260A1
: GENERAL INFORMATION:
: APPLICANT: Grubisic, Dan M.
: APPLICANT: Mac, Gregory R.
: TITLE OF INVENTION: USE OF FUNCTIONAL ANTIBODIES THAT DEFINE UNIQUE
: FILE REFERENCE: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
: FILE REFERENCE: COMPOSITIONS
: CURRENT APPLICATION NUMBER: US/09/910,552
: CURRENT FILING DATE: 2001-07-23
: PRIOR APPLICATION NUMBER: 09/494,822
: PRIOR FILING DATE: 2000-01-31
: NUMBER OF SEQ ID NOS: 68
: SOFTWARE: Patent Ver. 2.0
: SEQ ID NO 43
: LENGTH: 8
: TYPE: PRI
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: sequence from
US-09-910-552-43

Query Match 27.3% Score 3: DB 10: Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 3: Conservative 0 Mismatches 0 Indels 0 Gaps 0;

QY 3 ALN 5
   III
DB 5 ALN 7

RESULT 35
US-09-726-470A-68
: Sequence 68, Application US/09/726470A
: Publication No. US20030046628A1
: GENERAL INFORMATION:
: APPLICANT: Zheleva, Daniela I
: APPLICANT: Fischer, Peter M
: APPLICANT: McInnes, Campbell
```

APPLICANT: Andrews, Martin JI
APPLICANT: Chan, Weng C
APPLICANT: Atkinson, Gail E
TITLE OF INVENTION: p21 Peptides
FILE REFERENCE: CCI-014
CURRENT APPLICATION NUMBER: US/09/726.470A
CURRENT FILING DATE: 2000-11-24
PRIOR APPLICATION NUMBER: GB 992812A.1
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 275
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 68
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: p21 derived
OTHER INFORMATION: peptide
FEATURE:
OTHER INFORMATION: Synthesised with free amino terminus and as the
OTHER INFORMATION: C-terminal carboxamide
US-09-726-470A-68

Query Match 27.38; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 KPK 4

DB 4 KPK 6

RESULT 36
US-09-726-470A-125
Sequence 125, Application US/09/726.470A
Publication No. US20030036628A1
GENERAL INFORMATION:
APPLICANT: Zheleva, Daniela I
APPLICANT: Fischer, Peter M
APPLICANT: McInnes, Campbell
APPLICANT: Andrews, Martin JI
APPLICANT: Chan, Weng C
APPLICANT: Atkinson, Gail E
TITLE OF INVENTION: p21 Peptides
FILE REFERENCE: CCI-014
CURRENT APPLICATION NUMBER: US/09/726.470A
CURRENT FILING DATE: 2000-11-24
PRIOR APPLICATION NUMBER: GB 992812A.1
PRIOR FILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 275
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 125
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: p21 derived
OTHER INFORMATION: peptide
FEATURE:
OTHER INFORMATION: Synthesised with free amino terminus and as the
OTHER INFORMATION: C-terminal carboxamide
FEATURE:
NAME/KEY: SITE
LOCATION: (6)
OTHER INFORMATION: p-Fluorophenylalanine
US-09-726-470A-125

Query Match 27.38; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9

DB 111

DB 1 GAK 3

RESULT 37

US-09-876-904A-57
Sequence 57, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: IB-2002-00
CURRENT APPLICATION NUMBER: US/09/876.904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/216,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 57
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic Chicken Ets1
OTHER INFORMATION: Core NLS peptide
US-09-876-904A-57

Query Match 27.4%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11

DB 6 KPK 8

RESULT 38

US-09-876-904A-537
Sequence 537, Application US/09876904A
Publication No. US20030072794A1
GENERAL INFORMATION:
APPLICANT: BOULIKAS, TENI
TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
TITLE OF INVENTION: CONJUGATES INTO TARGETED LIPOSOME COMPLEXES
FILE REFERENCE: IB-2002-00
CURRENT APPLICATION NUMBER: US/09/876.904A
CURRENT FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/216,925
PRIOR FILING DATE: 2000-06-09
NUMBER OF SEQ ID NOS: 629
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 537
LENGTH: 8
TYPE: PRT
ORGANISM: Xenopus laevis
FEATURE:
OTHER INFORMATION: Xenopus laevis t1 ribosomal protein (homologous to
OTHER INFORMATION: yeast L2).
US-09-876-904A-537

Query Match 27.4%; Score 3; DB 11; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11

DB 2 KPK 4

RESULT 39

US-10-079-167-4

```
; Sequence 4, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Reece, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; CURRENT APPLICATION NUMBER: US/10/079,167
; PRIOR FILING DATE: 2002-02-19
; PRIOR FILING DATE: 2002-02-19
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/03681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 24204.3
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CTL Epitope of the Malaria Strain
US-10-079-167-4

Query Match      27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 KPK 11
DB      1 KPK 3

RESULT 40
US-10-350-258-2
; Sequence 2, Application US/10350258
; Publication No. US20030139345A1
; GENERAL INFORMATION:
; APPLICANT: MATTHIAS RATH
; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND METHODS FOR TREATING CANCER INVASION AND METASTASIS
; FILE REFERENCE: 11957/23
; CURRENT APPLICATION NUMBER: US/10/350,258
; CURRENT FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: 60/351,317
; PRIOR FILING DATE: January 23, 2002
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-350-258-2

Query Match      27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 KPK 11
DB      3 KPK 5

RESULT 41
US-10-209-187A-4
; Sequence 4, Application US/10209187A
; Publication No. US20030148383A1
; GENERAL INFORMATION:
; APPLICANT: Maurer-Stroh, Sebastian
; APPLICANT: Eisenhaber, Birgit
; TITLE OF INVENTION: Methods for Identifying Proteins with N-Terminal N-Myristoyle
; FILE REFERENCE: 0652.2560000
; CURRENT APPLICATION NUMBER: US/10/209,187A
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: EP 01 118 627.7
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Synthetic octapeptide
US-10-209-187A-4

Query Match      27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 KPK 11
DB      6 KPK 8

RESULT 42
US-10-209-187A-5
; Sequence 5, Application US/10209187A
; Publication No. US20030148383A1
; GENERAL INFORMATION:
; APPLICANT: Maurer-Stroh, Sebastian
; APPLICANT: Eisenhaber, Birgit
; TITLE OF INVENTION: Methods for Identifying Proteins with N-Terminal N-Myristoyle
; FILE REFERENCE: 0652.2560000
; CURRENT APPLICATION NUMBER: US/10/209,187A
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: EP 01 118 627.7
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Synthetic octapeptide
US-10-209-187A-5

Query Match      27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ARA 3
DB      2 ARA 4

RESULT 43
US-10-283-423-51
; Sequence 51, Application US/10283423
; Publication No. US20030162223A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David F.
; APPLICANT: Smith, Vaidin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Methods For Their Use
```



```

: TITLE OF INVENTION: Related To The Same
: FILE REFERENCE: PHRM0002-102
: Application Project
:
: CURRENT APPLICATION NUMBER: US/10/283.423
: CURRENT FILING DATE: 2002-10-30
: Earlier Applications
:
: PRIOR APPLICATION NUMBER: PriorAppNumber: 10/283.423
: PRIOR FILING DATE: PriorFilingDate: 2000-10-20
: PRIOR APPLICATION NUMBER: PriorAppNumber: 10/283.423
: PRIOR FILING DATE: PriorFilingDate: 1999-10-22
: NUMBER OF SEQ ID NOS: 187
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 51
: LENGTH: 6
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: No. US20030162223A1; Sequence
US 10-283-423 5;

Query Match          27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9
DB 2 GAK 4

RESULT 44
US-10-283-423-80
: Sequence 80, Application US/10/283.423
: Publication No. US20030162223A1
: GENERAL INFORMATION:
: APPLICANT: Lowery, David E.
: APPLICANT: Smith, Valdin G.
: APPLICANT: Kubiak, Teresa M.
: APPLICANT: Larsen, Martha J.
: TITLE OF INVENTION: Drosophila G Protein-Coupled Receptors, Nucleic Acids, And Method
: TITLE OF INVENTION: Related To The Same
: FILE REFERENCE: PHRM0002-102
: Application Project
:
: CURRENT APPLICATION NUMBER: US/10/283.423
: CURRENT FILING DATE: 2002-10-30
: Earlier Applications
:
: PRIOR APPLICATION NUMBER: PriorAppNumber: 10/283.423
: PRIOR FILING DATE: PriorFilingDate: 2000-10-20
: PRIOR APPLICATION NUMBER: PriorAppNumber: 10/283.423
: PRIOR FILING DATE: PriorFilingDate: 1999-10-22
: NUMBER OF SEQ ID NOS: 187
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 80
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: No. US20030162223A1; Sequence
US 10-283-423-80

Query Match          27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9
DB 2 GAK 4

RESULT 45
US-10-283-423-80
: Sequence 80, Application US/10/283.423
: Publication No. US20030162223A1
: GENERAL INFORMATION:
: APPLICANT: Lowery, David E.
: APPLICANT: Smith, Valdin G.
: APPLICANT: Kubiak, Teresa M.
: APPLICANT: Larsen, Martha J.
: TITLE OF INVENTION: Drosophila G Protein-Coupled Receptors, Nucleic Acids, And Method
: TITLE OF INVENTION: Related To The Same
: FILE REFERENCE: PHRM0002-102
: Application Project
:
: CURRENT APPLICATION NUMBER: US/10/283.423
: CURRENT FILING DATE: 2002-10-30
: Earlier Applications
:
: PRIOR APPLICATION NUMBER: PriorAppNumber: 10/283.423
: PRIOR FILING DATE: PriorFilingDate: 2000-10-20
: PRIOR APPLICATION NUMBER: PriorAppNumber: 10/283.423
: PRIOR FILING DATE: PriorFilingDate: 1999-10-22
: NUMBER OF SEQ ID NOS: 187
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 80
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: No. US20030162223A1; Sequence
US 10-283-423-80

Query Match          27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9
DB 2 GAK 4

RESULT 46
US-10-224-999A-1325
: Sequence 1325, Application US/10/224.999A
: Publication No. US20030171318A1
: GENERAL INFORMATION:
: APPLICANT: Myriad Genetics, Inc.
: APPLICANT: Morham, Scott
: APPLICANT: Zavitz, Kenton
: APPLICANT: Hobden, Adrian
: TITLE OF INVENTION: Composition and Method for Treating Viral Infection
: FILE REFERENCE: 5004.01
: CURRENT APPLICATION NUMBER: US/10/224.999A
: CURRENT FILING DATE: 2003-03-03
: PRIOR APPLICATION NUMBER: US 60/313,695
: PRIOR FILING DATE: 2001-08-20
: NUMBER OF SEQ ID NOS: 3484
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 1325
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Human papillomaviruses
US-10-224-999A-1325

Query Match          27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 6 KPK 8

RESULT 47
US-10-224-999A-1326
: Sequence 1326, Application US/10/224.999A
: Publication No. US20030171318A1
: GENERAL INFORMATION:
: APPLICANT: Myriad Genetics, Inc.
: APPLICANT: Morham, Scott
: APPLICANT: Zavitz, Kenton
: APPLICANT: Hobden, Adrian
: TITLE OF INVENTION: Composition and Method for Treating Viral Infection
: FILE REFERENCE: 5004.01
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; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1326
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-224-999A-1326

Query Match 27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KPK 11
DB 5 KPK 7

RESULT 48
US-10-293-580-41
; Sequence 41, Application US/10/293580
; Publication No. US20030170767A1
; GENERAL INFORMATION:
; APPLICANT: Aurora Biosciences Corporation
; TITLE OF INVENTION: Fluorescent Protein Sensors of Post-Translational Modifications
; FILE REFERENCE: AU01270 (08366/G31001)
; CURRENT APPLICATION NUMBER: US/10/293,580
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US/09/129,192
; PRIOR FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Adenovirus endoproteidase
US-10-293-580-41

Query Match 27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GAK 9
DB 4 GAK 5

RESULT 49
US-10-192-832-5
; Sequence 3, Application US/10192832
; Publication No. US20030176335A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, SHUGUANG
; APPLICANT: VAUTHEY, SYLVAIN
; TITLE OF INVENTION: SURFACTANT PEPTIDE NANOSTRUCTURES, AND USES THEREOF
; FILE REFERENCE: MTV-043.01
; CURRENT APPLICATION NUMBER: US/10/192,832
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/304,256
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-192-832-5

Query Match 27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARA 3
DB 4 ARA 6

RESULT 50
US-10-192-832-5
; Sequence 5, Application US/10192832
; Publication No. US20030176335A1
; GENERAL INFORMATION:
; APPLICANT: ZHANG, SHUGUANG
; APPLICANT: VAUTHEY, SYLVAIN
; TITLE OF INVENTION: SURFACTANT PEPTIDE NANOSTRUCTURES, AND USES THEREOF
; FILE REFERENCE: MTV-043.01
; CURRENT APPLICATION NUMBER: US/10/192,832
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/304,256
; PRIOR FILING DATE: 2001-07-10
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-192-832-5

Query Match 27.3%; Score 3; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARA 3
DB 2 ARA 4

Search completed: September 30, 2003, 10:32:54
Job time: 24.5 secs

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OM protein - protein search, using sw model

Run 06: September 30, 2003, 15:07:04 : Search time : 1.333 Seconds
(waypoint alignments)
93,440 Million cell updates/sec

File: US-09-787-443-4

Perfect score: 11

Sequence: AGSAVKLKKA III

Scoring table: UL:GO Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 6

Total number of hits satisfying chosen parameters.

Maximum: 88 seconds length: 8

Maximum 03 seq length: 15

Post-processing: Listing first 500 summaries

Database ; PIR_76: *

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Database:
PRK_70:
1: pirl:
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1: pir1:
2: pir2:
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z:=pir2;
      }:=pir3;
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3: birds:
4: birds:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query		Length	DB	Hit	Description
		Match	%				
1	4	36.4		9	2	A3576	xylose isomerase (
2	4	36.4		13	2	B6424	hypothetical prote
3	4	36.4		13	2	S01904	glucan-transporting
4	4	36.4		14	2	S14864	methyl-enzyme M-1
5	3	27.3		18	2	A47934	apolipoprotein A-1
6	3	27.3		9	2	I54379	gene NF2 protein -
7	3	27.3		9	2	PT0425	14 heavy chain C1g
8	3	27.3		9	2	P07376	spectrin alpha cha
9	3	27.3		11	2	A47555	20 alpha-hydroxys
10	3	27.3		11	2	S33519	probable secreted
11	3	27.3		11	2	D57783	galbladder stone
12	3	27.3		11	2	P00941	F-cell receptor be
13	3	27.3		11	2	P00334	dextranase (EC
14	3	27.3		12	2	C58502	58k kille and galb
15	3	27.3		13	2	S78519	ribosomal protein
16	3	27.3		13	2	S43210	cellulose alpha (V
17	3	27.3		13	2	S32475	lynnanamide 3 - a
18	3	27.3		14	2	P03109	porin por IB - Ara
19	3	27.3		14	2	B34135	DNA binding protei
20	3	27.3		14	2	S14336	mastoparan B - hor
21	3	27.3		14	2	A47421	leukotriene B-4 12
22	3	27.3		14	2	P00800	T-cell receptor al
23	3	27.3		14	2	P02010	T-cell receptor al
24	3	27.3		14	4	S00843	hypothetical prote
25	3	27.3		15	2	S21240	alpha-glucosidase
26	3	27.3		15	2	P00116	hemoglobin beta ch
27	3	27.3		15	2	P06117	hemoglobin alpha c
28	3	27.3		15	2	S36896	ribosomal protein
29	3	27.3		15	2	S14744	3-hydroxyphospho

103	2	18.2	9	2	A33527	fructose-2,6-bisph	176	2	18.2	11	2	YHXAE	morphogenetic neur
104	2	18.2	9	2	I52974	seminal vesicle pr	177	2	18.2	11	2	YHJFHY	morphogenetic neur
105	2	18.2	9	2	B30572	T-cell receptor be	178	2	18.2	11	2	B26744	megascoliakinin
106	2	18.2	9	2	S78426	52.5K protein - sp	179	2	18.2	11	2	S42449	anti-protein - pha
107	2	18.2	9	2	PC7073	uniquinol cytochro	180	2	18.2	11	2	A38502	38K kidney stone p
108	2	18.2	9	4	I73804	hypothetical E2 pr	181	2	18.2	11	2	F58501	43.5K bile stone p
109	2	18.2	10	1	EC123M	tachykinin 111 - m	182	2	18.2	11	2	JQ0395	hypothetical prote
110	2	18.2	10	2	S28055	cytochrome b559 co	183	2	18.2	11	2	S66606	hypothetical prote
111	2	18.2	10	2	C26497	unspecific monooxy	184	2	18.2	11	2	S58244	pyroloquinoline q
112	2	18.2	10	2	A43405	6-phosphofructo 2-	185	2	18.2	11	2	B43669	hypothetical prote
113	2	18.2	10	2	S24190	tryptase (EC 3.4.2	186	2	18.2	11	2	E41476	probable antigen 5
114	2	18.2	10	2	S33844	alpha-2-macroglobu	187	2	18.2	11	2	S70338	napin small chain
115	2	18.2	10	2	PG0177	neumomedin C - lau	188	2	18.2	11	2	S19775	wound-induced prot
116	2	18.2	10	2	A60547	neumomedin C - bov	189	2	18.2	11	2	A38590	transforming protei
117	2	18.2	10	2	I36893	apelinoprotein A-1	190	2	18.2	11	2	A34135	DNA-binding protei
118	2	18.2	10	2	C45474	thrombospondin 2 -	191	2	18.2	11	2	A61512	variant surface gl
119	2	18.2	10	2	C60787	sperm-activating p	192	2	18.2	11	2	S43626	cytochrome-c oxida
120	2	18.2	10	2	E60787	sperm-activating p	193	2	18.2	11	2	D42965	talin - chicken (f
121	2	18.2	10	2	E60584	sperm-activating p	194	2	18.2	11	2	S21727	gamma-interferon-1
122	2	18.2	10	2	H60586	gastric juice pept	195	2	18.2	11	2	PT0287	Ig heavy chain CRD
123	2	18.2	10	2	GXHU1	neurokinin A-relat	196	2	18.2	11	2	S57575	T-cell receptor V-
124	2	18.2	10	2	S27178	pneumadin - human	197	2	18.2	11	2	S51732	T-cell receptor al
125	2	18.2	10	2	B33143	pneumadin - rat	198	2	18.2	11	2	A32428	amine oxidase (cop
126	2	18.2	10	2	A61617	ecdysteroid upfqlu	199	2	18.2	11	2	A61483	pyridoxal kinase (
127	2	18.2	10	2	G58561	48K bile/gallblad	200	2	18.2	11	2	PD0442	NIPSNAP2 protein -
128	2	18.2	10	2	A24467	amicyanin - Paraco	201	2	18.2	11	2	PN0044	protein kinase C 1
129	2	18.2	10	2	S06954	hypothetical prote	202	2	18.2	11	2	PT0209	T-cell receptor al
130	2	18.2	10	2	JF0072	ribosomal protein	203	2	18.2	11	2	PT0218	T-cell receptor be
131	2	18.2	10	2	C39745	sphingomyelinase -	204	2	18.2	11	2	D41946	T-cell receptor ga
132	2	18.2	10	2	S69159	cystathionine gamm	205	2	18.2	11	2	B41946	T-cell receptor ga
133	2	18.2	10	2	C38925	seed storage prote	206	2	18.2	11	2	C38887	T-cell receptor ga
134	2	18.2	10	2	S70346	napin small chain	207	2	18.2	11	2	I41946	T-cell receptor ga
135	2	18.2	10	2	S66248	processing enzyme,	208	2	18.2	11	2	A49037	TCR gamma V-J regi
136	2	18.2	10	2	I28027	protein p7 - curle	209	2	18.2	11	2	B49037	TCR gamma V-J regi
137	2	18.2	10	2	PT0038	glutathione transt	210	2	18.2	11	2	C49037	TCR gamma V-J regi
138	2	18.2	10	2	C61440	polylacturonase	211	2	18.2	11	2	PD0441	translation elonga
139	2	18.2	10	2	E61512	variant surface gl	212	2	18.2	11	2	S65377	cytochrome-c oxida
140	2	18.2	10	2	S19617	glutelin - polychaet	213	2	18.2	11	2	S09349	microtubule-associ
141	2	18.2	10	2	S65728	hemoglobin, extrac	214	2	18.2	11	2	S18385	NADP-cytochrome P4
142	2	18.2	10	2	A58315	neuropeptide FRFA	215	2	18.2	11	2	S78422	ribosomal protein
143	2	18.2	10	2	B61108	hemocyanin subunit	216	2	18.2	11	2	PH0939	T-cell receptor be
144	2	18.2	10	2	A42085	transcription fact	217	2	18.2	11	2	PH0940	T-cell receptor be
145	2	18.2	10	2	C44787	calliferramide 12	218	2	18.2	11	2	PH0947	T-cell receptor be
146	2	18.2	10	2	JNC025	mesact - sea urchi	219	2	18.2	11	2	PC2254	cytochrome P450 3A
147	2	18.2	10	2	A24196	acetylcholinestera	220	2	18.2	11	2	A34243	H-phosphorin - Ja
148	2	18.2	10	2	PT0342	cytochrome-c oxida	221	2	18.2	11	2	H84082	hypothetical prote
149	2	18.2	10	2	PH1444	Ig heavy chain CRD	222	2	18.2	11	4	I52708	ELAV-like neuronal
150	2	18.2	10	2	S24371	T-cell receptor al	223	2	18.2	11	4	U06081	retinoic acid rece
151	2	18.2	10	2	S10765	T-cell receptor al	224	2	18.2	12	1	U06082	urotensin II - lon
152	2	18.2	10	2	E49024	transcription fact	225	2	18.2	12	1	A43975	locustamyotrophin -
153	2	18.2	10	2	E10212	transcription fact	226	2	18.2	12	1	JTJG0	tremorogen A-10 -
154	2	18.2	10	2	PT0213	T-cell receptor al	227	2	18.2	12	2	A25169	phospholipase A2 (
155	2	18.2	10	2	E41946	T-cell receptor ga	228	2	18.2	12	2	S11286	exo-alpha-sialidas
156	2	18.2	10	2	A41946	T-cell receptor ga	229	2	18.2	12	2	S09082	protease chain 1
157	2	18.2	10	2	C41946	placental lactogen	230	2	18.2	12	2	C49215	urease (EC 3.5.1.5
158	2	18.2	10	2	A47464	cytochrome-c oxida	231	2	18.2	12	2	S25485	transcription fact
159	2	18.2	10	2	S65387	lysosome-associate	232	2	18.2	12	2	S42765	urotensin II - tel
160	2	18.2	10	2	PX0060	T-cell receptor be	233	2	18.2	12	2	J50423	urotensin II - A pep
161	2	18.2	10	2	C30572	T-cell receptor be	234	2	18.2	12	2	S26541	T-cell receptor be
162	2	18.2	10	2	PH0927	T-cell receptor be	235	2	18.2	12	2	S25056	Ig heavy chain - m
163	2	18.2	10	2	C54226	light-harvesting p	236	2	18.2	12	2	S65409	histone H2B - huma
164	2	18.2	10	2	A32156	Na+/K+-exchanging	237	2	18.2	12	2	A19233	myosin heavy chain
165	2	18.2	10	2	PA0116	ferredoxin-NADP re	238	2	18.2	12	2	S15815	translation elonga
166	2	18.2	10	2	PS0220	ferredoxin-NADP re	239	2	18.2	12	2	E45691	probable minor cap
167	2	18.2	10	2	S74147	glyceraldehyde 3-p	240	2	18.2	12	2	E58502	43.2K bile stone p
168	2	18.2	11	1	IFTAME	probable trypsin lea	241	2	18.2	12	2	G49215	urease (EC 3.5.1.5
169	2	18.2	11	2	S66196	alcohol dehydrogen	242	2	18.2	12	2	E64573	hypothetical prote
170	2	18.2	11	2	A33917	dihydroorotase (EC	243	2	18.2	12	2	S56122	type I DNA methyl
171	2	18.2	11	2	A38841	rhodopsin homolog	244	2	18.2	12	2	S71034	potB protein - Sal
172	2	18.2	11	2	YHRT	morphogenetic neur	245	2	18.2	12	2	A26093	microbial collagen
173	2	18.2	11	2	YHHC	morphogenetic neur	246	2	18.2	12	2	S34447	binr protein - Sta
174	2	18.2	11	2	YHHC	morphogenetic neur	247	2	18.2	12	2	A60757	enterotoxin C-1 -
175	2	18.2	11	2	YHHC	morphogenetic neur	248	2	18.2	12	2	D28551	hypothetical prote

249	2	18.2	12	2	140663	hma protein - Cios	322	2	18.2	13	2	A38929	glutathione peroxi
250	2	18.2	12	2	PA0019	acidic ribosomal p	323	2	18.2	13	2	PQ0445	utensin II - lau
251	2	18.2	12	2	PA0047	protein QAI00045	324	2	18.2	13	2	A28505	neutensin [valid
252	2	18.2	12	2	S67528	napin - rape (frag	325	2	18.2	13	2	A61067	neutensin - comm
253	2	18.2	12	2	S70337	napin small chain	326	2	18.2	13	2	B35245	histone H1.c - mou
254	2	18.2	12	2	JU0356	cycloleucurinin -	327	2	18.2	13	2	A35245	histone H1.c - mou
255	2	18.2	12	2	P00696	1,4-alpha-glucac b	328	2	18.2	13	2	A23695	myosin heavy chain
256	2	18.2	12	2	PS0213	28K protein 4412 -	329	2	18.2	13	2	A60336	outer membrane pro
257	2	18.2	12	2	PQ0730	unidentified 5.4/3	330	2	18.2	13	2	S01119	photosystem II pro
258	2	18.2	12	2	PN0170	alcohol dehydrogen	331	2	18.2	14	2	E37390	trAA protein - Esc
259	2	18.2	12	2	PN0162	ma-ate dehydrogena	332	2	18.2	13	2	E39778	lactose phosphotra
260	2	18.2	12	2	T46656	hypothetical protei	333	2	18.2	13	2	PN0122	alpha-2 collagen -
261	2	18.2	12	2	C34135	hema-binding protei	334	2	18.2	13	2	S01773	bombesin-like pept
262	2	18.2	12	2	S65730	hemoglobin, extrac	335	2	18.2	13	2	A60409	VCAM-1 5'UTR bindi
263	2	18.2	12	2	J50424	utensin II-B pep	336	2	18.2	13	2	A59487	alpha-peptide/alg
264	2	18.2	12	2	S10626	lipovitellin - Afr	337	2	18.2	13	2	P00038	hypothetical prote
265	2	18.2	12	2	A49261	coagulation factor	338	2	18.2	13	2	T08533	hypothetical prote
266	2	18.2	12	2	A55637	5-aminimidazole r	339	2	18.2	13	2	S22955	oxfx protein - Esc
267	2	18.2	12	2	S29830	dimethylamine mo	340	2	18.2	13	2	B36042	microbial collagen
268	2	18.2	12	2	I77529	estrogen receptor	341	2	18.2	13	2	B26093	preabsorbing anti
269	2	18.2	12	2	PT0274	ig heavy chain CRD	342	2	18.2	13	2	A46463	spore proteinase g
270	2	18.2	12	2	PT0319	ig heavy chain CRD	343	2	18.2	13	2	A61288	botulinum toxins -
271	2	18.2	12	2	S43957	ig mu chain V regi	344	2	18.2	13	2	A01825	botulinum toxins -
272	2	18.2	12	2	S43170	kinesin light chai	345	2	18.2	13	2	S36887	ribosomal protein
273	2	18.2	12	2	S47391	T-cell antigen rec	346	2	18.2	13	2	S23103	erythronolide synt
274	2	18.2	12	2	S47395	T-cell antigen rec	347	2	18.2	13	2	S20578	ribosomal protein
275	2	18.2	12	2	PH1190	T-cell receptor al	348	2	18.2	13	2	S14316	photosystem I 9K c
276	2	18.2	12	2	PH1187	T-cell receptor al	349	2	18.2	13	2	S38736	lipid transfer pro
277	2	18.2	12	2	PH1184	T-cell receptor al	350	2	18.2	13	2	PA0049	protein QAI00046 -
278	2	18.2	12	2	PH1182	T-cell receptor al	351	2	18.2	13	2	JN0310	insulin-binding pr
279	2	18.2	12	2	PH1185	T-cell receptor al	352	2	18.2	13	2	S00316	photosystem I 13K
280	2	18.2	12	2	PH1180	T-cell receptor al	353	2	18.2	13	2	S09733	photosystem I prot
281	2	18.2	12	2	PH1183	T-cell receptor al	354	2	18.2	13	2	S60046	early nodulin 40 -
282	2	18.2	12	2	PH1188	T-cell receptor al	355	2	18.2	13	2	JQ2309	hypothetical 1.6K
283	2	18.2	12	2	PH1172	T-cell receptor al	356	2	18.2	13	2	JQ2319	hypothetical 1.6K
284	2	18.2	12	2	PH1171	T-cell receptor al	357	2	18.2	13	2	PS0453	36K protein 3124 -
285	2	18.2	12	2	PH1175	T-cell receptor al	358	2	18.2	13	2	PS0250	ribulose-bisphosph
286	2	18.2	12	2	PH1174	T-cell receptor al	359	2	18.2	13	2	PS0325	tetrahydroberberin
287	2	18.2	12	2	PH1174	T-cell receptor al	360	2	18.2	13	2	PQ0700	unidentified 6.3/4
288	2	18.2	12	2	PH1181	T-cell receptor al	361	2	18.2	13	2	JQ1350	hypothetical prote
289	2	18.2	12	2	A49034	T-cell receptor de	362	2	18.2	13	2	PA0089	protein QF200053 -
290	2	18.2	12	2	B49033	T-cell receptor de	363	2	18.2	13	2	B60396	antigen 7H6/2 - ma
291	2	18.2	12	2	C49033	T-cell receptor de	364	2	18.2	13	2	S32471	lymnaDFamide 1 - g
292	2	18.2	12	2	A69528	insulin-like growt	365	2	18.2	13	2	S32472	lymnaDFamide 2 - g
293	2	18.2	12	2	S74196	3-hydroxy-3-methyl	366	2	18.2	13	2	S32474	lymnaDFamide 4 - g
294	2	18.2	12	2	A37933	ig lambda chain J	367	2	18.2	13	2	S32475	lymnaDFamide 5 - g
295	2	18.2	12	2	PN0563	dyatrophin-associ	368	2	18.2	13	2	S29488	GTP-binding protei
296	2	18.2	12	2	A20937	ig kappa chain J1	369	2	18.2	13	2	S09018	hemolytic protein
297	2	18.2	12	2	C20937	ig kappa-1 chain J	370	2	18.2	13	2	A60379	factor X activator
298	2	18.2	12	2	D20937	ig kappa-1 chain J	371	2	18.2	13	2	A57789	galbladder stone
299	2	18.2	12	2	P20937	ig kappa-2 chain J	372	2	18.2	13	2	S52356	hypothetical prote
300	2	18.2	12	2	S65626	phosphorylase b -	373	2	18.2	13	2	PT0305	ig heavy chain CRD
301	2	18.2	12	2	S60228	ig kappa chain J1	374	2	18.2	13	2	PH1316	ig heavy chain DJ
302	2	18.2	12	2	PH1635	ig H chain V-D-J r	375	2	18.2	13	2	PH1316	ig kappa chain V-I
303	2	18.2	12	2	PH1587	ig H chain V-D-J r	376	2	18.2	13	2	B61458	ig kappa chain V-I
304	2	18.2	12	2	PH1511	ig H chain V-D-J r	377	2	18.2	13	2	D61458	ig kappa chain V-I
305	2	18.2	12	2	A35520	inhibitory diffus	378	2	18.2	13	2	E61458	ig kappa chain V-I
306	2	18.2	12	2	PH1454	T-cell receptor al	379	2	18.2	13	2	G61458	ig lambda chain V-
307	2	18.2	12	2	PH1458	T-cell receptor be	380	2	18.2	13	2	PH1772	T cell receptor al
308	2	18.2	12	2	PH1457	T-cell receptor be	381	2	18.2	13	2	S57571	T cell receptor al
309	2	18.2	12	2	PH1459	T-cell receptor be	382	2	18.2	13	2	S57567	T cell antigen rec
310	2	18.2	12	2	S39762	cytochrome P450 Uf	383	2	18.2	13	2	S47361	T-cell antigen rec
311	2	18.2	12	2	A42324	cytochrome P450c27	384	2	18.2	13	2	S47372	T-cell antigen rec
312	2	18.2	12	2	PH0930	T-cell receptor be	385	2	18.2	13	2	S47373	T-cell antigen rec
313	2	18.2	12	2	PH0931	T-cell receptor be	386	2	18.2	13	2	S47383	T-cell antigen rec
314	2	18.2	12	2	PH0920	T-cell receptor be	387	2	18.2	13	2	S47384	T-cell antigen rec
315	2	18.2	12	2	PC4377	telomeric and tet	388	2	18.2	13	2	S47388	T-cell antigen rec
316	2	18.2	12	2	S71380	lebetin 1 isoform	389	2	18.2	13	2	S23372	T-cell receptor al
317	2	18.2	12	2	PD0021	muconate cyclisom	390	2	18.2	13	2	PH0138	T-cell receptor be
318	2	18.2	12	2	A55524	ubiquinol cytochr	391	2	18.2	13	2	B61233	conceptus protein
319	2	18.2	12	4	PC2123	aminotransferase c	392	2	18.2	13	2	S66235	sperm motility inh
320	2	18.2	12	4	S49073	frame shifted cya	393	2	18.2	13	2	S78766	ribosomal protein
321	2	18.2	13	1	UNOPRT	neutrotenin - brus	394	2	18.2	13	2	B20907	ig kappa-1 chain J

A:Authors: Gohm, G.L.; McDonald, L.A.; Small, K.V.; Fraser, P.M.; Smith, H.O.; Venter, A.; Title: Whole genome random sequencing and assembly of *Haemophilus influenzae* Rd.
 A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:Accession: H64124
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-13 <TIGR>
 A:Cross-references: GB:032824; GB:14203; NID:01574299; PID:01574306; TIGR:H11460

Query Match 36.4%; Score 4; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 5; 1e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VKLK 8
 DB 3 VKLK 6

RESULT 3
 S01904
 H:Transporting two-sector ATPase (EC 3.6.3.14) beta chain - Arabidopsis thaliana chloroplast
 C:Species: Chloroplast Arabidopsis thaliana (mouse-ear cress)
 C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 03-Jun-2002
 C:Accession: S01904
 R:Chen, H.C.; Wintz, H.; Weil, J.H.; Pillay, D.; N
 Nucleic Acids Res. 16, 10372, 1988
 A:Title: Nucleotide sequence of chloroplast CF1-ATPase epsilon subunit and elongator ERN
 A:Reference number: S01903; MUID:89057486; PMID:240414
 A:Accession: S01904
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-15 <CHES>
 A:Cross-references: EMBL:X14889; NID:011162; PID:0AA14961; PID:0825297
 C:Genetics: atpB
 A:Gene: atpB
 A:Genome: chloroplast
 C:Keywords: ATP biosynthesis; chloroplast; hydrolase; thylakoid

Query Match 36.4%; Score 4; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 5; 1e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9
 DB 10 KLKK 13

RESULT 4
 S13864
 methyl coenzyme M reductase (EC 1.8.1.7) from strain Methanobacterium thermophilum
 C:Species: Methanobacterium thermophilum
 A:Variety: strain Marburg
 C:Date: 19-Mar-1997 #sequence_revision 19-Sep-1997 #text_change 30-Oct-1998
 C:Accession: S13864
 R:Rospert, S.; Binder, D.; Ellermann, J.; Hammer, K.K.
 Eur. J. Biochem. 194, 871-877, 1996
 A:Title: Two genetically distinct methyl coenzyme M reductases in Methanobacterium thermophilum
 A:Reference number: S13864; MUID:01093470; PMID:225700
 A:Accession: S13864
 A:Molecule type: protein
 A:Residues: 1-14 <ROS>
 A:Experimental source: strain Marburg
 C:Keywords: methanogenesis; oxidoreductase

Query Match 36.4%; Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5; 4e-02;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 LKKK 10
 DB 11 LKKK 14

RESULT 5
 I48934
 apolipoprotein A-II - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: I48934
 R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, Mamm. Genome 5, 349-355, 1994
 A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
 A:Reference number: I48934; MUID:94319082; PMID:8043949
 A:Accession: I48934
 A:Status: preliminary; translated from GR/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-8 <RES>
 A:Cross-references: EMBL:U05691; NID:0497010; PID:0AAB60462.1; PID:0642826

Query Match 27.3%; Score 3; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2; 8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4
 DB 4 GSA 6

RESULT 6
 I54379
 gene NF2 protein - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
 C:Accession: I54379
 R:Arai, E.; Ikeuchi, T.; Nakamura, Y.
 Hum. Mol. Genet. 3, 937-939, 1994
 A:Title: Characterization of the translocation breakpoint on chromosome 22q12.2 in a
 A:Reference number: I54379; MUID:95038750; PMID:7951241
 A:Accession: I54379
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-9 <RES>
 A:Cross-references: GB:S75841; NID:0861532; PID:0AAD14190.1; PID:04261890
 C:Genetics: NF2
 A:Gene: GDB:NF2
 A:Cross-references: GDB:126242; OMIM:101000
 A:Map position: 22q12.2-22q12.2

Query Match 27.3%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2; 8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKK 8
 DB 4 KKK 6

RESULT 7
 PT0225
 Ig heavy chain CDR3 region (clone 1-103) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0225
 R:Yamada, M.; Wasserman, K.; Reichard, H.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 355-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity 2
 A:Reference number: PT0225; MUID:91108337; PMID:1899102
 A:Accession: PT0225
 A:Molecule type: DNA
 A:Residues: 1-9 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 27.3%; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2; 8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGS 4
 III
 DB 7 AGS 9

RESULT 8
 PC7076
 Spectrin alpha chain, non-erythrocyte (fragment)
 N:Alternate names: fodrin alpha chain
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Aug-2000 #sequence_revision 18 Aug 2000 #text_change 14 Aug 2000
 C:Accession: PC7076
 R:Tsukida, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kana, M.; Matsui, I.; Watanabe, Y.
 Electrophoresis 21: 1853-1871, 2000
 A:Title: Proteome analysis of mouse brain: two dimensional electrophoresis profiles of
 A:Reference number: PC7076
 A:Accession: PC7076
 A:Molecule type: protein
 A:Residues: 1-9 <TSU>
 A:Experimental source: strain C57BL/6J Slc, male; brain, striatum
 C:Keywords: brain

Query Match 27.38; Score 3; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2 8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KKK 10
 III
 DB 6 KKK 5

RESULT 9
 A44755
 20alpha hydroxysteroid dehydrogenase (EC 1.1.1.147) cDNA from sea lamprey
 C:Species: Glostetridium scindens
 C:Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 17-Mar-1999
 C:Accession: A44755
 R:Kallits, A.E.; Hylemon, P.B.
 J. Biol. Chem. 268: 2925-2932, 1993
 A:Title: Purification and characterization of a novel form of 20alpha hydroxysteroid dehydrogenase (A44755) MUD:625504; PMID:2722796
 A:Reference number: A44755
 A:Accession: A44755
 A:Molecule type: protein
 A:Residues: 1-11 <KRA>
 C:Comment: This enzyme was purified to homogeneity and shown to have 20alpha hydroxysteroid dehydrogenase (GAPDH) activity and the fragment shows heat stability to known
 C:Keywords: hemotetrimer; NAD; NADP; oxidoreductase

Query Match 27.38; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1 1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AVK 6
 III
 DB 1 AVK 3

RESULT 10
 S33519
 Probable secreted protein - Acholeplasma laidlawii (fragment)
 C:Species: Acholeplasma laidlawii
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Oct-1999
 C:Accession: S33519
 R:Boyer, M.J.; Jarhede, T.K.; Tegmar, V.; Wieslander, A.
 submitted to the EMBL Data Library, June 1993
 A:Description: Sequence regions from Acholeplasma laidlawii which restore export of beta
 A:Reference number: S33518
 A:Accession: S33519
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-11 <ROY>
 A:Cross-references: EMBL:222875; NID:331176; PID:CA89049; FID:3311708

Query Match 27.38; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKK 8
 III
 DB 3 KKK 5

RESULT 11
 C57789
 Gallbladder stone matrix protein, 14.5K - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 23-Feb-1996
 C:Accession: C57789
 R:Binette, J.P.; Binette, M.F.
 submitted to the Protein Sequence Database, February 1996
 A:Description: The proteins of gallbladder stones.
 A:Reference number: A57789
 A:Accession: C57789
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-11 <BIN>

Query Match 27.38; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGS 3
 III
 DB 7 AGS 9

RESULT 12
 PH0941
 T cell receptor beta chain V-D-J region (clone 12) - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 C:Accession: PH0941
 R:Good, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
 J. Exp. Med. 174: 1467-1476, 1991
 A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic encephalomyelitis
 A:Reference number: PH0941; MUD:92078857; PMID:1836012
 A:Accession: PH0941
 A:Molecule type: mRNA
 A:Residues: 1-11 <GGL>
 A:Experimental source: Complete Freund's adjuvant-immunized lymph node
 C:Keywords: T cell receptor

Query Match 27.38; Score 3; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SAV 5
 III
 DB 4 SAV 6

RESULT 13
 PU0034
 Dextranucrase (EC 2.4.1.5) Streptococcus bovis (fragment)
 C:Species: Streptococcus bovis
 C:Date: 01-Feb-1994 #sequence_revision 01-Feb-1994 #text_change 18-Sep-1996
 C:Accession: PU0034
 R:Dezono, Y.; Tsumori, H.; Mukasa, H.
 submitted to JIPID, October 1993
 A:Description: Purification and properties of glucosyltransferase synthesizing 1,6-a
 A:Reference number: PU0034
 A:Accession: PU0034
 A:Molecule type: protein
 A:Residues: 1-11 <DEZ>
 A:Experimental source: ATCC 9809

C:Keywords: glycosyltransferase; hexosyltransferase

Query Match: 27.3%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SAV 5

DB 4 SAV 6

RESULT 14

C58502

58K bile and gallbladder stone protein - unidentified bacterium (fragment)

C:Species: unidentified bacterium

C:Date: 07-Feb-1997 #sequence_revision 07 Feb 1997 #text_change 10-Jul-1998

C:Accession: C58502

R:Binette, J.P.; Binette, M.B.

A:Submitted to the Protein Sequence Database, October 1998

A:Description: The proteins of kidney and gallbladder stones.

A:Reference number: A58501

A:Accession: C58502

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-12 <BIN>

A:Experimental source: human bile and gallbladder stones

Query Match: 27.3%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4

DB 8 GSA 10

RESULT 15

S78519

Ribosomal protein S16, chloroplast - *Ginkgo biloba* (fragment)

C:Species: chloroplast *Ginkgo biloba* (fragment)

C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Jul-1998

C:Accession: S78519

R:Richard, M.; Tremblay, C.; Bellemare, G.

A:Gene: Genet. 26, 159-165, 1994

A:Title: Chloroplastic genomes of *Ginkgo biloba* and *Chlamydomonas monensis* contain a chl

A:Reference number: S45486; MUID:950943.3; PMID:950943

A:Molecule type: DNA

A:Residues: 1-13 <R1C>

A:Cross-references: EMBL:U01531

C:Genetics:

A:Gene: rps16

A:Genome: chloroplast

C:Superfamily: Escherichia coli ribosomal protein S16

C:Keywords: chloroplast; protein biosynthesis; ribosome

Query Match: 27.3%; Score 3; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VKL 7

DB 2 VKL 4

RESULT 16

S48210

collagen alpha 1(V) chain - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 15-Jul-1995 #sequence_revision 25-Jul-1996 #text_change 16-Feb 1997

C:Accession: S48210

R:Niyibizi, C.; Eyre, D.R.

A:Biochem. 224, 943-950, 1994

A:Title: Structural characteristics of cross-linking sites in type V collagen of bo

A:Reference number: S48210; MUID:95010086; PMID:7925418

A:Accession: S48210

A:Molecule type: protein

A:Residues: 1-13 <NIY>

C:Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homo

Query Match: 27.3%; Score 3; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGS 3

DB 10 AGS 12

RESULT 17

S32473

LymnaeaDFamide 3 - great pond snail

C:Species: Lymnaea stagnalis (great pond snail)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999

C:Accession: S32473

R:Johnsen, A.H.; Rehfeld, J.F.

A:Biochem. 213, 875-879, 1993

A:Title: LymnaeaDFamides, a new family of neuropeptides from the pond snail, Lymnaea s

A:Reference number: S32471; MUID:9423877; PMID:8477756

A:Accession: S32473

A:Molecule type: protein

A:Residues: 1-13 <JOH>

A:Cross-references: PIDN:AAB26364.1; PID:q299831

A:Experimental source: ganglia

C:Keywords: amidated carboxyl end; neuropeptide

F.13/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match: 27.3%; Score 3; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4

DB 7 GSA 9

RESULT 18

PA0109

porin por 1B - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 07-Apr-1995 #sequence_revision 26-May-1995 #text_change 30-Jun-1995

C:Accession: PA0109

R:Kamo, M.; Kawakami, I.; Tsugita, A.

A:Submitted to JIPID, March 1995

A:Reference number: PA0109

A:Accession: PA0109

A:Molecule type: protein

A:Residues: 1-14 <KAM>

A:Experimental source: root

Query Match: 27.3%; Score 3; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 5.3e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KKA 11

DB 12 KKA 14

RESULT 19

B34135

DNA-binding protein g - Crithidia fasciculata mitochondrion (fragment)

C:Species: mitochondrion Crithidia fasciculata

C:Date: 30-Sep 1991 #sequence_revision 30-Sep-1991 #text_change 07-Dec-1999

C:Accession: B34135

R:Tittawella, I.

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FEBS Lett. 260, 57-61, 1990
A:Title: Kinoplast DNA-aggregating proteins from the parasitic protozoan Crithidia fasciculata
A:Reference number: A34135
A:Accession: B34135
A:Molecule type: protein
A:Residues: 1-14 <TIT>
C:Genetics:
A:Genome: mitochondrion
A:Genetic code: SGC6
C:Keywords: mitochondrion

Query Match 27.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 KKA 11
DB 7 KKA 9

RESULT 20
S14336
mastoparan B - hornet (Vespa basalis)
C:Species: Vespa basalis
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Apr-1999
C:Accession: S14336
R:Ho, C.L.; Hwang, L.L.
Biochem. J. 274, 453-456, 1991
A:Title: Structure and biological activities of a new mastoparan isolated from the venom of Vespa basalis
A:Reference number: S14336; MUID:91174755; PMID:2006909
A:Accession: S14336
A:Molecule type: protein
A:Residues: 1-14 <HOC>
A:Experimental source: venom
A:Function:
A:Description: possesses a potent hemolytic activity which acts in synergy with the lethal venom of Vespa basalis
C:Keywords: amidated carboxyl end; mast cell; venom
F:14/Modified site: amidated carboxyl end (res) #status experimental

Query Match 27.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLK 8
DB 2 KLK 4

RESULT 21
A47421
leukotriene B 4 12-hydroxydehydrogenase (EC 1.1.1.13) (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 17-Mar-1999
C:Accession: A47421
R:Yokomizo, T.; Izumi, T.; Takahashi, T.; Kasama, T.; Kikayashi, Y.; Sato, F.; Taketani, J. Biol. Chem. 268, 18128-18135, 1993
A:Title: Enzymatic inactivation of leukotriene B 4 by a novel enzyme found in the porcine leukocyte
A:Reference number: A47421; MUID:93352633; PMID:8383941
A:Accession: A47421
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <YOK>
C:Keywords: oxidoreductase

Query Match 27.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKK 9
DB 8 LKK 10

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RESULT 22
PH0800
T-cell receptor alpha chain (J3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0800
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0800
A:Molecule type: mRNA
A:Residues: 1-14 <CAS>
A:Cross-references: EMBL:X60907
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 27.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4
DB 7 GSA 9

RESULT 23
PT0210
T-cell receptor alpha chain V-J region (4-1-K.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C:Accession: PT0210
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted
A:Reference number: PT0209; MUID:91217621; PMID:1902501
A:Accession: PT0210
A:Molecule type: mRNA
A:Residues: 1-14 <NAK>
C:Keywords: T-cell receptor

Query Match 27.3%; Score 3; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4
DB 11 GSA 13

RESULT 24
S00843
hypothetical protein ksqA 5'-region - Escherichia coli
C:Species: Escherichia coli
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: S00843
R:van Gemen, B.; Koets, H.J.; Plooy, C.A.M.; Bodlaender, J.; van Knippenberg, P.H.
Biochimie 69, 841-848, 1987
A:Title: Characterization of the ksqA gene of Escherichia coli determining kasugamycin resistance
A:Reference number: S00843; MUID:88107880; PMID:3122846
A:Accession: S00843
A:Molecule type: DNA
A:Residues: 1-14 <DNA>
A:Cross-references: EMBL:X06536; NID:q41884; PIDN:CAA29785.1; PID:q41885
C:Comment: This is the hypothetical translation of a sequence that was not reported

Query Match 27.3%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SAV 5
DB 11

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Db          2 SAV 4          Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

RESULT 25
S21240
alpha-glucosidase (EC 3.2.1.20) I - Bacillus "thermoamylobacteriens" (fragment)
C:Species: Bacillus "thermoamylobacteriens"
C:Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 27-Aug-1998
C:Accession: S21240
R:Suzuki, Y.; Yonezawa, K.; Hattori, M.; Takii, Y.
E: J. Biochem. 205, 249-256, 1992
A:Title: Assignment of Bacillus thermoamylobacteriens KPI071 alpha-glucosidase I to an
ence and in structural parameters calculated from the amino acid composition.
A:Reference number: S21202; MUID:92209510; PMID:1555585
A:Accession: S21240
A:Molecule type: protein
A:Residues: 1-15 <SUZ>
A:Experimental source: strain KPI071
C:Superfamily: alpha-glucosidase; alpha-amylose core homology
C:Keywords: glycosidase; hydrolase

Query Match          27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY          9 KKA 11
          III
Db          2 KKA 4

RESULT 26
PN0118
hemoglobin beta chain - red fox (fragment)
C:Species: Vulpes vulpes (red fox)
C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 13-May-2000
C:Accession: PN0118
R:Sukhomlinov, B.F.; Konoshenko, S.V.
Mol. Biol. (Mosk.) 5, 415-418, 1971
A:Title: Study on N-terminal sequence of the haemoglobin of Vulpes vulpes fox.
A:Reference number: PN0117
A:Accession: PN0118
A:Molecule type: protein
A:Residues: 1-15 <SUK>
C:Superfamily: globin; globin homology
C:Keywords: blood; erythrocyte; heme; heterotetramer; oxygen carrier;

Query Match          27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY          4 AVK 6
          III
Db          10 AVK 12

RESULT 27
PN0117
hemoglobin alpha chain - red fox (fragment)
C:Species: Vulpes vulpes (red fox)
C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 13-May-2000
C:Accession: PN0117
R:Sukhomlinov, B.F.; Konoshenko, S.V.
Mol. Biol. (Mosk.) 5, 415-418, 1971
A:Title: Study on N-terminal sequence of the haemoglobin of Vulpes vulpes fox.
A:Reference number: PN0117
A:Accession: PN0117
A:Molecule type: protein
A:Residues: 1-15 <SUK>
C:Superfamily: globin; globin homology
C:Keywords: blood; erythrocyte; heme; heterotetramer; oxygen carrier;

Query Match          27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY          4 AVK 6
          III
Db          10 AVK 12

Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY          4 AVK 6
          III
Db          8 AVK 10

RESULT 28
S36896
ribosomal protein S16 - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C:Accession: S36896
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Myc
A:Reference number: S36887; MUID:94009653; PMID:8405418
A:Accession: S36896
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <OHA>
C:Keywords: protein biosynthesis; ribosome

Query Match          27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY          4 AVK 6
          III
Db          1 AVK 3

RESULT 29
S14749
3-dehydroquinase - Neurospora crassa (fragment)
C:Species: Neurospora crassa
C:Date: 21-Nov-1993 #sequence_revision 01-Sep-1995 #text_change 01-Sep-1995
C:Accession: S14749
R:Chaudhuri, S.; Duncan, K.; Graham, L.D.; Coggins, J.R.
Biochem. J. 275, 1-6, 1991
A:Title: Identification of the active-site lysine residues of two biosynthetic 3-de
A:Reference number: S14749; MUID:91207275; PMID:1826831
A:Accession: S14749
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <CHA>

Query Match          27.3%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY          5 VKL 7
          III
Db          8 VKL 10

RESULT 30
G41299
T-cell receptor alpha chain precursor J region (39) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 05-Nov-1999
C:Accession: G41299
R:Uematsu, Y.; Wege, H.; Straus, A.; Ott, M.; Bannwarth, W.; Lanchbury, J.; Panayil,
Proc. Natl. Acad. Sci. U.S.A. 88, 8534-8538, 1991
A:Title: The T-cell-receptor repertoire in the synovial fluid of a patient with rheu
A:Reference number: A41299; MUID:92020887; PMID:1656449
A:Accession: G41299
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <DEM>
A:Cross-references: GB:S57457; NID:g236330; PIDN:AAB19962.1; PID:g236331
C:Keywords: T-cell receptor

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Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGS 3
 III
 7 AGS 9

DB

RESULT 31
 PH0775
 T-cell receptor alpha chain (B2B) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PH0775
 R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
 allelic exclusion and antigen-specific repertoire
 A:Reference number: PH0746; MUID:92078846; PMID:1836016
 A:Accession: PH0775
 A:Molecule type: mRNA
 A:Residues: 1-15 <CAS>
 A:Cross-references: EMBL:X60871
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4
 III
 6 GSA 8

DB

RESULT 32
 PH0779
 T-cell receptor alpha chain (B83) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PH0779
 R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
 allelic exclusion and antigen-specific repertoire
 A:Reference number: PH0746; MUID:92078846; PMID:1836016
 A:Accession: PH0779
 A:Molecule type: mRNA
 A:Residues: 1-15 <CAS>
 A:Cross-references: EMBL:X60877
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4
 III
 6 GSA 8

DB

RESULT 33
 PH1455
 T-cell receptor alpha chain (clone A24/PEP4) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 1; Apr-1995
 C:Accession: PH1455
 R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barillet, C.; Pannatier, C.; Reynault, A.; Ko
 J. Exp. Med. 177, 811-820, 1993
 A:Title: T cell receptor selection by and recognition of two class I major histocompatib
 A:Reference number: PH1430; MUID:93171421; PMID:8445911

A:Accession: PH1455
 A:Molecule type: mRNA
 A:Residues: 1-15 <CAS>
 A:Experimental source: cytolytic T-lymphocyte
 C:Superfamily: immunoglobulin homology
 C:Keywords: receptor; T-cell

Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4
 III
 6 GSA 8

DB

RESULT 34
 A49887
 Transcription factor HNF-1 beta - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 07-May-1999
 C:Accession: A49887
 R:Sasaki, H.; Hogan, B.L.M.
 Cell 76, 103-115, 1994
 A:Title: HNF-3beta as a regulator of floor plate development.
 A:Reference number: A49887; MUID:94116056; PMID:8287471
 A:Accession: A49887
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-15 <SAS>
 C:Keywords: alternative initiators; alternative splicing; transcription factor

Query Match 27.1% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AVK 6
 III
 10 AVK 12

DB

RESULT 35
 S09073
 Cytochrome P450-3b - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1993
 C:Accession: S09073
 R:Imaoka, S.; Terano, Y.; Funae, Y.
 Arch. Biochem. Biophys. 278, 168-178, 1990
 A:Title: Changes in the amount of cytochrome P450s in rat hepatic microsomes with st
 A:Reference number: S09072; MUID:90210577; PMID:2321956
 A:Accession: S09073
 A:Molecule type: protein
 A:Residues: 1-15 <IMA>

Query Match 27.3% Score 3; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGS 3
 III
 5 AGS 7

DB

RESULT 36
 PL0110
 complement factor B1-Bb and B2-Bb - guinea pig (fragment)
 C:Species: Cavia porcellus (guinea pig)
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 15-Nov-1996
 C:Accession: PL0110
 R:Matsushita, M.; Okada, H.
 Mol. Immunol. 26, 669-676, 1989
 A:Title: Two forms of guinea pig factor B of the alternative complement pathway with

A:Reference number: A93136; MWID:89484665; PMID:2779589
 A:Accession: P10110
 A:Molecule type: protein
 A:Residues: 1-15 <MAT>
 C:Keywords: complement alternate pathway; glycoprotein

Query Match 27.3%; Score 2; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGS 3
 ||
 DB 2 AGS 3

RESULT 47

LEPAME

Probable msra leader peptide - Staphylococcus epidermidis

C:Species: Staphylococcus epidermidis
 C:Date: 30-Sep-1991 #sequence_revision 10-Sep-1991 #text_change 16-Jul-1999
 C:Accession: S11157
 R:Ross, J.L.; Eady, E.A.; Cove, J.H.; Cunliffe, W.J.; Baumbard, S.; Wootton, J.C.
 Mol. Microbiol. 4, 1207-1214, 1990
 A:Title: Inducible erythromycin resistance in staphylococci is encoded by a member of the

A:Reference number: S11157; MWID:91041740; PMID:2243255
 A:Accession: S11157
 A:Molecule type: DNA
 A:Residues: 1-8 <ROS>
 A:Cross-references: EMBL:X52085; NID:q47400; PIDN:CAA6404.1; PID:q581653
 C:Superfamily: probable msra leader peptide

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LK 8
 ||
 DB 7 LK 8

RESULT 38

S3741

tpsa protein - Erwinia chrysanthemi

C:Species: Erwinia chrysanthemi
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Oct-1999
 C:Accession: S3741
 R:Deuillie, A.; Toussaint, A.; Faes, M.
 Submitted to the EMBL Data Library, August 1994
 A:Description: Identification of the integration host factor genes of E. chrysanthemi.

A:Reference number: S37139
 A:Accession: S3741
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-8 <DOU>

A:Cross-references: EMBL:X74750; NID:q344669; PIDN:CAA62769.1; PID:q581108

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SA 4
 ||
 DB 4 SA 5

RESULT 39

S16324

hypothetical protein 2 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 21-Nov-1993 #sequence_revision 12-May-1994 #text_change 21-Jan-2000
 C:Accession: S16324
 R:Ruberti, L.; Sessa, G.; Lucchetti, S.; Morel, L. G.
 EMBO J. 10, 1787-1791, 1991

A:Title: A novel class of plant proteins containing a homeodomain with a closely lin
 A:Reference number: S16323; MWID:91266907; PMID:1675603

A:Accession: S16324
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-8 <RUH>

A:Cross-references: EMBL:X58821; NID:q16327; PIDN:CAA1624.1; PID:q579259

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KL 7
 ||
 DB 4 KL 5

RESULT 40

P00726

unidentified 4.5/45K [imported] - rice (fragment)

C:Species: Oryza sativa (rice)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: P00726
 R:Komatsu, S.; Kakiwara, H.; Hirano, H.

Theor. Appl. Genet. 86, 935-942, 1993

A:Title: A rice protein library: a data-file of rice proteins separated by two-dime

A:Reference number: P00696

A:Accession: P00726

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <KOM>

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AV 5
 ||
 DB 1 AV 2

RESULT 41

JS0315

leucokinin V - Madeira cockroach

C:Species: Leucophaea maderae (Madeira cockroach)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C:Accession: JS0315
 R:Holman, G.M.; Cook, R.J.; Nachman, R.J.
 Comp. Biochem. Physiol. C 88, 27-30, 1987

A:Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotr

A:Reference number: JS0315

A:Accession: JS0315

A:Molecule type: protein

A:Residues: 1-8 <HOL>

C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile

C:Keywords: amidated carboxyl end; cephalomyotropic peptide

F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GS 3
 ||
 DB 1 GS 2

RESULT 42

A61467

penalbumin - Adelie penguin (fragment)

C:Species: Pygoscelis adeliae (Adelie penguin)
 C:Date: 07-Oct-1994 #sequence_revision 04-Nov-1994 #text_change 04-Nov-1994
 C:Accession: A61467

R:Osega, D.T.; Aninlari, M.; Ho, C.Y.K.; Allison, R.G.; Feeney, R.E.
 J. Protein Chem. 2, 43-62, 1983
 A:Title: Sulfhydryl proteins of penguin egg white: ovalbumin and penalbumin. Comparisons
 A:Reference number: A61467
 A:Accession: A61467
 A:Molecule type: protein
 A:Residues: 1-8 <OSU>
 C:Comments: Penalbumin is a major protein component of egg whites from penguins but not of
 C:Keywords: egg white; glycoprotein

Query Match 18.2% Score 2: DB 2: Length 8:
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 GS 3
 II
 Db 1 GS 2

RESULT 44
 PT0411
 A:Title: Heavy chain CDR3 region (clone 6-106) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0411
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shorer, S.; Gahan, A.; Rivera, G.
 J. Exp. Med. 273, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PT0222; MUID:91108337, PMID:899162
 A:Accession: PT0411
 A:Molecule type: DNA
 A:Residues: 1-8 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 18.2% Score 2: DB 2: Length 8:
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 3 SA 4
 II
 Db 2 SA 3

RESULT 44
 PT0423
 A:Title: Heavy chain CDR3 region (clone 62 1066) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0423
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shorer, S.; Gahan, A.; Rivera, G.
 J. Exp. Med. 273, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PT0222; MUID:91108337, PMID:899162
 A:Accession: PT0423
 A:Molecule type: DNA
 A:Residues: 1-8 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 18.2% Score 2: DB 2: Length 8:
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 GS 3
 II
 Db 1 GS 2

RESULT 45
 PT0603
 A:Title: T cell receptor alpha chain (J2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PH0803
 R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A:Title: T cell receptor genes in a series of class I major histocompatibility comp
 allelic exclusion and antigen-specific repertoire
 A:Reference number: PH0746; MUID:92078846; PMID:1836010
 A:Accession: PH0803
 A:Molecule type: mRNA
 A:Residues: 1-8 <CAS>
 A:Cross-references: EMBL:X6912
 A:Experimental source: T lymphocyte
 C:Keywords: T-cell receptor

Query Match 18.2% Score 2: DB 2: Length 8:
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AG 2
 II
 Db 3 AG 4

RESULT 46
 A35769
 A:Title: T-cell receptor alpha chain V-J region (34S-281) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 30-May-1997
 C:Accession: A35769
 R:Kosaki, H.; Imai, K.; Nakayama, F.; Sado, T.; Moriuchi, K.; Taniguchi, M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5248-5252, 1990
 A:Title: Homogenous junctional sequence of the VJ4+ T-cell antigen receptor alpha c
 A:Reference number: A35768; MUID:90319089; PMID:2371269
 A:Accession: A35768
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-8 <KOS>
 A:Note: the sequence shown follows the authors' translation at position 1 of IGT
 C:Keywords: T-cell receptor

Query Match 18.2% Score 2: DB 2: Length 8:
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 GS 3
 II
 Db 7 GS 8

RESULT 47
 PT0627
 A:Title: T-cell receptor beta chain V-D-J region (100-2H) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0627
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N region
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0627
 A>Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-8 <FE>
 A:Experimental source: newborn thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 18.2% Score 2: DB 2: Length 8:
 Best Local Similarity 100.0% Pred. No. 2.8e+05;
 Matches 2: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AG 2
 II
 Db 5 AG 6

A:Title: A novel class of plant proteins containing a homeodomain with a closely li:
A:Reference number: S16323; MUID:91266907; PMID:1675603
A:Accession: S16324
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <RUB>
A:Cross-references: EMBL:X58821; NID:g16327; PIDN:CAA41624.1; PID:g579259

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KL 7
DB 4 KL 5

RESULT 40
PQ0726
unidentified 4.5/45k [imported] - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PQ0726
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A:Title: A rice protein library: a data-file of rice proteins separated by two-dimer
A:Reference number: PQ0696
A:Accession: PQ0726
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <KOM>

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 AV 5
DB 1 AV 2

RESULT 41
JS0315
leucokinin V - Maduira cockroach
C:Species: Leucophaea maderae (Madeira cockroach)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C:Accession: JS0315
R:Holman, G.M.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 27-30, 1987
A:Title: Isolation, primary structure, and synthesis of leucokinin V and VI: myotr
A:Reference number: JS0315
A:Accession: JS0315
A:Molecule type: protein
A:Residues: 1-8 <HOL>
C:Comment: Leucokinin, a family of cephalomyotropic peptides, stimulate contractile
C:Keywords: amidated carboxyl end; cephalomyotropic peptide
F:8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GS 3
DB 1 GS 2

RESULT 42
A61467
penalubum - Adelle penguin (fragment)
C:Species: Pygoscelis adelle (Adelle penguin)
C:Date: 07-Oct-1994 #sequence_revision 04-Nov-1994 #text_change 04-Nov-1994
C:Accession: A61467

A:Reference number: A93136; MUID:89384686; PMID:2779589
A:Accession: P10110
A:Molecule type: protein
A:Residues: 1-15 <MA>
C:Keywords: complement alternate pathway; glycoprotein.

Query Match 27.3% Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGS 3
DB 7 AGS 9

RESULT 37
LFSAME
probable msra leader peptide - Staphylococcus epidermidis
C:Species: Staphylococcus epidermidis
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C:Accession: S11157
R:Ross, J.L.; Eady, E.A.; Cove, J.H.; Cunliffe, W.J.; Hamberg, S.; Wootton, J.C.
Mol. Microbiol. 4, 1207-1214, 1990
A:Title: Inducible erythromycin resistance in Staphylococci is encoded by a member of the
A:Reference number: S11157; MUID:91041740; PMID:2233255
A:Accession: S11157
A:Molecule type: DNA
A:Residues: 1-8 <ROS>
A:Cross-references: EMBL:X52085; NID:g47000; PIDN:CAA46403.1; PID:g581653
C:Superfamily: probable msra leader peptide

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LR 8
DB 7 LR 8

RESULT 38
S17141
tpsa protein - Erwinia chrysanthemi
C:Species: Erwinia chrysanthemi
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1995
C:Accession: S17141
R:Douville, A.; Rousseau, A.; Faelen, M.
Submitted to the EMBL Data Library August 1994
A:Description: Identification of the integrated host factor genes of E. chrysanthemi.
A:Reference number: S17139
A:Accession: S17141
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <DOU>
A:Cross-references: EMBL:X74750; NID:g39966; PIDN:CAA42769.1; PID:g581108

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SA 4
DB 4 SA 5

RESULT 39
S16324
hypothetical protein 2 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 21-Nov-1993 #sequence_revision 12-May-1995 #text_change 21-Jun-2000
C:Accession: S16324
R:Robert, I.; Sessa, G.; Lucchetti, S.; Morelli, G.
EMBO J. 10, 1787-1791, 1991

R:Gusaga, D.T.; Aminlari, M.; Ho, C.Y.K.; Allison, R.G.; Feeney, A.E.
 J. Protein Chem. 2: 43-62, 1983
 A:Title: Sulfhydryl proteins of penquin egg white: ovalbumin and penatubulin. Comparisons
 A:Reference number: A61467
 A:Accession: PT0311
 A:Molecule type: protein
 A:Residues: 1-8 <GS>
 C:Comment: Penatubulin is a major protein component of egg whites from penquins but not B
 C:Keywords: egg white; glycoprotein

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GS 3
 II
 DB 1 GS 2

RESULT 43

PT0311
 Ig heavy chain CRO3 region (clone 6-103) human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0311
 R:Yamada, M.; Wasserman, K.; Reichard, B.A.; Shauer, S.; Caton, A.J.; Rivera, G.
 J. Exp. Med. 173: 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PT0222; MUID:91108337; PMID:1899102
 A:Accession: PT0311
 A:Molecule type: DNA
 A:Residues: 1-8 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SA 4
 II
 DB 2 SA 3

RESULT 44

PT0323
 Ig heavy chain CRO3 region (clone J2-106B) human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0323
 R:Yamada, M.; Wasserman, K.; Reichard, B.A.; Shauer, S.; Caton, A.J.; Rivera, G.
 J. Exp. Med. 173: 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PT0222; MUID:91108337; PMID:1899102
 A:Accession: PT0323
 A:Molecule type: DNA
 A:Residues: 1-8 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GS 3
 II
 DB 1 GS 2

RESULT 45

PT0803
 T-cell receptor alpha chain (J2) - mouse (fragment)
 C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0803
 R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174: 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility compl
 allelic exclusion and antigen-specific repertoire

A:Reference number: PT0746; MUID:92078846; PMID:1836010

A:Accession: PT0803

A:Molecule type: mRNA

A:Residues: 1-8 <CAS>

A:Cross-references: EMBL:X60912

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
 II
 DB 3 AG 4

RESULT 46

A35768
 T-cell receptor alpha chain V-J region (34S-281) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 30-May-1997
 C:Accession: A35768
 R:Koseki, H.; Imai, K.; Nakayama, F.; Sado, T.; Moriwaiki, K.; Taniguchi, M.
 Proc. Natl. Acad. Sci. U.S.A. 87: 5248-5252, 1990
 A:Title: Homogenous junctional sequence of the V14+ T-cell antigen receptor alpha ch
 A:Reference number: A35768; MUID:90319089; PMID:2371269
 A:Accession: A35768
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-8 <KOS>
 A:Note: the sequence shown follows the authors' translation at position 1 of TGT
 C:Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GS 3
 II
 DB 7 GS 8

RESULT 47

PT0627
 T-cell receptor beta chain V D J region (100-2H) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0627
 R:Feeney, A.J.
 J. Exp. Med. 174: 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N region
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0627
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-8 <FE>
 A:Experimental source: newborn thymus, strain BALB/c
 C:Keywords: T-cell receptor

Query Match 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
 II
 DB 5 AG 6

RESULT 48
PT0530
T-cell receptor beta chain V-D-J region (100-48K) - Mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30 May-1997
C:Accession: PT0530
R:Feeney, A.J.
J:Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of total T-cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711559
A:Accession: PT0530
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <FE>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match: 18.2%; Score 2; Len 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2 de-95;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 4
DB 3 SA 4

RESULT 49
PT0527
T-cell receptor beta chain V-D-J region (100-41) - Mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30 May-1997
C:Accession: PT0527
R:Feeney, A.J.
J:Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T-cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0527
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <FE>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match: 18.2%; Score 2; Len 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2 de-95;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
DB 5 AG 6

RESULT 50
PT0509
T-cell receptor beta chain V-D-J region (100-48K) - Mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0509
R:Feeney, A.J.
J:Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of total T-cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0509
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-8 <FE>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match: 18.2%; Score 2; Len 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2 de-95;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
DB 5 AG 6

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
DB 5 AG 6

Search completed: September 30, 2003, 10:09:44
Job time : 12.4167 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:04 / Search time 5.25 Seconds

{without alignment}

62,767 million c.e.1 updates/sec

Title: US-09-787-443-4

Perfect score: 11

Sequence: 1 AGSAVKKKKA 11

Scoring table: G130

Gapop 50.0 / Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size: 9

Total number of hits satisfying chosen parameters: 707

Minimum DB seq length: 8

Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database: SwissProt_41.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	46.4	9	1	XVIA_STRSQ
2	4	46.4	14	1	MRX_METIM
3	4	27.3	12	1	RR16_GINRI
4	3	27.3	13	1	TP55_BOVIN
5	4	27.3	13	1	NPL_YMST
6	4	27.3	13	1	UP71_LILHW
7	3	27.3	14	1	MAST_VENBA
8	3	27.3	14	1	MY14_PHEV
9	3	27.3	14	1	TNK1_SCHUR
10	3	27.3	15	1	DIDH_PSEFL
11	3	27.3	15	1	MA17_PATIS
12	3	27.3	15	1	ONC1_GNOMY
13	3	27.3	15	1	SD09_PEPIS
14	3	27.3	15	1	THE_CUGRA
15	3	27.3	15	1	UP02_METAN
16	2	18.2	8	1	AL15_CARMA
17	2	18.2	8	1	AL18_CARMA
18	2	18.2	8	1	CAG1_ENEFA
19	2	18.2	8	1	PAK7_ASNSU
20	2	18.2	8	1	LCK5_LEINA
21	2	18.2	8	1	LPMS_STAPP
22	2	18.2	8	1	RS1_ERWHH
23	2	18.2	8	1	VGI6_HSVJB
24	2	18.2	8	1	WPL_PERAL
25	2	18.2	9	1	ALC_CHLKE
26	2	18.2	9	1	BUR_CUGRA
27	2	18.2	9	1	DSIP_PARIT
28	2	18.2	9	1	FAR2_PANKE
29	2	18.2	9	1	FAR2_CALVO
30	2	18.2	9	1	LTC6_LITAN
31	2	18.2	9	1	LMP_LACM
32	2	18.2	9	1	LPCA_STAAJ
33	2	18.2	9	1	MOSF_CLYJA

34	2	18.2	9	1	MOSH_CLYJA
35	2	18.2	9	1	PPH1_LYCES
36	2	18.2	9	1	PPK1_PERAM
37	2	18.2	9	1	PTSP_BOMMO
38	2	18.2	9	1	RE42_LITRU
39	2	18.2	9	1	THYF_PIG
40	2	18.2	9	1	ULAD_HUMAN
41	2	18.2	10	1	AMPN_HILAM
42	2	18.2	10	1	COXK_ONCMY
43	2	18.2	10	1	COXM_RAT
44	2	18.2	10	1	FARC_CALVO
45	2	18.2	10	1	FARP_WYTED
46	2	18.2	10	1	FIRB_PERSI
47	2	18.2	10	1	GAJU_HUMAN
48	2	18.2	10	1	GRP_RANRI
49	2	18.2	10	1	LABA_JATMU
50	2	18.2	10	1	MALE_KLEPN
51	2	18.2	10	1	MOSU_CLYJA
52	2	18.2	10	1	NO40_TOBAC
53	2	18.2	10	1	ODP2_BOVIN
54	2	18.2	10	1	PNEU_HUMAN
55	2	18.2	10	1	PNEU_RAT
56	2	18.2	10	1	PPCK_FASHE
57	2	18.2	10	1	PSHF_CAPAN
58	2	18.2	10	1	PVK_LOCHI
59	2	18.2	10	1	RT02_BOVIN
60	2	18.2	10	1	SPI_HALRO
61	2	18.2	10	1	SYK_CAMUP
62	2	18.2	10	1	TEMK_RANTE
63	2	18.2	10	1	TKL3_LOCHI
64	2	18.2	10	1	TKNB_RANRI
65	2	18.2	10	1	TKU1_UREUN
66	2	18.2	10	1	TK02_UREUN
67	2	18.2	10	1	TRP6_LEUMA
68	2	18.2	10	1	UPA3_HUMAN
69	2	18.2	10	1	UPA8_HUMAN
70	2	18.2	10	1	URA6_HUMAN
71	2	18.2	10	1	UXA6_CHLTR
72	2	18.2	10	1	XYNB_DICB4
73	2	18.2	11	1	RRK_MEGFL
74	2	18.2	11	1	CA41_LITCI
75	2	18.2	11	1	CA42_LITCI
76	2	18.2	11	1	COXA_CANFA
77	2	18.2	11	1	CS15_BACSU
78	2	18.2	11	1	CX11_CONMR
79	2	18.2	11	1	LPW_THETH
80	2	18.2	11	1	MIB1_KLEPN
81	2	18.2	11	1	MORN_HUMAN
82	2	18.2	11	1	NUHM_CANFA
83	2	18.2	11	1	PGOC_PSEFL
84	2	18.2	11	1	Q29A_COMTE
85	2	18.2	11	1	RS30_ONCMY
86	2	18.2	12	1	FAR7_PENMO
87	2	18.2	12	1	H2AX_ONCMY
88	2	18.2	12	1	LMT1_LOCHI
89	2	18.2	12	1	NO40_LOTJA
90	2	18.2	12	1	NO40_SESRO
91	2	18.2	12	1	NO40_SOYBN
92	2	18.2	12	1	PORD_METIM
93	2	18.2	12	1	PSP1_PHYPA
94	2	18.2	12	1	PKV2_PERAM
95	2	18.2	12	1	RS19_CLYEP
96	2	18.2	12	1	RS19_ELYEP
97	2	18.2	12	1	RS19_TOBBP
98	2	18.2	12	1	SO15_BACSU
99	2	18.2	12	1	TA10_TREME
100	2	18.2	12	1	TM2A_METMA
101	2	18.2	12	1	UH03_RAT
102	2	18.2	12	1	UR2A_CATCO
103	2	18.2	12	1	UR2B_CATCO
104	2	18.2	12	1	UR2_GILMI
105	2	18.2	12	1	UR2_POLSP
106	2	18.2	13	1	AUF8_TENMO

P19852	clypeaster
P83380	lycopersico
P82691	periplaneta
P82003	bombyx mori
P82075	litoria rub
P01255	sus scrofa
P31929	homo sapien
P81731	helicoverpa
P80332	oncorhynch
P80431	rattus norv
P41867	calliphora
P42560	mytilus edu
P14537	ceratotheri
P01358	homo sapien
P23260	rana ridibu
P13270	jatropha mu
Q05564	klebsiella
P19962	clypeaster
P55962	nicotiana t
P11180	bos taurus
P22103	homo sapien
P21996	rattus norv
P80525	fasciola he
Q04367	capsicum an
P83382	locusta mig
P82923	bos taurus
Q10997	halocynthia
Q46464	campylobact
P56923	rana tempor
P30249	locusta mig
P29135	rana ridibu
P40751	urechis uni
P81738	leucophaea
P40930	homo sapien
P32080	homo sapien
P38007	chlamydia t
P80717	dictyoglomu
P12797	megascollia
P82091	litoria cit
P82092	litoria cit
P99501	canis fami
P81095	bacillus su
P58807	conus marmo
P05624	thermus the
P80580	klebsiella
P01163	homo sapien
P49820	canis fami
P22395	pseudomonas
P55173	pseudomonas
P80464	comamonas t
P83328	oncorhynch
P83327	penaeus mon
P83327	oncorhynch
P22395	locusta mig
Q24246	lotus japon
Q24369	seebania ro
P55960	glycine max
P80903	methanobact
P80662	physcomitre
P81555	periplaneta
Q46490	clover yell
Q47881	elm yellows
Q56251	tomato big
P80863	bacillus su
P01371	tremella me
P80652	methanosarc
P56572	rattus norv
P04558	catostomus
P04559	catostomus
P01427	gillichthys
P81022	polyodon sp
P83109	tenebrio mo

107	2	18.2	13	1	AUL1_LITRA	P82385	litoria ran	180	2	18.2	15	1	AFIL_MALPA	P83141	malva parvi
108	2	18.2	13	1	AUL2_LITRA	P82387	litoria ran	181	2	18.2	15	1	ARCA_STRPS	P58827	streptococc
109	2	18.2	13	1	BML_PSGG	P42991	pseudophryn	182	2	18.2	15	1	ASPI_IACSN	P82648	lactobacilli
110	2	18.2	13	1	B371_LEUMA	P41754	leucophaea	183	2	18.2	15	1	ATP2_SPIOL	P80083	spinacia ol
111	2	18.2	13	1	CHEP_PARIC	P42718	paripolybia	184	2	18.2	15	1	CIQA_RAT	P31720	rattus norv
112	2	18.2	13	1	CP1_AKCA	Q10998	apiysia cal	185	2	18.2	15	1	CDN5_LITCE	P82077	litoria cae
113	2	18.2	13	1	CHP1_VESAN	P17245	vespa arali	186	2	18.2	15	1	CH11_PEA	P82078	litoria cae
114	2	18.2	13	1	CHP2_VESSE	P17245	vespa arali	187	2	18.2	15	1	CH11_PEA	P21225	pisum sativ
115	2	18.2	13	1	CHP3_VESNA	P17244	vespa manda	188	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
116	2	18.2	13	1	CHP4_VESNA	P17244	vespa manda	189	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
117	2	18.2	13	1	CHP5_VESNA	P17244	vespa manda	190	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
118	2	18.2	13	1	CHP6_VESNA	P17244	vespa manda	191	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
119	2	18.2	13	1	CHP7_VESNA	P17244	vespa manda	192	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
120	2	18.2	13	1	CHP8_VESNA	P17244	vespa manda	193	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
121	2	18.2	13	1	CHP9_VESNA	P17244	vespa manda	194	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
122	2	18.2	13	1	CHP10_VESNA	P17244	vespa manda	195	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
123	2	18.2	13	1	CHP11_VESNA	P17244	vespa manda	196	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
124	2	18.2	13	1	CHP12_VESNA	P17244	vespa manda	197	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
125	2	18.2	13	1	CHP13_VESNA	P17244	vespa manda	198	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
126	2	18.2	13	1	CHP14_VESNA	P17244	vespa manda	199	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
127	2	18.2	13	1	CHP15_VESNA	P17244	vespa manda	200	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
128	2	18.2	13	1	CHP16_VESNA	P17244	vespa manda	201	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
129	2	18.2	13	1	CHP17_VESNA	P17244	vespa manda	202	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
130	2	18.2	13	1	CHP18_VESNA	P17244	vespa manda	203	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
131	2	18.2	13	1	CHP19_VESNA	P17244	vespa manda	204	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
132	2	18.2	13	1	CHP20_VESNA	P17244	vespa manda	205	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
133	2	18.2	13	1	CHP21_VESNA	P17244	vespa manda	206	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
134	2	18.2	13	1	CHP22_VESNA	P17244	vespa manda	207	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
135	2	18.2	13	1	CHP23_VESNA	P17244	vespa manda	208	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
136	2	18.2	13	1	CHP24_VESNA	P17244	vespa manda	209	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
137	2	18.2	13	1	CHP25_VESNA	P17244	vespa manda	210	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
138	2	18.2	13	1	CHP26_VESNA	P17244	vespa manda	211	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
139	2	18.2	13	1	CHP27_VESNA	P17244	vespa manda	212	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
140	2	18.2	13	1	CHP28_VESNA	P17244	vespa manda	213	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
141	2	18.2	13	1	CHP29_VESNA	P17244	vespa manda	214	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
142	2	18.2	13	1	CHP30_VESNA	P17244	vespa manda	215	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
143	2	18.2	13	1	CHP31_VESNA	P17244	vespa manda	216	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
144	2	18.2	13	1	CHP32_VESNA	P17244	vespa manda	217	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
145	2	18.2	13	1	CHP33_VESNA	P17244	vespa manda	218	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
146	2	18.2	13	1	CHP34_VESNA	P17244	vespa manda	219	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
147	2	18.2	13	1	CHP35_VESNA	P17244	vespa manda	220	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
148	2	18.2	13	1	CHP36_VESNA	P17244	vespa manda	221	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
149	2	18.2	13	1	CHP37_VESNA	P17244	vespa manda	222	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
150	2	18.2	13	1	CHP38_VESNA	P17244	vespa manda	223	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
151	2	18.2	13	1	CHP39_VESNA	P17244	vespa manda	224	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
152	2	18.2	13	1	CHP40_VESNA	P17244	vespa manda	225	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
153	2	18.2	13	1	CHP41_VESNA	P17244	vespa manda	226	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
154	2	18.2	13	1	CHP42_VESNA	P17244	vespa manda	227	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
155	2	18.2	13	1	CHP43_VESNA	P17244	vespa manda	228	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
156	2	18.2	13	1	CHP44_VESNA	P17244	vespa manda	229	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
157	2	18.2	13	1	CHP45_VESNA	P17244	vespa manda	230	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
158	2	18.2	13	1	CHP46_VESNA	P17244	vespa manda	231	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
159	2	18.2	13	1	CHP47_VESNA	P17244	vespa manda	232	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
160	2	18.2	13	1	CHP48_VESNA	P17244	vespa manda	233	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
161	2	18.2	13	1	CHP49_VESNA	P17244	vespa manda	234	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
162	2	18.2	13	1	CHP50_VESNA	P17244	vespa manda	235	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
163	2	18.2	13	1	CHP51_VESNA	P17244	vespa manda	236	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
164	2	18.2	13	1	CHP52_VESNA	P17244	vespa manda	237	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
165	2	18.2	13	1	CHP53_VESNA	P17244	vespa manda	238	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
166	2	18.2	13	1	CHP54_VESNA	P17244	vespa manda	239	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
167	2	18.2	13	1	CHP55_VESNA	P17244	vespa manda	240	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
168	2	18.2	13	1	CHP56_VESNA	P17244	vespa manda	241	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
169	2	18.2	13	1	CHP57_VESNA	P17244	vespa manda	242	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
170	2	18.2	13	1	CHP58_VESNA	P17244	vespa manda	243	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
171	2	18.2	13	1	CHP59_VESNA	P17244	vespa manda	244	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
172	2	18.2	13	1	CHP60_VESNA	P17244	vespa manda	245	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
173	2	18.2	13	1	CHP61_VESNA	P17244	vespa manda	246	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
174	2	18.2	13	1	CHP62_VESNA	P17244	vespa manda	247	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
175	2	18.2	13	1	CHP63_VESNA	P17244	vespa manda	248	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
176	2	18.2	13	1	CHP64_VESNA	P17244	vespa manda	249	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
177	2	18.2	13	1	CHP65_VESNA	P17244	vespa manda	250	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
178	2	18.2	13	1	CHP66_VESNA	P17244	vespa manda	251	2	18.2	15	1	COX1_THUOB	P80978	thunus obe
179	2	18.2	13	1	CHP67_VESNA	P17244	vespa manda	252	2	18.2	15	1	COX1_THUOB	P80978	thunus obe

253	1	9.1	8	1	FUSS_FUSSO	P81010 fusarium so	326	1	9.1	9	1	OXYA_SQUAC	P42999 squalus aca
254	1	9.1	8	1	GLUR_HUMAN	P02729 homo sapien	327	1	9.1	9	1	OXYF_SCYCA	P42997 scyllorhinu
255	1	9.1	8	1	HTF1_PERAM	P04548 periplaneta	328	1	9.1	9	1	OXYT_BUFRE	P42995 bufo regula
256	1	9.1	8	1	HTF2_PERAM	P04549 periplaneta	329	1	9.1	9	1	OXYT_CYPCA	P23879 cyprinus ca
257	1	9.1	8	1	HTF_TENNO	P25419 tenebrio mo	330	1	9.1	9	1	OXYT_EISFO	P42998 esenita foe
258	1	9.1	8	1	LCK1_LEUMA	P21140 leucophaea	331	1	9.1	9	1	OXYT_OCTVO	P80027 octopus vul
259	1	9.1	8	1	LCK2_LEUMA	P21141 leucophaea	332	1	9.1	9	1	OXYT_RABIT	P32878 oryctolagus
260	1	9.1	8	1	LCK3_LEUMA	P21142 leucophaea	333	1	9.1	9	1	OXYT_RAJCL	P42994 raja clavat
261	1	9.1	8	1	LCK4_LEUMA	P21143 leucophaea	334	1	9.1	9	1	OXYV_SQUAC	P43000 squalus aca
262	1	9.1	8	1	LCK6_LEUMA	P19988 leucophaea	335	1	9.1	9	1	PGLK_DIAAB	P81179 diaprepes a
263	1	9.1	8	1	LCK7_LEUMA	P19989 leucophaea	336	1	9.1	9	1	RT33_BOVIN	P82926 bos taurus
264	1	9.1	8	1	LCK8_LEUMA	P19990 leucophaea	337	1	9.1	9	1	SAMP_MUSCA	P19095 mustelus ca
265	1	9.1	8	1	LMT2_LOCOM	P22396 locusta mig	338	1	9.1	9	1	SAP_STOVA	P24047 stomopneute
266	1	9.1	8	1	LPK_LEUMA	P10049 leucophaea	339	1	9.1	9	1	TAL1_PICJA	P17440 pichia jadi
267	1	9.1	8	1	NFB_BOVIN	P15507 bos taurus	340	1	9.1	9	1	TAL3_PICJA	P17441 pichia jadi
268	1	9.1	8	1	NS3_NYCTU	P41152 mycobacteri	341	1	9.1	9	1	TKC1_CALVO	P41517 calliphora
269	1	9.1	8	1	OMY_OROLI	P42455 orconectes	342	1	9.1	9	1	TKL1_LOCOM	P16223 locusta mig
270	1	9.1	8	1	PJP_BRANA	P81707 brassica na	343	1	9.1	9	1	TRP4_LEUMA	P81736 leucophaea
271	1	9.1	8	1	PKK2_PERAM	P82692 periplaneta	344	1	9.1	9	1	UHA2_HUMAN	P40929 homo sapien
272	1	9.1	8	1	PKK3_PERAM	P82618 periplaneta	345	1	9.1	9	1	ULAE_HUMAN	P31931 homo sapien
273	1	9.1	8	1	RPH_PANHO	P08939 pandalus bo	346	1	9.1	9	1	ULAH_HUMAN	P31934 homo sapien
274	1	9.1	8	1	RS7_MYC17	P33564 mycobacteri	347	1	9.1	9	1	ULAK_MOUSE	P99031 mus musculu
275	1	9.1	8	1	RT34_BOVIN	P82929 bos taurus	348	1	9.1	9	1	UN19_CLOPA	P81355 clostridium
276	1	9.1	8	1	UC26_MAIZE	P80632 zea mays (m	349	1	9.1	9	1	UPA3_HUMAN	P30089 homo sapien
277	1	9.1	8	1	UG6_MOUSE	P36844 mus musculu	350	1	9.1	9	1	UPA6_HUMAN	P30092 homo sapien
278	1	9.1	8	1	UH09_RAT	P56575 rattus norv	351	1	9.1	9	1	UPA7_HUMAN	P30093 homo sapien
279	1	9.1	8	1	UPA1_HUMAN	P30087 homo sapien	352	1	9.1	9	1	YBFR_AZOV1	P25825 azotobacter
280	1	9.1	8	1	UPAA_HUMAN	P30096 homo sapien	353	1	9.1	9	1	AEGL_AGRAE	P83465 agroclybe ae
281	1	9.1	9	1	ALI10_CARMA	P41813 carcinus ma	354	1	9.1	10	1	AH3_PRUSE	P29261 prunus sero
282	1	9.1	9	1	ALI11_CERUL	P81814 carcinus ma	355	1	9.1	10	1	AKHX_LOCOM	P81626 locusta mig
283	1	9.1	9	1	BS43_SERUL	P33375 serratia pl	356	1	9.1	10	1	ALI9_CARMA	P81822 carcinus ma
284	1	9.1	9	1	CCAP_CARMA	P38586 carcinus ma	357	1	9.1	10	1	ANG1_BOTJA	Q10581 bothrops ja
285	1	9.1	9	1	CONG_CONGE	P05486 conus geogr	358	1	9.1	10	1	ANGT_BOVIN	P01017 bos taurus
286	1	9.1	9	1	CONO_CONST	P05487 conus stria	359	1	9.1	10	1	ANGT_CHICK	P01018 gallus gall
287	1	9.1	9	1	COW_CONVE	P83047 conus ventr	360	1	9.1	10	1	APE_CAPGI	P80474 capocytoph
288	1	9.1	9	1	COW_THUOB	P83975 thunnus obe	361	1	9.1	10	1	BPP8_BOTIN	P80426 bothrops in
289	1	9.1	9	1	DL_NEPNO	P24816 nephrops no	362	1	9.1	10	1	BPP_VIPAS	P31351 vipera aspi
290	1	9.1	9	1	DNF1_LOCOM	P16349 locusta mig	363	1	9.1	10	1	BRK_ONCHY	Q9PRZ1 oncorhynch
291	1	9.1	9	1	FAE2_CALVO	P41857 calliphora	364	1	9.1	10	1	CA12_LITCI	P82086 littoria cit
292	1	9.1	9	1	FAE3_CALVO	P41858 calliphora	365	1	9.1	10	1	CAER_LITXA	P56264 littoria xan
293	1	9.1	9	1	FAE3_MARS	P83276 macrobrachi	366	1	9.1	10	1	CATB_SHEEP	P83205 ovis aries
294	1	9.1	9	1	FAE3_PENNO	P83319 penaeus mon	367	1	9.1	10	1	COXA_ONCHY	P80328 oncorhynch
295	1	9.1	9	1	FAE4_CALVO	P41859 calliphora	368	1	9.1	10	1	COXH_RAT	P80331 oncorhynch
296	1	9.1	9	1	FAE4_PENNO	P83319 penaeus mon	369	1	9.1	10	1	COXO_RAT	P80432 rattus norv
297	1	9.1	9	1	FAE5_ASYU	P43170 ascaris suu	370	1	9.1	10	1	COXO_THUOB	P80982 thunnus obe
298	1	9.1	9	1	FAE5_CALVO	P41860 calliphora	371	1	9.1	10	1	COXO_RABIT	P80336 oryctolagus
299	1	9.1	9	1	FAE5_PANNE	P42661 panagrellus	372	1	9.1	10	1	COXO_SHEEP	P80337 ovis aries
300	1	9.1	9	1	FAE5_PENNO	P83320 penaeus mon	373	1	9.1	10	1	CU30_LOCOM	P11735 locusta mig
301	1	9.1	9	1	FAE6_CALVO	P41861 calliphora	374	1	9.1	10	1	ESL_LACCA	P81758 lactobacilli
302	1	9.1	9	1	FAE6_MARS	P83279 macrobrachi	375	1	9.1	10	1	ESTA_SCHGA	P81012 schizaphis
303	1	9.1	9	1	FAE7_CALVO	P41862 calliphora	376	1	9.1	10	1	FAE2_PENNO	P83317 penaeus mon
304	1	9.1	9	1	FAE6_MARS	P83281 macrobrachi	377	1	9.1	10	1	FAE5_MARS	P83278 macrobrachi
305	1	9.1	9	1	FAE6_ASYU	P43172 ascaris suu	378	1	9.1	10	1	FAE6_PANRE	P82660 panagrellus
306	1	9.1	9	1	FAE7_ASYU	P48495 callinectes	379	1	9.1	10	1	FAE7_MARS	P83280 macrobrachi
307	1	9.1	9	1	FIBB_ASYU	P39346 erythrocebu	380	1	9.1	10	1	FARP_LOCOM	P38553 locusta mig
308	1	9.1	9	1	FIBB_MACHU	P19345 macaca tusc	381	1	9.1	10	1	FARP_MANSE	P18523 manduca sex
309	1	9.1	9	1	FIBB_PAPAN	P19344 papio anubi	382	1	9.1	10	1	GLEM_HUMAN	P02728 homo sapien
310	1	9.1	9	1	FIBB_PAPER	P19343 papio hamad	383	1	9.1	10	1	GONI_ALUMI	P37041 alligator m
311	1	9.1	9	1	FIBB_THERE	P19342 theropitheo	384	1	9.1	10	1	GONI_CHEPR	P80677 chelysoma
312	1	9.1	9	1	FLA2_TREHY	P80159 trepomena h	385	1	9.1	10	1	GONI_CLUPA	P81749 clupea pall
313	1	9.1	9	1	FREF_SARBU	P83350 sarcophaga	386	1	9.1	10	1	GONI_PETMA	P04378 petromyzon
314	1	9.1	9	1	HUTU_KLEAE	P12381 klebsiella	387	1	9.1	10	1	GON2_CHEPR	P80678 chelysoma
315	1	9.1	9	1	IPVR_RHOVI	P82992 rhodopsendo	388	1	9.1	10	1	GON2_CHICK	P37043 gallus gall
316	1	9.1	9	1	ISOT_CYPCA	P42997 cyprinus ca	389	1	9.1	10	1	GON3_ONCRE	P20367 oncorhynch
317	1	9.1	9	1	KNL3_HUMVA	P83058 bombina var	390	1	9.1	10	1	GON3_PETMA	P30948 petromyzon
318	1	9.1	9	1	LITR_PHYKO	P08946 phyllomedusa	391	1	9.1	10	1	GONL_SQUAC	P27429 squalus aca
319	1	9.1	9	1	LITR_LOCOM	P41489 locusta mig	392	1	9.1	10	1	GS09_BACSU	P80243 bacillus su
320	1	9.1	9	1	MGMT_BOVIN	P29177 bos taurus	393	1	9.1	10	1	HTF1_ROMMI	P18110 romalea mic
321	1	9.1	9	1	NEF_HIV25	P12483 human immun	394	1	9.1	10	1	HTF2_CARMO	P11385 carausius m
322	1	9.1	9	1	NEUO_CAVIPO	P44966 cavia porce	395	1	9.1	10	1	HTF_HELZE	P16353 heliothis z
323	1	9.1	9	1	NEUX_HUMAN	P04277 homo sapien	396	1	9.1	10	1	HTF_NAUCI	P10939 nauphoeta c
324	1	9.1	9	1	NEUX_SARHC	P41492 sarcophaga	397	1	9.1	10	1	HTF_TABAT	P14596 tabanus atr
325	1	9.1	9	1	OXYA_SCYCA	P42996 scyllorhinu	398	1	9.1	10	1	LCMS_LEUMA	P21144 leucophaea

399	1	9.1	10	1	LPK2_LUHM:	P41488 locusta mig	472	1	9.1	11	1	TKN1_PSEGU	P42986 pseudophryn
400	1	9.1	10	1	LSK2_LEUMA	P05039 leucophaea	473	1	9.1	11	1	TKN1_OPERU	P82026 uperoleia r
401	1	9.1	10	1	MP2_MCOCC	P61533 microplitis	474	1	9.1	11	1	TKN1_OPERU	P08612 uperoleia r
402	1	9.1	10	1	NS1_MYCTE	P81135 mycobacteri	475	1	9.1	11	1	TKN2_PSEGU	P42987 pseudophryn
403	1	9.1	10	1	PAP1_PARMA	P81863 pardachuris	476	1	9.1	11	1	TKN2_PSEGU	P08616 uperoleia r
404	1	9.1	10	1	POR6_MFTIM	P80501 methanobact	477	1	9.1	11	1	TKN3_PSEGU	P42988 pseudophryn
405	1	9.1	10	1	QZ06_COMTE	P80465 romamonas t	478	1	9.1	11	1	TKN4_PSEGU	P42989 pseudophryn
406	1	9.1	10	1	QZ06_COMTE	P80465 romamonas t	479	1	9.1	11	1	TKN5_PSEGU	P42990 pseudophryn
407	1	9.1	10	1	RCA_PINS	P81084 pinus pinas	480	1	9.1	11	1	TKNA_CHICK	P19850 gallus gall
408	1	9.1	10	1	RL15_ACHLA	P25221 acholop:asm	481	1	9.1	11	1	TKNA_GADMO	P28498 gadus morhu
409	1	9.1	10	1	RNPL_PHVU	P45946 phorine dis	482	1	9.1	11	1	TKNA_HORSE	P01290 equus cabal
410	1	9.1	10	1	SLAP_BAVIG	P49325 bacillus th	483	1	9.1	11	1	TKNA_ONCMY	P28499 oncorhynch
411	1	9.1	10	1	SP34_DPMO	P81545 diacyostelli	484	1	9.1	11	1	TKNA_RANCA	P22688 rana catesb
412	1	9.1	10	1	TKL2_LUHM	P16224 locusta mig	485	1	9.1	11	1	TKNA_RANRI	P29207 rana ridibu
413	1	9.1	10	1	TKL2_LUHM	P16224 locusta mig	486	1	9.1	11	1	TKNA_SCYCA	P42333 scyllorhinu
414	1	9.1	10	1	TKN1_SCYCA	P06308 scyllorhinu	487	1	9.1	11	1	TKND_RANCA	P22691 rana catesb
415	1	9.1	10	1	TKNB_CHICK	P19850 gallus gall	488	1	9.1	11	1	TKN_ELEMO	P01293 eledone mos
416	1	9.1	10	1	TKNB_ONCMY	P26500 oncorhynch	489	1	9.1	11	1	TKN_PHVU	P08615 physalaemus
417	1	9.1	10	1	TKNB_RANCA	P22689 rana catesb	490	1	9.1	11	1	UF05_MOUSE	P38643 mus musculu
418	1	9.1	10	1	TKNC_RANCA	P22690 rana catesb	491	1	9.1	11	1	ULAG_HUMAN	P31933 homo sapien
419	1	9.1	10	1	TKNK_PIG	P01292 sus scrofa	492	1	9.1	11	1	UXB2_YEAST	P99013 saccharomyc
420	1	9.1	10	1	TKN1_FHYBI	P05610 phyllomedus	493	1	9.1	11	1	CALM_FETTH	Q05055 tetrahymena
421	1	9.1	10	1	TKS1_AEAE	P42634 aedes aegypt	494	1	9.1	11	1	CD11_LITXA	P56245 litorea xan
422	1	9.1	10	1	TKS2_AEAE	P42634 aedes aegypt	495	1	9.1	11	1	CD14_LITXA	P56246 litorea xan
423	1	9.1	10	1	TKOF_AEAE	P19425 aedes aegypt	496	1	9.1	11	1	CXAL_CONIM	P50983 conus imper
424	1	9.1	10	1	TPIS_NICBE	P19418 nicotiana p	497	1	9.1	11	1	CXL3_CONMR	P58809 conus marmo
425	1	9.1	10	1	TKPS_LEUMA	P81717 leucophaea	498	1	9.1	11	1	CXST_CONTE	P58846 conus texti
426	1	9.1	10	1	TKP5_LEUMA	P81719 leucophaea	499	1	9.1	11	1	FARI_CALVO	P41869 calliphora
427	1	9.1	10	1	TKP5_LEUMA	P81719 leucophaea	500	1	9.1	11	1	FIFI_SARBU	P83349 sarcophaga
428	1	9.1	10	1	TKP5_LEUMA	P81719 leucophaea							
429	1	9.1	10	1	TKP5_LEUMA	P81719 leucophaea							
430	1	9.1	10	1	UPA2_HUMAN	P40288 homo sapien							
431	1	9.1	10	1	UPA4_HUMAN	P30590 homo sapien							
432	1	9.1	10	1	UPA5_HUMAN	P30591 homo sapien							
433	1	9.1	10	1	URA1_HUMAN	P24118 homo sapien							
434	1	9.1	10	1	URA1_HUMAN	P24118 homo sapien							
435	1	9.1	10	1	USE3_MORNO	P17339 moronelella							
436	1	9.1	10	1	UXA2_CHLIF	P38093 chlamydia l							
437	1	9.1	10	1	UXB1_YEAST	P99012 saccharomyc							
438	1	9.1	10	1	VEG6_BANSE	P80699 bacillus su							
439	1	9.1	11	1	ANG1_CRIGE	P09077 ericia geor							
440	1	9.1	11	1	ASL1_BANSE	P81146 bacteroides							
441	1	9.1	11	1	ASL2_BANSE	P81147 bacteroides							
442	1	9.1	11	1	BPP1_HOJIN	P41425 bothrops in							
443	1	9.1	11	1	BPP4_HOJIN	P41426 bothrops in							
444	1	9.1	11	1	BPP6_AKHA	P10221 agkistrodon							
445	1	9.1	11	1	BPP6_AKHA	P10221 agkistrodon							
446	1	9.1	11	1	CA21_LITXA	P82087 litorea cit							
447	1	9.1	11	1	CA22_LITXA	P82088 litorea cit							
448	1	9.1	11	1	CA23_LITXA	P82089 litorea cit							
449	1	9.1	11	1	CA24_LITXA	P82090 litorea cit							
450	1	9.1	11	1	CEP1_AKHA	P23290 calliphora							
451	1	9.1	11	1	CEP2_FESAR	P11449 periplaneta							
452	1	9.1	11	1	CEP6_AKHA	P88649 conus ulic							
453	1	9.1	11	1	ERG2_AKHA	P81350 castridium							
454	1	9.1	11	1	ESI1_FAT	P16571 ratius norv							
455	1	9.1	11	1	FAR6_PENMO	P41332 penaeus mon							
456	1	9.1	11	1	FAP9_CALVO	P41864 calliphora							
457	1	9.1	11	1	HS70_PINS	P81672 pinus pinas							
458	1	9.1	11	1	LAG6_PENMO	P81678 oncorhynch							
459	1	9.1	11	1	LSK1_LEUMA	P46248 leucophaea							
460	1	9.1	11	1	LSKP_PERAM	P46248 leucophaea							
461	1	9.1	11	1	MIC3_THEIS	P41989 thecocyton							
462	1	9.1	11	1	NKSN_PSELE	P49072 pscodanaja							
463	1	9.1	11	1	PKCL_CARMO	P82684 carausius p							
464	1	9.1	11	1	PKVL_PERAM	P41837 periplaneta							
465	1	9.1	11	1	RANC_RANRI	P08951 rana pipen							
466	1	9.1	11	1	RE41_LITXA	P82074 litorea rub							
467	1	9.1	11	1	RR2_CONAM	P42341 eucnopolis							
468	1	9.1	11	1	RRL1_CHAV	P11179 chandipura							
469	1	9.1	11	1	TIN4_PROVU	P31641 proteus vul							
470	1	9.1	11	1	TIN4_PROPT	P82654 hoplobatrax							
471	1	9.1	11	1	TKC2_CALVO	P41518 calliphora							

ALIGNMENTS

RESULT 1	XYLA_STRSQ	STANDARD:	PRT:	9 AA.
AC	XYLA_STRSQ			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DF	XYlose isomerase (bC 5.3.1.5) (Fragment).			
GN	XYLA.			
OS	Streptomyces sp. (strain NCL 82-5-1).			
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;			
OC	Streptomycineae; Streptomycetaceae; Streptomyces.			
OX	NCL1_TaxID-1941;			
RN	SEQUENCE.			
RP	MEDLINE-88326345; PubMed 3415697;			
RK	Pawar H.S., Kannan K., Srinivasan M.C., Vartak H.G.;			
KA	*Purification and characterisation of glucose (xylose) isomerase from			
RT	Chainia sp. (NCL 82-5-1).*			
RL	Brocher, Biophys. Res. Commun. 155:411-417(1988).			
CC	-1- FUNCTION: Involved in D-xylose catabolism.			
CC	-1- CATALYTIC ACTIVITY: D-xylose = D-xylose.			
CC	-1- Cofactor: Binds 2 magnesium ions per subunit (Potential).			
CC	-1- SUBUNIT: Homotetramer.			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-1- SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.			
DR	P18; A31576; A31576.			
DR	HMAP; MF_00455; ?			
DR	InterPro: IPR001998; Xylose isom.			
DR	PROSITE: PS00172; XYLOSE ISOMERASE.1; PARTIAL.			
DR	PROSITE: PS00173; XYLOSE ISOMERASE.2; PARTIAL.			
RW	Isomerase; Pentose shunt; Xylose metabolism; Metal-binding; Magnesium.			
FT	NON_TER			
SQ	SEQUENCE 9 AA: 983 MW: P64BA1EDC5B87DD1 CRC64;			

Query Match 16.4% Score 4: DB 1: Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ACSS 4
DB 1
ACSS 6

RESULT 2
MCRX_METIM STANDARD; PRI: 14 AA;
AC P58615;
DI 28-FEB-2003 (Rel. 41, Created)
DI 28-FEB-2003 (Rel. 41, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Methyl-coenzyme M reductase II alpha subunit (partial) (MCR II
BE alpha) (Fragment).
GN MKIA.
OS Methanobacterium thermoautotrophicum (Strain Marburg / DSM 2153).
OC Archaea: Euryarchaeota: Methanobacteria: Methanobacteriales.
CC Methanobacteriales; Methanobacteriales.
CX NCBI_TaxID:79929;
RN [1]
RP SEQUENCE.
RX MEDLINE:9109470; PubMed:2269306;
RA Kospert S., Linder D., Ellermann J., Thauer R.K.
RI "Two genetically distinct methyl-coenzyme M reductases in
R1 Methanobacterium thermoautotrophicum Strain Marburg and delta H."
R2 Eur. J. Biochem. 194:871-877(1990).
CC -1- FUNCTION: Reduction of methyl-coenzyme M (2-methylthio)
ethanesulfonic acid) with 7-mercaptoheptanoylthreonine phosphate
to methane and an heterodisulfide.
CC -1- CATALYTIC ACTIVITY: CH(3)-S-CoM + H-S-HEP -> CH(4) + CoM-S-S-HEP.
CC -1- COFACTOR: THE ENZYME COMPLEX BINDS TIGHTLY (BUT NOT COVALENTLY)
TO TWO MOLECULES OF COENZYME F430. F430 IS A YELLOW NICKEL
PORPHINOID.
CC -1- PATHWAY: Methanogenesis; last step.
CC -1- SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO GAMMA CHAINS.
CC -1- DEVELOPMENTAL STAGE: THERE ARE TWO MCR COMPLEXES IN THIS BACTERIA.
CC -1- MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE. LATE GROWTH CELLS
CONTAINS MOSTLY MCR I.
CC Methanobacteriales; Oxidoreductases; Methylase family.
KW Methanobacteriales; Oxidoreductases; Methylase family.
FT NON_TER 14
SQ SEQUENCE 14 AA: 1718 MW; D31730562F00E29 CRC64.

Query Match 36.4%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.8e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKKK 10
DB 1
LKKK 14

RESULT 4
RR15_GINBI STANDARD; PRI: 12 AA;
AC P36207;
DI 01-JUN-1994 (Rel. 29, Created)
DI 01-JUN-1994 (Rel. 29, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chloroplast 30S ribosomal protein S16 (Fragment).
GN RPS16.
OS Ginkgo biloba (Ginkgo).
OC Chlorophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Ginkgophyta; Ginkgoales; Ginkgoaceae; Ginkgo.
CX NCBI_TaxID:3311;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:95094313; PubMed:8001171;
RA Richard M., Tremblay C., Bellmore G.
RI "Chloroplastic genomes of Ginkgo biloba and Chlamydomonas moewusii
RT contain a chlB gene encoding one subunit of a light-independent
RT protochlorophyllide reductase."
R2 Curr. Genet. 26:159-165(1994).

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CC -1- SIMILARITY: BELONGS TO THE S16P FAMILY OF RIBOSOMAL PROTEINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC
CC EMBL: J01531; AAA66977.1;
CC HAMAP: MF_00385; 1;
CC INTERPRO: IPR000307; Ribosomal_S16.
CC PROSITE: PS00732; RIBOSOMAL_S16; 1;
CC KW Ribosomal protein; Chloroplast.
CC FT NON_TER 12
CC SQ SEQUENCE 12 AA: 1488 MW; 5700EDAF9D033734 CRC64;

Query Match 27.1%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.7e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VKL 7
DB 2
VKL 4

RESULT 4
ITB5_BOVIN STANDARD; PRI: 13 AA;
AC P80747;
DI 01-NOV-1997 (Rel. 35, Created)
DI 01-NOV-1997 (Rel. 35, Last sequence update)
DI 28-FEB-2003 (Rel. 41, Last annotation update)
DE Integrin beta-5 (Fragment).
GN ITGB5.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Rovidae; Bovinae; Bos.
CX NCBI_TaxID:9913;
RN [1]
RP SEQUENCE
TISSUE:Mammary gland;
RX MEDLINE:97299777; PubMed:9154926;
RA Andersen M.H., Berlund L., Rasmussen J.T., Petersen T.E.;
RT "Bovine PAS-6/7 binds alpha v beta 5 integrins and anionic
RT phospholipids through two domains."
R1 Biochemistry 36:5441-5446(1997).
CC -1- FUNCTION: INTEGRIN ALPHA-V/BETA-5 IS A RECEPTOR FOR FIBRONECTIN.
CC IT RECOGNIZES THE SEQUENCE R-G-D IT ITS LIGAND.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5
CC ASSOCIATES WITH ALPHA-V.
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein (By similarity).
CC -1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
CC INTERPRO: IPR001169; Integrin_beta_C.
CC PROSITE: PS00243; INTEGRIN_BETA; PARTIAL
CC Integrin; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
CC Repeat.
CC FT NON_TER 13
CC SQ SEQUENCE 13 AA: 1299 MW; 844197D005B9865 CRC64;

Query Match 27.1%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.8e-03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSA 4
DB 7
GSA 9

RESULT 5
NP3_LYMSY

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ID NP4_LYNS7 STANDARD: PRT: 13 AA.
AC P8080;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE Lymnaea DF-amide 3
OS Lymnaea stagnalis (Great pond snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora.
OC Lymnaeoidae; Lymnaeidae; Lymnaea.
OX NCBI_TaxID=6523;
RA (1)
RP SEQUENCE.
RC TISSUE: Gasteron.
RX MEDLINE=9424877; PubMed=847775;
RA Johnson A.H., Reicheld J.F.;
RI Lymnaeidae; a new family of neuro-peptides from the pond snail.
RI Lymnaea stagnalis. Clue to cholecystokinin immunoreactivity in
RT invertebrates?;
RL Eur. J. Biochem. 213:875-879(1993).
CC -1- SIMILARITY: RELATED TO THE CHOLECYSTOKININ (CCK) FAMILY.
DR PIR: S12473; S14336.
KW Neuropeptide; Amidation.
FT MOD_RES 13 13
FT UNSURE 12 12
SQ SEQUENCE 13 AA: 1462 MW: 9CA07BA45D58855 CRC64:

Query Match 27.3%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GSA 4
DB 7 GSA 9

RESULT 6
ID NP71_LITFW STANDARD: PRT: 14 AA.
AC P82050;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 7.1 [contains: Uperin 7.1.1].
OS Citraria ewingi (Brown tree frog) (Ewing's tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104896;
RA (1)
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE: Skin secretion;
RA Steininger S., Bowle J.H., Lyons M., Watanabe T.;
RT "An unusual combination of peptides from the skin glands of Ewing's
RT tree frog, Litoria ewingi. Sequence determination and antimicrobial
RT activity.";
RL Aust. J. Chem. 50:889-894(1997).
CC -1- FUNCTION: UPERIN 7.1 SHOWS AN BACTERIAL ACTIVITY AGAINST L. LACTIS
CC AND S. UBERIS. UPERIN 7.1.1 IS INACTIVE.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=1427; METHOD: FAB; RANGE 1-13.
CC -1- MASS SPECTROMETRY: MW=1184; METHOD: FAB; RANGE 1-13.
KW Amphibian defense peptide; Antibiotic; Amidation.
FT PEPTIDE 1 13
FT MOD_RES 3 13
FT MOD_RES 13 13
SQ SEQUENCE 13 AA: 1429 MW: DE17C243CAE322 CRC64:

Query Match 27.3%; Score 4; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 2.0e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SAV 5

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DB 11 SAV 13

RESULT 7
ID MAST_VESBA STANDARD: PRT: 14 AA.
AC P21654;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mastoparan B.
OS Vespa basalis (Hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7444;
RA (1)
RP SEQUENCE.
RC TISSUE: Venom;
RX MEDLINE=91174755; PubMed=2006909;
RA Lo C.-L., Hwang L.-C.;
RT "Structure and biological activities of a new mastoparan isolated
RT from the venom of the hornet Vespa basalis.";
RL Biochem. J. 274:453-456(1991).
CC -1- FUNCTION: Mast cell degranulating peptide. Activates G proteins
CC that couple to phospholipase C.
CC PIR: S14336; S14336.
KW Mast cell degranulation; Amidation.
FT MOD_RES 14 14
FT MOD_RES 14 14
SQ SEQUENCE 14 AA: 1613 MW: D35944CA193A19A2 CRC64:

Query Match 27.3%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKK 8
DB 2 KKK 4

RESULT 8
ID MY14_PHEVI STANDARD: PRT: 14 AA.
AC P46980;
DT 01-NOV-1995 (Rel. 42, Created)
DT 01-NOV-1995 (Rel. 42, Last sequence update)
DT 01-NOV-1995 (Rel. 42, Last annotation update)
DE Myoactive tetradecapeptide (PTP).
OS Pheretima vittata (Earthworm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
OC Lumbricina; Megascolicidae; Pheretima.
OX NCBI_TaxID=46674;
RA (1)
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE: Gut;
RX MEDLINE=96087879; PubMed=8512604;
RA Ukena K., Ouml T., Matsushima O., Ikeda T., Fujita T., Minakata H.,
RA Nomoto K.;
RT "A novel gut tetradecapeptide isolated from the earthworm, Eisenia
RT foetida.";
RL Peptides 16:995-999(1995).
CC -1- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT
CC MUSCLES.
CC -1- SIMILARITY: TO INSECTS ALLATOTROPIN.
KW Neuropeptide; Amidation.
FT MOD_RES 14 14
FT MOD_RES 14 14
SQ SEQUENCE 14 AA: 1522 MW: DA40BEE67CCD91AD CRC64:

Query Match 27.3%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RN [1]
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
 RC TISSUE=SKIN;
 RA *Fernandes J.M.O., Smith V.J., Kemp G.L.
 RT *Partial and N-terminal sequencing of a 4 kDa antibacterial
 RL peptide from skin secretions of *Labeo rohita*.
 RL Submitted (MAY-2002) to the SWISS PRO database.
 CC *FUNCTION: Has antibacterial activity against Gram positive
 CC Lactobacium *L. citreus*.
 CC *SUBCELLULAR LOCATION: Secreted
 CC *TISSUE SPECIFICITY: Skin.
 DR 33-03-2005576; Extracellul:NAS
 DR 33-03-2005745; Plant:Microbial peptide:2005-03-23:NAS
 DR 33-03-2006665; P: xenobiotic metabolism:NAS
 KW Antibiotic.
 FT UNSURE 4 4 OR C.
 FT UNSURE 5 9 OR T.
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA: 1601 MW: 49250.28061267 (8204)

 Query Match: 27.3% Score 3; DB 1; Length 15;
 Best Local Similarity: 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 9 KKA 11
 DB [1]
 4 KKA 6

 RESULT 13
 SODC_PINS
 ID SODC_PINS STANDARD: PRL 15 AA
 AC P81082;
 DT 15-JUL-1998 (Rel. 36, Created)
 DI 15-JUL-1998 (Rel. 36, Last sequence update)
 DI 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Probable superoxide dismutase [Cu,Zn], chloroplast (EC 1.15.1.1)
 DE [Water stress responsive protein 15; (Fragment).
 OS Pinus pinaster (Maritime pine).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 CX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE
 RC TISSUE=Needle.
 RX MEDLINE:98418576; PubMed:9747604;
 RA Costa P., Rahman N., Frigerio J. M., Kromer A., Pionneau C.
 RT *Water deficit-responsive proteins in maritime pine.
 RL Plant Mol. Biol. 38:587-594(1992).
 RN [2]
 RP SEQUENCE
 RC TISSUE=Needle.
 RX MEDLINE:99274068; PubMed:10444293;
 RA Costa P., Pionneau C., Bauw G., Babos G., Rahman N., Kromer A.,
 RA Frigerio J. M., Plomion C.
 RT *Separation and characterization of needle and xylem maritime pine
 RT proteins.
 RC Electrophoresis 20:1098-1108(1999)
 CC *FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems.
 CC *CATALYTIC ACTIVITY: 2 superoxide + 2 H⁺ + O₂ -> H₂O₂ + O₂ (2)
 CC *COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
 CC similarity).
 CC 1 SUBUNIT. Homodimer (By similarity).
 CC *INDUCTION: By water stress.
 CC *SIMILARITY: BELONGS TO THE CU,ZN SUPEROXIDE DISMUTASE FAMILY.
 DR InterPro: IPR001424; SOD_CU_ZN.
 DR Pfam: PF00080; SODcu; 1.
 DR PROSITE: PS00087; SOD_CU_ZN_1; PARTIAL.
 DR PROSITE: PS00432; SOD_CU_ZN_2; PARTIAL.
 KW Antioxidant; oxidoreductase; Metal-binding; P: pin; zinc; Chloroplast.
 FT NON_TER 1 1
 FT NON_TER 15 15

SO SEQUENCE 15 AA: 1381 MW: 0369BF9DBB69CA8 CRC64;

 Query Match: 27.3% Score 3; DB 1; Length 15;
 Best Local Similarity: 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 AAS 3
 DB [1]
 10 AAS 12

 RESULT 14
 THL_CoAFA
 ID THL_CoAFA STANDARD: LFT 15 AA
 AC P81347;
 DT 15-JUL-1998 (Rel. 36, Created)
 DI 15-JUL-1998 (Rel. 36, Last sequence update)
 DI 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Acetyl-CoA acetyltransferase (EC 2.3.1.9) (Acetoacetyl-CoA thiolase)
 DE (CP 13) (Fragment).
 GN THL.
 OS Clostridium pasteurianum.
 CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 CC Clostridium.
 CX NCBI_TaxID=1501;
 RN [1]
 RP SEQUENCE
 RC STRAIN=W5;
 RX MEDLINE:98291870; PubMed:9629918;
 RA Flensburg R., Skjeldal L.
 RT *Two-dimensional gel electrophoresis separation and N-terminal
 RT sequence analysis of proteins from *Clostridium pasteurianum* W5.
 RC Electrophoresis 19:802-806(1998)
 CC *CATALYTIC ACTIVITY: 2 acetyl-CoA -> CoA + acetoacetyl-CoA.
 CC *PATHWAY: JUNCTION IN THE PATHWAY LEADING TO THE PRODUCTION OF
 CC EITHER ACIDS (ACETATE OR BUTYRATE) OR SOLVENTS (ACETONE, BUTANOL
 CC OR ETHANOL).
 CC *SUBUNIT: Heterotrimer (By similarity).
 CC *SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC *SIMILARITY: BELONGS TO THE THIOLEASE FAMILY.
 DR InterPro: IPR002155; Thiolase.
 DR PROSITE: PS00098; THIOLEASE_1; PARTIAL.
 DR PROSITE: PS00737; THIOLEASE_2; PARTIAL.
 DR PROSITE: PS00049; THIOLEASE_3; PARTIAL.
 KW Transferase; Acyltransferase.
 FT NON_TER 15 15
 SO SEQUENCE 15 AA: 1496 MW: 9735820D61BB35FC CRC64;

 Query Match: 27.3% Score 3; DB 1; Length 15;
 Best Local Similarity: 100.0%; Pred. No. 2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 3 SAV 5
 DB [1]
 6 SAV 10

 RESULT 15
 UPO2_METAN
 ID UPO2_METAN STANDARD: PRT 15 AA
 AC P84439;
 DT 28-FEB-2003 (Rel. 41, Created)
 DI 28-FEB-2003 (Rel. 41, Last sequence update)
 DI 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Unknown 70 kDa protein (Fragment).
 OS Metarhizium anisopliae.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Hypocreomycetidae; Hypocreales; Clavicipitaceae;
 CC mitosporic Clavicipitaceae; Metarhizium.
 CX NCBI_TaxID=5530;
 RN [1]
 RP SEQUENCE
 RC STRAIN=54A-1b;

RX MEDLINE:22343006; PubMed:12455610;
 RA Kamp A.M., Bidochna M.J.;
 RT "Protein analysis in a pleomorphically deteriorated strain of the
 insect-pathogenic fungus *Metarhizium anisopliae*."
 RL Can. J. Microbiol. 48:787-792(2002).
 CC -!- MISCELLANEOUS: On the 2D-gel the determined Mw of this unknown
 CC protein is: 70 kDa.
 KW NON_TER 15 15
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 15 AA: 1483 MW: 260A74F07C6B8153 CRC64;

Query Match 27.3%; Score 3; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2e-05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 3
 DB 3 AGS 5

RESULT 16

AL15_CARMA STANDARD: PRT: 8 AA.
 ID AL15_CARMA
 AC P81818;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinus maenas.
 OS Carcinus maenas (Common shore crab) (Green Crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 CC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 CC NCBI_TaxID=5759;
 RN [1]

RP SEQUENCE.
 RC TISSUE: Cerebral ganglion, and Thoracic ganglion.
 RX MEDLINE:98121193; PubMed:9461295;
 RA Drove H., Johnson A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT *allatostatin* superfamily in the shore crab *Carcinus maenas*."
 RL Eur. J. Biochem. 250:727-734(1997).

CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptides; Amides; Multigene family.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 811 MW: 922879D5A476E7D CRC64.

Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
 DB 1 AG 2

RESULT 17

AL15_CARMA STANDARD: PRT: 8 AA.
 ID AL15_CARMA
 AC P81818;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinus maenas.
 OS Carcinus maenas (Common shore crab) (Green Crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 CC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 CC NCBI_TaxID=5759;
 RN [1]

RP SEQUENCE.

RC TISSUE: Cerebral ganglion, and Thoracic ganglion;

RX MEDLINE:98121193; PubMed:9461295;

RA Drove H., Johnson A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT *allatostatin* superfamily in the shore crab *Carcinus maenas*."
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
 CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptides; Amides; Multigene family.
 FT MOD_RES 8 8 AMIDATION.
 SQ SEQUENCE 8 AA: 795 MW: 922879D5A47687D CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
 DB 1 AG 2

RESULT 18

CAD1_ENTFA STANDARD: PRT: 8 AA.
 ID CAD1_ENTFA
 AC P13268;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE Sex pheromone CAD1.
 OS Enterococcus faecalis (Streptococcus faecalis).
 CC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
 CC NCBI_TaxID=1351;
 RN [1]

RP SEQUENCE.
 RX MEDLINE:85051889; PubMed:6437872;
 RA Mori M., Sadaikani Y., Narita M., Fujino M., Kitada C.,
 RA Craig R.A., Clewell D.R., Suzuki A.;
 RT "Isolation and structure of the bacterial sex pheromone, CAD1, that
 RT induces plasmid transfer in *Streptococcus faecalis*."
 RL FEBS Lett. 178:97-100(1984).

CC -!- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
 CC HEMOLYSIN PLASMID PADI.
 KW Pheromone.
 SQ SEQUENCE 8 AA: 819 MW: 047DD732C735B9C7 CRC64;

Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.3e-05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
 DB 7 AG 6

RESULT 19

FAR7_ASCSU STANDARD: PRT: 8 AA.
 ID FAR7_ASCSU
 AC P43171;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 42, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRamide-like neuropeptide AF7.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaris.
 CC NCBI_TaxID=6253;
 RN [1]

RP SEQUENCE.
 RX MEDLINE:95380362; PubMed:7651904;
 RA Cowden C., Stretton A.O.W.;
 RT "Eight novel FMRamide-like neuropeptides isolated from the nematode
 RT *Ascaris suum*."
 RL Peptides 16:491-500(1995).

CC -!- SIMILARITY: BELONGS TO THE FARP (FMRAMIDE RELATED PEPTIDE)

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-!- FUNCTION: MAY REGULATE EXPRESSION OF THE ERYTHROMYCIN RESISTANCE
PROTEIN.
-----
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-----
EMBL: X52085; CAA36403.1; -
PIR: S11157; LFSAME.
Leader peptide: P.asmid.
SEQUENCE 8 AA: 937 MW: FA37340685BDC1A6 CRC64;
-----
Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0
-----
QY 7 LK 8
DB 7 LK 8
-----
RESULT 22
RS1_ERWCH STANDARD; PKT; 8 AA.
AC P37985;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE 30S ribosomal protein S1 (Fragment).
GN RPSA.
OS Erwinia chrysanthemi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID:556;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-3937;
RA Doullie A.; Jousset A.; Faelen M.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: BINDS MRNA: THUS FACILITATING RECOGNITION OF THE
INITIATION POINT. IT IS NEEDED TO TRANSLATE MRNA WITH A SHORT
SHINE-DALGARNO (SD) PURINE-RICH SEQUENCE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.
-----
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or send an email to license@isb-sib.ch).
-----
EMBL: X74750; CAA52769.1; -
PIR: S37141; S37141.
Ribosomal protein; Repeat; RNA-binding.
NON_TER 1
FT 1
SQ SEQUENCE 8 AA: 837 MW: 9E18733DC5B339CD CRC64;
-----
Query Match 18.2%; Score 2; DB 1; Length 8;
Best Local Similarity 100.0%; Prod. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0
-----
QY 3 SA 4
DB 4 SA 5
-----
RESULT 23
VGJG_HSV2H

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ID VGLG_HSV2B STANDARD: PRT: 8 AA.
 AC P81783;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Glycoprotein G (Fragment).
 OS Glycoprotein G (Fragment).
 OC Herpes simplex virus (type 2 / strain B422/BR).
 OC Viruses: JSNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OX NCBI_TaxID=103921;
 RN 1;
 RP SEQUENCE.
 RA Liljeqvist J.-A., Svennerholm H., Bengtsson L.;
 RL Submitted (APR 1999) to the SWISS-prot data bank.
 CC -!- MISCELLANEOUS: THERE ARE SEVEN EXTERNAL GLYCOPROTEINS IN HSV1 AND
 CC 2: GH, GB, GC, GD, GI, AND GE.
 CC -!- MISCELLANEOUS: GLYCOPROTEIN G IS MUCH LARGER IN HSV 2 THAN IN
 CC HSV-1.
 CC Glycoprotein. 8
 KW Glycoprotein. 8
 FT NON_TER
 SQ SEQUENCE 8 AA: 683 MW; 7847686772086486 CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1 3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 2 GS 3
 DB 1 GS 2

 RESULT 24
 WPI_PERAT STANDARD: PRT: 6 AA.
 AC P83195;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Wall protein-1 (PWP-1) (Fragment).
 OS Perkinsus atlanticus.
 OC Eukaryota; Alveolata; Perkinsea; Perkinsida; Perkinsidae; Perkinsus.
 OX NCBI_TaxID=106964;
 RN 1;
 RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND DEVELOPMENTAL STAGE.
 RA MEDLINE=22044350; PubMed=12049410;
 RA Montes J.F., Durfort M., Llido A., Garcia-Vallejo J.;
 RL *Characterization and immunolocalization of a main proteomic
 RL component of the cell wall of the protozoan parasite Perkinsus
 RL atlanticus*;
 RL Parasitology 124:477-484(2002).
 CC -!- FUNCTION: Is a major protein component of the cell wall. May play
 CC a key role in the organization of the cell wall and in promoting
 CC the survival of this parasite.
 CC -!- SUBCELLULAR LOCATION: Cell wall. Disulfide linked to other cell
 CC wall components.
 CC -!- DEVELOPMENTAL STAGE: Expressed throughout all walled developmental
 CC stages.
 KW Cell wall.
 FT NON_TER
 SQ SEQUENCE 8 AA: 765 MW; F17670687816A815 CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1 3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 AG 2
 DB 6 AG 7

 RESULT 25
 ALQ_CHLRE STANDARD: PRT: 9 AA.
 ID ALQ_CHLRE

AC P82678;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Allantoicase (EC 3.5.3.4) (Allantoate amidinohydrolase) (Fragment).
 OS Chlamydomonas reinhardtii.
 OC Chlamydomonas reinhardtii.
 OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
 OC Chlamydomonadaceae; Chlamydomonas.
 OX NCBI_TaxID=3055;
 RN 1;
 RP SEQUENCE.
 RA STRAIN=6145C;
 RX MEDLINE=20318328; PubMed=10860551;
 RA Piedras P., Mucoz A., Aguilar M., Pineda M.;
 RL *Allantoate amidinohydrolase (Allantoicase) from Chlamydomonas
 RL reinhardtii: its purification and catalytic and molecular
 RL characterization*;
 RL Arch. Biochem. Biophys. 378:340-348(2000).
 CC -!- FUNCTION: Catalyzes the degradation of allantoate to (-)-
 CC ureidoglycolate and (-)-ureidoglycolate to glyoxylate.
 CC -!- CATALYTIC ACTIVITY: Allantoate + H(2)O - (-)-ureidoglycolate +
 CC urea.
 CC -!- PATHWAY: Degradation of allantoin (purine catabolism); second
 CC step.
 CC -!- SUBUNIT: Homohexamer.
 CC -!- MISCELLANEOUS: Optimum pH is 6.5 and 8 for the reactions with
 CC allantoate and ureidoglycolate, respectively.
 CC -!- SIMILARITY: BELONGS TO THE ALLANTOICASE FAMILY.
 KW Hydrolase; Purine metabolism.
 FT UNSURE 5 5 OR Y.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA: 943 MW; D934ADD9D6D871F2 CRC64;

 Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1 3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 4 AV 5
 DB 1 AV 2

 RESULT 26
 BUK_CLOPA STANDARD: PRT: 9 AA.
 ID BUK_CLOPA
 AC P81337;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Butyrate kinase (EC 2.7.2.7) (BK) (CP 38) (Fragment).
 GN BUK.
 OS Clostridium pasteurianum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1501;
 RN 1;
 RP SEQUENCE.
 RA STRAIN=W5;
 RX MEDLINE=98291870; PubMed=9629918;
 RA Flengsrud R., Skjeldal L.;
 RL *Two-dimensional gel electrophoresis separation and N-terminal
 RL sequence analysis of proteins from Clostridium pasteurianum W5*;
 RL Electrophoresis 19:802-806(1998).
 CC -!- FUNCTION: Catalyzes the conversion of butyryl-CoA through butyryl
 CC phosphate to butyrate (By similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + 2-butanolate - ADP + butanoyl phosphate.
 CC -!- PATHWAY: Involved in the acidogenic phase of fermentation.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the acetokinase family.
 DR HAMAP: MF_00542; 1.
 DR InterPro: IPR000890; Acetate_kin.
 DR PROSITE: PS01075; ACETATE_KINASE_1; PARTIAL.
 DR PROSITE: PS01076; ACETATE_KINASE_2; PARTIAL.

KW Transferase: Kinase. 9
 FT N-TER 9 AA: 1104 MW: 0550405657272428 CRC64:
 SQ SEQUENCE 9 AA: 1104 MW: 0550405657272428 CRC64:
 Query Match 18.2% Score 2: DB 1: Length 9:
 Best Local Similarity 100.0% Pred. No. 1.3e-05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 AG 2
 DB 1 AG 3
 RESULT 27
 USIP_RABIT
 ID USIP_RABIT STANDARD: PRT: 9 AA:
 AC P01158:
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DB Delta sleep inducing peptide (DSIP)
 DB Delta sleep inducing peptide (DSIP)
 DB Oryctolagus cuniculus (Rabbit)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
 CC NCBI_TaxID:9986;
 RN [1]
 RP SEQUENCE
 RX MEDLINE:7718524; PubMed:862769;
 RA Manier M., Dudler L., Gacster R., Maier P.F., Ruder H.J.,
 RA Schoenberger G.A.;
 K: "the delta sleep inducing peptide (DSIP): Comparative properties of
 K: the original and synthetic nonapeptide";
 K: Experimental 43:548-552(1977);
 RN [2]
 RP SEQUENCE AND SYNTHESIS
 RX MEDLINE:73054421; PubMed:568769;
 RA Schoenberger G.A., Maier P.F., Ruder H.J., Manier M.,
 RA "the delta EEG (sleep)-inducing peptide (DSIP); X: Amino acid
 RI analysis, sequence, synthesis and activity of the nonapeptide";
 RL Pflügers Arch. 376:119-124(1978);
 RN [3]
 RP REVIEW
 RX MEDLINE:87175129; PubMed:3550726;
 RA Graf M.V., Kastin A.J.;
 K: "Delta-sleep-inducing peptide (DSIP): an update";
 RL Peptides 7:1165-1187(1986);
 CC -1- FUNCTION: WHEN INFUSED INTO THE MESOCEPHALIC VENTRICLE OF
 CC RECENT RABBITS INDUCES SLEEPING AND DECREASES ACTIVITY AND
 CC REDUCED MOTOR ACTIVITIES.
 CC -1- MISCELLANEOUS: THIS PEPTIDE WAS OBTAINED FROM ANALYSES OF
 CC OCCIPITAL VENOUS SINUS BLOOD FROM RABBITS KEPT ASLEEP BY ELECTRIC
 CC STIMULATION OF THE THALAMUS.
 CC -1- DATABASE: NAME-Protein Spotlight;
 CC Note-Issue 8 of March 2001;
 CC WWW:"http://www.expasy.org/spotlight/articles/spotlight.html".
 OR PIR: A01422; GDB:
 SQ SEQUENCE 9 AA: 849 MW: 100365804AA07873 CS764;
 Query Match 18.2% Score 2: DB 1: Length 9:
 Best Local Similarity 100.0% Pred. No. 1.3e-05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AG 2
 DB 2 AG 3
 RESULT 28
 FAR2_PANRE
 ID FAR2_PANRE STANDARD: PRT: 9 AA:
 AC P41873:
 DT 21-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide PF2 (SADPNFLRF-amide).
 OS Panagrellus redivivus.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 CC Panagrolaimoidea; Panagrolaimidae; Panagrellus.
 CC NCBI_TaxID:6233;
 RN [1]
 RP SEQUENCE
 RX MEDLINE:93027659; PubMed:1408999;
 RA Geary J.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
 RA Garrison R.D., Williams J.F., Friedman A.R.;
 RT "Two FMRFamide-like peptides from the free-living nematode
 R: Panagrellus redivivus";
 RL Peptides 13:209-214(1992);
 CC -1- FUNCTION: NEURONIC.
 CC -1- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED
 CC CAUDALLY TO THE BASE OF THE PHARYNX.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide: Amidation.
 FT MOD_RES 9 AA: 1066 MW: DA00729C4576AAD CRC64:
 SQ SEQUENCE 9 AA: 1066 MW: DA00729C4576AAD CRC64:
 Query Match 18.2% Score 2: DB 1: Length 9:
 Best Local Similarity 100.0% Pred. No. 1.3e-05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SA 4
 DB 1 SA 2
 RESULT 29
 FAR2_CALVO
 ID FAR2_CALVO STANDARD: PRT: 9 AA:
 AC P41868:
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Calliphramide 13.
 OS Calliphora vomitoria (Blue blowfly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 CC Calliphoridae; Calliphora.
 CC NCBI_TaxID:27454;
 RN [1]
 RP SEQUENCE
 RX MEDLINE:92196111; PubMed:1549595;
 RA Duve H., Johnson A.H., Sewell J.C., Scott A.G., Orchard I.,
 RA Rehfeld J.F., Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
 RT neuropeptides (designated calliphramides) from the blowfly
 R: Calliphora vomitoria";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 CC PIR: D44787; D44787.
 KW Neuropeptide: Amidation.
 FT MOD_RES 9 AA: 1028 MW: 22010699C87AB6D8 CRC64:
 SQ SEQUENCE 9 AA: 1028 MW: 22010699C87AB6D8 CRC64:
 Query Match 18.2% Score 2: DB 1: Length 9:
 Best Local Similarity 100.0% Pred. No. 1.3e-05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AG 2
 DB 1 AG 2
 RESULT 30
 FAR2_CITAC

ID LITG_LITAU STANDARD: PRT: 9 AA.
 AC 2089457;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Litorin
 OS Litoria aurea (Green and golden bell frog)
 OC Amphibia; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Pelodyadinae; Litoria.
 CX NCBI_TaxID:8371;
 RN [1]
 KW TISSUE: Skin secretion;
 RX MEDLINE:75187011; PubMed:1143241;
 RA Anastasi A., Espamer V., Endean R.,
 RF "Amino acid composition and sequence of litorin, a bombesin-like
 RF nonapeptide from the skin of the Australian leopard frog
 RF Litoria aurea."
 RC Experientia 31:510-511(1975).
 RN [2]
 RP SEQUENCE (METHYLATED VARIANT).
 KC TISSUE: Skin secretion;
 RX MEDLINE:78003546; PubMed:908397;
 RA Anastasi A., Montecucchi R.C., Angeloni F., Espamer V., Endean R.,
 RT "Guinea's litorin, the second bombesin-like peptide occurring in
 RT methanol extracts of the skin of the Australian frog Litoria aurea."
 RL Experientia 33:1289-1289(1977).
 CC -1 SUBCELLULAR LOCATION: Secreted.
 CC -1 TISSUE SPECIFICITY: Skin.
 CC -1 SIMILARITY: BELONGS TO THE BOMBESIN/NEUR-PEPTIN B/RANATENSIN
 CC FAMILY.
 DT PIR: S07204; S07204.
 DK InterPro: IPR000874; Bombesin.
 LK Pfam: PF02044; Bombesin; 1.
 CR PROSITE: PS00257; BOMBESIN; 2.
 KW Amphibian defense peptide; Bombesin family; Acetyl-L-homo-methyl-L-
 KW pyrrolidone carboxylic acid.
 FT MISC_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MISC_RES 2 2 METHYLATION (PARIAL).
 FT MISC_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA: 1103 MW: 1103 MW: D70CC1EW6JTC006 (1994).
 Query Match 18.2% Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1; Gap 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CY 4 AV 5
 DB 4 AV 5
 RESULT 31
 LIMP_LOCMI
 ID LIMP_LOCMI STANDARD: PRT: 9 AA.
 AC P11799;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE Locust amyloid-inhibiting peptide (LAIM-IP)
 OS Locusta migratoria (Migratory locust)
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Polyptera;
 OC Neoptera; Orthoptera; Acridoidea; Orthoptera; Acridomorpha;
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.
 CX NCBI_TaxID:7004;
 RN [1]
 KW SEQUENCE.
 RX MEDLINE:92179466; PubMed:1796179;
 RA Schoofs L., Holman G.M., Hayes T.K., Natchus W., de Zool A.L.
 RF "Isolation, identification and synthesis of locust amyloid-inhibiting
 RF peptide (LAIM-IP), a novel biologically active non-peptide from
 RF Locusta migratoria."
 RL Regul. Pept. 36:111-119(1991).

CC -1 FUNCTION: SUPPRESSES SPONTANEOUS CONTRACTIONS OF THE HINOGUT AND
 CC CVIDUCT.
 CC -1 TISSUE SPECIFICITY: NEURONS LOCATED IN TWO VENTRAL CELL CLUSTERS
 CC IN THE SUBESOPHAGEAL GANGLION.
 DR PIR: A60065; AKLQIM.
 KW Amidation; Neuropeptide
 FT MISC_RES 9 AMIDATION.
 SQ SEQUENCE 9 AA: 1050 MW: 1050 MW: 48D7D04472AB6C3 CRC64;
 Query Match 18.2% Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1; Gap 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CY 1 AG 2
 DB 7 AG 8
 RESULT 32
 LIPCA_STAAC
 ID LIPCA_STAAC STANDARD: PRT: 9 AA.
 AC P36884;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Chloramphenicol resistance leader peptide.
 OS Staphylococcus aureus, and
 OS Streptococcus agalactiae.
 OG Plasmid pSCS6, Plasmid pSCS7, and Plasmid pIP501.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 CX NCBI_TaxID:1280, 1311;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES: S. aureus; STRAIN: 436; PLASMID: pSCS7;
 RX MEDLINE:92027652; PubMed:1925326;
 RA Schwarz S., Cardoso M.,
 RT "Nucleotide sequence and phylogeny of a chloramphenicol
 RT acetyltransferase encoded by the plasmid pSCS7 from Staphylococcus
 RT aureus."
 RL Antimicrob. Agents Chemother. 35:1551-1556(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES: S. aureus; PLASMID: pSCS6;
 RX MEDLINE:92388047; PubMed:1517170;
 RA Cardoso M., Schwarz S.,
 RT "Nucleotide sequence and structural relationships of a
 RT chloramphenicol acetyltransferase encoded by the plasmid pSCS6 from
 RT Staphylococcus aureus."
 RL J. Appl. Bacteriol. 72:289-293(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES: S. aureus; PLASMID: pJB112;
 RX MEDLINE:86081739; PubMed:3865770;
 RA Brueckner R., Matzura H.,
 RT "Regulation of the inducible chloramphenicol acetyltransferase gene
 RT of the Staphylococcus aureus plasmid pJB112."
 RL EMBO J. 4:2295-2300(1985).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES: S. agalactiae; PLASMID: pIP501;
 RX MEDLINE:93096867; PubMed:1461942;
 RA Trieu-Cuot P., de Cespedes G., Haurand T.,
 RT "Nucleotide sequence of the chloramphenicol resistance determinant of
 RT the streptococcal plasmid pIP501."
 RL Plasmid 28:272-276(1992).
 CC -----
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DI 16-OCT-2001 (Rel. 40, Last sequence update)
 DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE PYROKININ-1 (Pea-PK-1) (EXPRL-amide)
 OS Euplanetia americana (American cockroach)
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea;
 CC Blattellidae; Periplaneta
 CX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE: Corpora cardiaca;
 RX MEDLINE=57151923; PubMed=9210164;
 KA Predel K., Kellner R., Kaufmann K., Penzlin H., Juedo B.;
 RT "Isolation and structural elucidation of two pyrokinins from the
 RT retrocerebral complex of the American cockroach."
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA
 CC -!- MASS SPECTROMETRY: MW=1010.4; METHOD MALDI-
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro: IPR001484; PYROKININ.
 KW PROSITE: PS00539; PYROKININ; FALSE_NEG.
 DR Neuropeptide; Amidation; Pyrokinin
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA: 1011 MW: 88501760596987061 CRC64:
 Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AG 2
 DB 1 AG 4
 RESULT 47
 PTSP_HOMMO STANDARD; PRI: 9 AA.
 AC P82003;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Prothoracicostatic peptide (Bom. PISP).
 CC Prothoracicostatic peptide (Bom. PISP).
 CC Bombyx mori (Silk moth).
 CC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Lepidoptera; Glossata; Tortysia; Bombycoidea;
 CC Bombycidae; Bombyx.
 CX NCBI_TaxID=7091;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=C145 X N140; TISSUE=Brain;
 RX MEDLINE=2002634; PubMed=10531308;
 RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Naitata S.,
 RA Katoka H.;
 RT "Identification of a prothoracicostatic peptide in the larval brain of
 RT the silkworm, Bombyx mori."
 RL J. Biol. Chem. 274:31169-31173(1999).
 RN [2]
 RP ERATOJ.
 RA Hua Y.-J., Tanaka Y., Nakamura K., Sakakibara M., Naitata S.,
 RA Katoka H.;
 RL J. Biol. Chem. 275:9892-9892(2000).
 CC -!- FUNCTION: Inhibits ecdysteroid biosynthesis in the prothoracic
 CC gland.
 CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- DEVELOPMENTAL STAGE: EARLY FIFTH INSTAR.
 KW Hormone; Amidation.
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA: 1090 MW: 3878C5B4472AB6C3 CRC64:
 Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 SA 4
 DB 7 SA 8
 RESULT 38
 RE42_LITRU STANDARD; PRI: 9 AA.
 ID RE42_LITRU
 AC P82075; P82093;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Rubellidin 4.2/4.3.
 CC Litoria rubella (Desert tree frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 CC Pelodyadidae; Litoria.
 CX NCBI_TaxID=104895;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
 RA Tyler M.J., Wallace J.C.;
 RT "The structure of new peptides from the Australian red tree frog
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study
 RT of evolutionary trends of amphibians."
 RL Aust. J. Chem. 49:955-963(1996).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Skin secretion;
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
 RT "Peptides from the skin glands of the Australian buzzing tree frog
 RT Litoria electrica. Comparison with the skin peptides from Litoria
 RT rubella".
 RL Aust. J. Chem. 52:639-645(1999).
 CC -!- FUNCTION: Shows neither neuropeptide activity nor antibiotic
 CC activity.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- PTM: Rubellidin 4.2 seems to differ from Rubellidin 4.3 by its C-
 CC terminal amidation.
 CC -!- MASS SPECTROMETRY: MW=883; METHOD=FAB.
 KW Amphibian defense peptide; Amidation.
 FT MOD_RES 9 9 AMIDATION.
 SQ SEQUENCE 9 AA: 884 MW: 2C2D77205AA72728 CRC64:
 Query Match 18.2%; Score 2; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AG 2
 DB 1 AG 2
 RESULT 39
 THYF_PIG STANDARD; PRI: 9 AA.
 ID THYF_PIG
 AC P01255;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Thymic factor.
 OS Sus scrofa (Pig).


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RESULT 43
COMM_RAT:
ID COXM_RAT STANDARD: PRT: 10 AA.
AC P80431:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide VIIb, Mitochondrion (Ref. 19,3,1)
DE (Fragment).
GN COX7B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Rattus
OX NCBI_TaxID=10116;
FN [1]
RP SEQUENCE.
RC SPRAIN-Mistral; TISSUE=Liver;
RX MEDLINE=95124529; PubMed=7601105;
RA Schaeffer H., Noack H., Halandik W., Prandt D., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart: Enzymic properties and
RT amino terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform."
RL Eur. J. Biochem. 230:235-241(1995)
CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-ENCODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyanide + 2 e- + 2 H+(2) -> 4 ferrocyanide
CC c + 2 H(2).
DR PIR: S65387; S65387.
KW oxidoreductase; Mitochondrion.
FT NIN_TIR 10
SQ SEQUENCE 10 AA: 1210 MW: 280708771A3328 DPC64;

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KK 9
DB 4 KK 5

RESULT 44
FARG_CALVO:
ID FARG_CALVO STANDARD: PRT: 1 AA
AC P41867:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE CalliPMRFamide 12.
DE Calliphora vomitoria (Blue blowfly).
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Protophaga;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscophora; Gastrophila;
OC Calliphoridae; Calliphora.
OX NCBI_TaxID=27454;
FN [1]
RP SEQUENCE.
RC TISSUE=Thoracic ganglion;
RX MEDLINE=92196111; PubMed=1549595;
RA Dyer H., Johnson A.H., Sewell J.C., Scott A.G., Orchard L.;
RA Reletho J.F., Thorpe A.;
RT "Isolation, structure, and activity of the Met and Pro-NW2
RT neuropeptides (designated calliPMRFamides) from the blowfly
RT Calliphora vomitoria."
RL Proc. Natl. Acad. Sci. U.S.A. 89:2347-2350(1992)
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: C44787; C44787.
KW Neuropeptide; Amidation.
FT MOD_RFS 10
SQ SEQUENCE 10 AA: 1156 MW: 22810399C44A86D8 CKE64;

Query Match 18.2% Score 2; DB 1; Length 10;

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Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
DB 2 AG 3

RESULT 45
FARP_MYTED:
ID FARP_MYTED STANDARD: PRT: 10 AA.
AC P42560:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE FMRFamide-like neuropeptide ALAGDHFRF-amide.
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
FN [1]
RP SEQUENCE.
RX MEDLINE=93047883; PubMed=1358534;
RA Walker R.J.;
RT "Neuroactive peptides with an N-terminus or Famide or Famide carboxyl terminal."
RL Comp. Biochem. Physiol. 102C:213-222(1992).
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: A58365; A58365.
KW Neuropeptide; Amidation.
FT MOD_RES 10
SQ SEQUENCE 10 AA: 1180 MW: C2F80CC9C1EAA87D CRC64;

Query Match 18.2% Score 2; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AG 2
DB 3 AG 4

RESULT 46
FIBB_CERS1:
ID FIBB_CERS1 STANDARD: PRT: 10 AA.
AC P14537:
DT 01-JAN-1996 (Rel. 13, Created)
DT 01-JAN-1996 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB.
OS Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
OX NCBI_TaxID=9807;
FN [1]
RP SEQUENCE.
RC O'Neill P.B., Poolittle R.F.;
RA "Mammalian phylogeny based on fibrinopeptide amino acid sequences."
RL Syst. Zool. 22:590-595(1973).
CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR InterPro: IPR002181; Fibrinogen_C.
DR PROSITE: PS00514; FIBRIN_AG_C_DOMAIN; PARTIAL.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 10 FIBRINOPEPTIDE B.

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FI NON_ERK 10 10
 SQ SEQUENCE 10 AA: 9402H2b27H2G05AA (8/9/4)
 Query Match 18.2% Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 AV 5
 ID 11
 ID 5 AV 7
 RESULT 47
 CAJUL_HUMAN STANDARD: PRT: 10 AA
 AC P01358;
 DT 21-JUL-1996 (Rel. 01, Created)
 DT 21-JUL-1996 (Rel. 01, Last sequence update)
 DE 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Gastric juice peptide.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN 111
 RP SEQUENCE
 RX MEDLINE 75150948; PubMed 5549485;
 RA "Peptides of normal human gastric juice."
 RL FALCZ L. Proc 018 Res. 2:117-126(1972).
 DR PIR: A01428; GXR01.
 DR CAC: G339027986; P01358; NAS.
 FT PEPTIDE 1 10 CASPRLDPTPEPTIDE 1;
 FT PEPTIDE 2 10 CASPRLDPTPEPTIDE 2;
 SQ SEQUENCE 10 AA: 1004 MW: 6785.60 203489.758942
 Query Match 18.2% Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AG 2
 ID 1 AG 4
 RESULT 48
 GRP_RANK1 STANDARD: PRT: 10 AA
 AC P42263;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DE 26-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuroendocrine.
 OS Rana tigrinoides (laughing frog) (Bates 1964)
 OC Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyla; Hylinae; Hyla;
 OX NCBI_TaxID=8406;
 RN 111
 RP SEQUENCE
 RX MEDLINE 91315477; PubMed-18764100;
 RA Connors J.M., Hartle P., Vardany H.
 RT "Primary structures of the bombesin-like peptides of the genus Hyla." show that bombesin is not the archetypal question mark peptide.
 RL Biochem. Biophys. Res. Commun. 198:226-234(1994)
 OC 1 SUBCELLULAR LOCATION: Secreted.
 CC 1 SIMILARITY: BELONGS TO THE BOMBESIN-LIKE PEPTIDE FAMILY.
 DR PIR: P00177; P00177.
 DR Inferred from G08874; Bombesin.
 DR Clam; P04644; Bombesin; 1;
 DR PROSITE, P50247; BOMBESIN; 1

KW Bombesin family; Amidation.
 FI MOD_RES 10 10
 SQ SEQUENCE 10 AA: 1094 MW: P81FBAB862CDC371 CRC64;
 Query Match 18.2% Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GS 3
 ID 11
 ID 1 GS 2
 RESULT 49
 LABA_JATMU STANDARD: PRT: 10 AA
 AC P11270;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Labadiin.
 OS Jatropha multifida (Physic nut).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids 1; Malpighiales; Euphorbiales; Jatropha.
 OX NCBI_TaxID=3996;
 RN 111
 RP SEQUENCE
 RX MEDLINE 115502; Latex;
 RA Kosari S., van der Sluis W.G., Boelens R., T'Hart L.A., Labadie R.P.;
 RT "Labadiin, a novel cyclic decapeptide from the latex of Jatropha multifida L. (Euphorbiaceae). Isolation and sequence determination by means of two-dimensional NMR".
 RL PERS Lett. 25:591-95(1989).
 CC 1 FUNCTION: LABADIIN IS AN ACTIVE PEPTIDE WHICH INHIBITS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION IN VITRO. ACTIVITY SEEMS TO BE BASED ON AN INTERACTION WITH C1.
 CC 1 PIN: This is a cyclic peptide.
 CC 1 DISEASE: LATEX OF THIS PLANT IS USED IN FOLKLORIC MEDICINE FOR TREATMENT OF INFECTED WOUNDS, SKINS INFECTIONS AND SCABIES.
 SQ SEQUENCE 10 AA: 1089 MW: D98AA06362C1B362 CRC64;
 Query Match 18.2% Score 2; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AG 2
 ID 1 AG 2
 RESULT 50
 MALE_KLEPN STANDARD: PRT: 10 AA
 AC G05564;
 DT 01-DEC-1994 (Rel. 30, Created)
 DT 01-DEC-1994 (Rel. 30, Last sequence update)
 DT 30-MAY-2003 (Rel. 39, Last annotation update)
 DE Maltose-binding periplasmic protein (Maltodextrin-binding protein) (MBP) (Bacterial).
 OX NCBI_TaxID=574;
 RN 111
 RP SEQUENCE FROM N A
 RC STRAIN 1033 5P14 / KAY2026;
 RX MEDLINE 94211295; PubMed-8459773;
 RA Bachelier S., Petit L., Bulteau M., Glisson E.;
 RT "Bacterial maltodextrin-binding protein (MBP) are present in the genome of Klebsiella".
 RL Nucleic Acids Res. 27:667-671(1999).

```

CC -!- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE
CC TRANSPORT SYSTEM. INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AND
CC CHEMOAXIS TOWARD MALTOSE/GUSACCHARIDES
CC -!- SUBCELLULAR LOCATION: Periplasmic
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE BINDING
CC PROTEIN FAMILY 1.
CC .....
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC .....
DR EMBL: X68129; CAA48406.1;
DR InterPro: IPR006061; SRP_dom1.
DR PROSITE: PS01037; SRP_BACTERIAL_1; PARTIAL.
KW Transport; Sugar transport; Periplasmic.
FT NON_TER 1
SU SEQUENCE 10 AA: 1159 MW: 850862441566244A 0.6764:
Query Match 18.2% Score 27 DB 1 Length 107
Best Local Similarity 100.0% Pred. No. 2.5e+04
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 7 1K 8
DB 1 1K 2

```

Search completed: September 30, 2003, 10:26:02
 Job Time : 8.25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 30, 2003, 10:07:04 : Search time: 31.966 / Seconds
(without alignment)
89.339 Million cell updates/sec

Title: US-09-787-443-4
Perfect score: 11
Sequence: 1 AGSAVKLKKA 1:

Scoring table: OL100
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 3

Total number of hits satisfying chosen parameters: 3459

Minimum DB seq length: 8
Maximum DB seq length: 15

Post-processing: Listing first 500 summaries

Database : SPTRMBL23:
1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacteriap:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	36.4	9	2	Q46179 clostridium
2	4	36.4	14	2	Q9R782 bacillus li
3	4	36.4	14	2	Q52616 escherichia
4	4	36.4	15	2	Q52304 escherichia
5	3	27.3	8	2	Q9A3P4 artibroacte
6	3	27.3	8	2	Q56429 thermus the
7	3	27.3	8	3	Q9HDS4 aspergillus
8	3	27.3	8	3	Q36808 nicotiana p
9	3	27.3	8	8	Q34909 locusta mig
10	3	27.3	8	11	Q50615 mus musculu
11	3	27.3	9	2	Q45852 clostridium
12	3	27.3	9	4	Q16276 homo sapien
13	3	27.3	9	4	Q9BX14 homo sapien
14	3	27.3	9	5	Q8W119 drosophila
15	3	27.3	9	11	Q9QW63 mus musculu
16	3	27.3	9	11	Q9QW60 mus musculu

17	3	27.3	9	12	Q69100 herpes simp
18	3	27.3	10	2	Q60194 spiroplasma
19	3	27.3	10	3	Q9HDS2 aspergillus
20	3	27.3	10	3	Q9HDS1 aspergillus
21	3	27.3	11	2	Q9S618 prochloroco
22	3	27.3	11	2	Q44090 acholeptasm
23	3	27.3	11	3	Q9HDS9 aspergillus
24	3	27.3	11	3	Q43131 aspergillus
25	3	27.3	11	3	Q9HDS8 aspergillus
26	3	27.3	11	3	Q9HDS7 aspergillus
27	3	27.3	11	3	Q42762 aspergillus
28	3	27.3	11	3	Q43130 aspergillus
29	3	27.3	11	3	Q9HDS3 aspergillus
30	3	27.3	11	7	Q77908 oreochromis
31	3	27.3	11	11	Q9QXM6 mus musculu
32	3	27.3	12	4	Q9CE14 homo sapien
33	3	27.3	12	5	Q9TY79 panulirus i
34	3	27.3	12	5	Q61574 ostertagia
35	3	27.3	12	10	Q41744 zea mays (m
36	3	27.3	12	10	P94011 arabidopsis
37	3	27.3	12	11	Q8CJ30 mus musculu
38	3	27.3	12	13	Q8JHC1 cyprinus ca
39	3	27.3	12	13	Q90XT2 larus glauc
40	3	27.3	12	13	Q90XT5 puffinus gr
41	3	27.3	12	13	Q90XU4 phalacrocor
42	3	27.3	12	13	Q90XT0 grus canade
43	3	27.3	12	13	Q8JHC2 carassius a
44	3	27.3	13	2	Q9R3R6 prochloroco
45	3	27.3	13	4	Q16141 homo sapien
46	3	27.3	13	4	Q9UJ73 homo sapien
47	3	27.3	13	6	Q9TQS2 equus cabal
48	3	27.3	13	6	Q9TQS1 equus cabal
49	3	27.3	13	8	Q9T569 zea mays (m
50	3	27.3	13	8	Q33417 digitalis p
51	3	27.3	13	11	Q9QV14 rattus sp.
52	3	27.3	13	11	Q9WT26 mus musculu
53	3	27.3	14	2	Q8KSE3 enterococu
54	3	27.3	14	2	Q47335 escherichia
55	3	27.3	14	3	Q8JIG5 ashbya goss
56	3	27.3	14	4	Q96Q50 homo sapien
57	3	27.3	14	6	Q8HYM2 felis silve
58	3	27.3	14	11	Q91Y24 mus musculu
59	3	27.3	14	11	Q99PB8 mus musculu
60	3	27.3	14	12	Q66201 transmissib
61	3	27.3	14	15	Q98Y97 human immun
62	3	27.3	15	2	Q52586 agrobacteri
63	3	27.3	15	2	Q46456 clostridium
64	3	27.3	15	2	Q9R544 mycobacteri
65	3	27.3	15	2	Q9R4F0 desulfovibr
66	3	27.3	15	2	Q5S0V1 nitrogen fi
67	3	27.3	15	4	Q9UCC7 homo sapien
68	3	27.3	15	6	Q9TR45 bos taurus
69	3	27.3	15	8	Q37016 nicotiana a
70	3	27.3	15	10	Q9SQ16 oryza sativ
71	3	27.3	15	10	Q9S8D5 cynara card
72	3	27.3	15	10	Q9S814 zea mays (m
73	3	27.3	15	10	P82431 nicotiana t
74	3	27.3	15	10	P82439 nicotiana t
75	3	27.3	15	11	P82446 nicotiana t
76	3	27.3	15	11	Q9QVA9 rattus sp.
77	3	27.3	15	11	Q9QVNO rattus sp.
78	2	18.2	8	2	Q9RQ49 buchnera ap
79	2	18.2	8	2	Q9J5R0 staphylococ
80	2	18.2	8	2	Q56759 xanthobacte
81	2	18.2	8	2	O87471 haemophilus
82	2	18.2	8	2	Q9Z1E9 neisseria m
83	2	18.2	8	2	Q9R9E0 bacillus su
84	2	18.2	8	2	Q9R5R0 shigella dy
85	2	18.2	8	2	Q9R4M3 enterococu
86	2	18.2	8	2	Q51594 escherichia
87	2	18.2	8	2	P72221 pseudomonas
88	2	18.2	8	2	P83158 anabaena sp
89	2	18.2	8	2	P83152 anabaena sp

90	2	18.2	8	2	Q94PX7	Q94PX7	felis silve
91	2	18.2	8	8	Q8MC34	Q8MC34	heimia myrt
92	2	18.2	8	8	Q8MC32	Q8MC32	rotaria indi
93	2	18.2	8	8	Q8MC32	Q8MC32	sonneratia
94	2	18.2	8	8	Q8MC32	Q8MC32	telis libye
95	2	18.2	8	8	Q8MC32	Q8MC32	mesata lued
96	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
97	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
98	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
99	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
100	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
101	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
102	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
103	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
104	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
105	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
106	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
107	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
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112	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
113	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
114	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
115	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
116	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
117	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
118	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
119	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
120	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
121	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
122	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
123	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
124	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
125	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
126	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
127	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
128	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
129	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
130	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
131	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
132	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
133	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
134	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
135	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
136	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
137	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
138	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
139	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
140	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
141	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
142	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
143	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
144	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
145	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
146	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
147	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
148	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
149	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
150	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
151	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
152	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
153	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
154	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
155	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
156	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
157	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
158	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
159	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
160	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
161	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph
162	2	18.2	8	8	Q8MC32	Q8MC32	bacterioph


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KW TRANSFORMER.
SQ SEQUENCE 4 AA: 1041 MW: 492402.24ZD106.05 CRE64.

Query Match
Best Local Similarity 100.0% Pred. No. 8 3e-05
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

2Y 4 AVKX 7
III
DL 4 AVKX 7

RESULT 2
Q52604 PRELIMINARY: PRI: 4 AA
AC Q9R782
BT 01 MAY 2003 (EMBL:rel. 13, Created)
DT 01 MAY 2003 (EMBL:rel. 13, Last sequence update)
DI 01 MAY 2003 (EMBL:rel. 13, Last annotation update)
DE beta lactamase (Fragment);
OS Bacillus licheniformis;
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OX NCBI_TaxID:1492;
RN [1];
RP SEQUENCE FROM N.A.;
RA MESLINE-8659219; PubMed 2999074;
RA Frost L.S., Finlay B.B., Oquendoth A., Paranchych W., Lee J.S.;
RT "Cloning, expression, and sequence analysis of pilin from F-like
plasmids";
RC J. Bacteriol. 164:1248-1247(1985);
DR EMBL: M19710; AAA92663.1;
DK EMBL: K03091; AAA92759.1;
KW Plasmid;
FT NON-TER 14
SQ SEQUENCE 14 AA: 1665 MW: 987442.41ZD106.05 CRE64

Query Match
Best Local Similarity 100.0% Pred. No. 1 4e-05
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

2Y 6 KLKK 9
III
DL 9 KLKK 12

RESULT 3
Q52604 PRELIMINARY: PRI: 4 AA
AC Q52604
BT 01 NOV 1996 (EMBL:rel. 01, Created)
DT 01 NOV 1996 (EMBL:rel. 01, Last sequence update)
DI 01 FEB 2001 (EMBL:rel. 19, Last annotation update)
DE beta lactamase (Fragment);
OS Escherichia coli;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OX NCBI_TaxID:562;
RN [1];
RP SEQUENCE FROM N.A.;
RA MESLINE-8659219; PubMed 2999074;
RA Frost L.S., Finlay B.B., Oquendoth A., Paranchych W., Lee J.S.;
RT "Cloning, expression, and sequence analysis of pilin from F-like
plasmids";
RC J. Bacteriol. 164:1248-1247(1985);
DR EMBL: M05794; CAA29241.1;
DK EMBL: K03092; AAA92759.1;
KW Plasmid;
FT NON-TER 14
SQ SEQUENCE 14 AA: 1713 MW: 507591188B3511A CRE64

Query Match
Best Local Similarity 100.0% Pred. No. 1 4e-05
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

2Y 6 KLKK 9
III
DL 9 KLKK 12

RESULT 4
Q52604 PRELIMINARY: PRI: 15 AA
AC Q52604
BT 01 NOV 1996 (EMBL:rel. 01, Created)
DT 01 NOV 1996 (EMBL:rel. 01, Last sequence update)
DI 01 NOV 1999 (EMBL:rel. 12, Last annotation update)
DE beta lactamase (Fragment);
OS Escherichia coli;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OX NCBI_TaxID:562;
RN [1];
RP SEQUENCE FROM N.A.;
RA MESLINE-8659219; PubMed 2999074;
RA Frost L.S., Finlay B.B., Oquendoth A., Paranchych W., Lee J.S.;
RT "Cloning, expression, and sequence analysis of pilin from F-like
plasmids";
RC J. Bacteriol. 164:1248-1247(1985);
DR EMBL: M19710; AAA92663.1;
DK EMBL: K03091; AAA92759.1;
KW Plasmid;
FT NON-TER 15
SQ SEQUENCE 15 AA: 1844 MW: 507591188B3511A CRE64

Query Match
Best Local Similarity 100.0% Pred. No. 1 5e+03
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

2Y 6 KLKK 9
III
DL 8 KLKK 11

RESULT 5
Q52604 PRELIMINARY: PRI: 8 AA
AC Q9A394
BT 01 JUN 2001 (EMBL:rel. 17, Created)
DT 01 JUN 2001 (EMBL:rel. 17, Last sequence update)
DI 01 MAR 2002 (EMBL:rel. 20, Last annotation update)
DE Serine hydrolase (Fragment);
OS Actinobacter sp. 11N;
OC Bacteria; Actinobacteriales; Actinomycetales;
OX NCBI_TaxID:154692;
RN [1];
RP SEQUENCE FROM N.A.;
RA STRAIN 11N;
RA Meskys R., Harris R.J., Casati V., Hasran J., Scrutton N.S.;
RT "Genetic organization of the genes involved in dimethylglycine and
serine degradation in Actinobacter spp.: implications for glycine
betaine catabolism";
RC J. Bacteriol. 183:1248-1247(1985);
DR EMBL: AF129478; AAK16481.1;
DK EMBL: K03092; AAA92759.1;
KW Methyltransferase; Translocase;
FT NON-TER 1
SQ SEQUENCE 8 AA: 898 MW: 6R:8705333372457 CRE64

Query Match
Best Local Similarity 100.0% Pred. No. 8 3e-05
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

2Y 7 KLKK 9
III

```

```

KW TRANSFORMER.
SQ SEQUENCE 4 AA: 1041 MW: 492402.24ZD106.05 CRE64.

Query Match
Best Local Similarity 100.0% Pred. No. 8 3e-05
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

2Y 6 KLKK 9
III
DL 7 KLKK 10

RESULT 4
Q52604 PRELIMINARY: PRI: 15 AA
AC Q52604
BT 01 NOV 1996 (EMBL:rel. 01, Created)
DT 01 NOV 1996 (EMBL:rel. 01, Last sequence update)
DI 01 NOV 1999 (EMBL:rel. 12, Last annotation update)
DE beta lactamase (Fragment);
OS Escherichia coli;
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OX NCBI_TaxID:562;
RN [1];
RP SEQUENCE FROM N.A.;
RA MESLINE-8659219; PubMed 2999074;
RA Frost L.S., Finlay B.B., Oquendoth A., Paranchych W., Lee J.S.;
RT "Cloning, expression, and sequence analysis of pilin from F-like
plasmids";
RC J. Bacteriol. 164:1248-1247(1985);
DR EMBL: M19710; AAA92663.1;
DK EMBL: K03091; AAA92759.1;
KW Plasmid;
FT NON-TER 15
SQ SEQUENCE 15 AA: 1844 MW: 507591188B3511A CRE64

Query Match
Best Local Similarity 100.0% Pred. No. 1 5e+03
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

2Y 6 KLKK 9
III
DL 8 KLKK 11

RESULT 5
Q52604 PRELIMINARY: PRI: 8 AA
AC Q9A394
BT 01 JUN 2001 (EMBL:rel. 17, Created)
DT 01 JUN 2001 (EMBL:rel. 17, Last sequence update)
DI 01 MAR 2002 (EMBL:rel. 20, Last annotation update)
DE Serine hydrolase (Fragment);
OS Actinobacter sp. 11N;
OC Bacteria; Actinobacteriales; Actinomycetales;
OX NCBI_TaxID:154692;
RN [1];
RP SEQUENCE FROM N.A.;
RA STRAIN 11N;
RA Meskys R., Harris R.J., Casati V., Hasran J., Scrutton N.S.;
RT "Genetic organization of the genes involved in dimethylglycine and
serine degradation in Actinobacter spp.: implications for glycine
betaine catabolism";
RC J. Bacteriol. 183:1248-1247(1985);
DR EMBL: AF129478; AAK16481.1;
DK EMBL: K03092; AAA92759.1;
KW Methyltransferase; Translocase;
FT NON-TER 1
SQ SEQUENCE 8 AA: 898 MW: 6R:8705333372457 CRE64

Query Match
Best Local Similarity 100.0% Pred. No. 8 3e-05
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

2Y 7 KLKK 9
III

```


RA STRAIN:1X12_10_2S;
 RA Geiser D.M., Gerner J.W., Horn B.W., Taylor J.W.;
 "The phylogenetics of mycotoxin and sclerotium production in
 Aspergillus flavus and Aspergillus oryzae."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBS databases.
 KW EMBL: AF261877; AAG16361.1;
 KW Polyprotein.
 FT NON_TER
 ST 11
 SQ SEQUENCE 11 AA: 114 MW: 8F0HEH03H2C72AB5 CRC64;
 Query Match 27.4% Score 3; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.2e-04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGS 4
 DB 2 AGS 4
 RESULT 27
 042762 PRELIMINARY; PRT; 11 AA
 AC 042762;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE TrpC polyprotein (Fragment).
 GN TRPC.
 OS Aspergillus flavus.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Mitosporic Trichocomaceae; Aspergillales.
 OX NCBI_TaxID:5059;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN:5.1;
 RA Geiser D.M., Pitt J.L., Taylor J.W.;
 "Cryptic speciation and recombination in the aflatoxin producers
 Aspergillus flavus."
 RL EMBL: AF046857; AAC01692.1;
 RL EMBL: AF046857; AAC01692.1;
 KW Polyprotein.
 FT NON_TER
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 DB 2 AGS 4
 RESULT 28
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 AC 043130;
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 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 18, Last annotation update)
 DE TrpC polyprotein (Fragment).
 GN TRPC.
 OS Aspergillus parasiticus.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
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 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN:CA3-CL, and CA1-05;
 RA Geiser D.M., Pitt J.L., Taylor J.W.;
 "Cryptic speciation and recombination in the aflatoxin producers

RE Fungus Aspergillus flavus."
 RA Proc. Natl. Acad. Sci. U.S.A. 95:368-393(1998).
 DR EMBL: AF036970; AAC01705.1;
 DR EMBL: AF036869; AAC01704.1;
 KW Polyprotein.
 FT NON_TER
 ST 11
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 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE TrpC polyprotein (Fragment).
 GN TRPC.
 OS Aspergillus flavus.
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 OX NCBI_TaxID:5059;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC STRAIN:A12C;
 RA Geiser D.M., Gerner J.W., Horn B.W., Taylor J.W.;
 "The phylogenetics of mycotoxin and sclerotium production in
 Aspergillus flavus and Aspergillus oryzae."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBS databases.
 KW Polyprotein.
 FT NON_TER
 ST 11
 SQ SEQUENCE 11 AA: 1133 MW: 8F0HEH03H2C72AB5 CRC64;
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 Best Local Similarity 100.0%; Pred. No. 1.2e-04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 AC 077908;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class II B locus 2 (Fragment).
 GN Oryzomys niloticus (Nile tilapia).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
 OC Cichlidae; Oreochromis
 OX NCBI_TaxID:8128;
 RN 1;
 RP SEQUENCE FROM N.A.
 RC MEDLINE:9835113; PubMed:7649549;
 RA Malaga Trillo E., Zaleska-Rozcynska Z., McAndrew B., Vincek V.,
 RA Figueroa F., Sultmann H., Krell J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci."
 RL Genetics 149:1527-1547(1998).


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CX CYPRINIDAE: CARASSIUS.
CX NCBI: TaxID 7957;
RN
SE
SA 01-NOV-1996 (TRENBLER). 01, Created;
SI 01-NOV-1996 (TRENBLER). 01, Last sequence update;
SI 01-DEC-2001 (TRENBLER). 19, Last annotation update;
DR EMBL: AF51602; AAM77902.1;
DR NCBI: AF51602; AAM77902.1;
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AC C99496;
DT 01-MAY-2000 (TRENBLER). 19, Created;
DT 01-MAY-2000 (TRENBLER). 19, Last sequence update;
DT 01-DEC-2001 (TRENBLER). 19, Last annotation update;
DE Cytochrome b6/f complex subunit IV (Fragment);
GN PEP2;
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
CX NCBI: TaxID 9606;
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SEQUENCE FROM N.A.
RX MEDLINE: 92220069; PubMed: 7548922;
RA Sadekane Y., Masda K., Kuroda Y., Hori K.;
RT "Identification of mutations in DNA polymerase beta (PNAS) from patients with Werner syndrome";
RL Gene 247:241-253(2000);
DR EMBL: AF076221; AAG21273.1;
DR NCBI: AF076221; AAG21273.1;
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Query Match
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Matches 3; Conservative 0; Mismatches 0; Gaps 0;
QY 7 LKK 9
LD 4 LKK 6
RESULT 45
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AC C99496;
DT 01-MAY-2000 (TRENBLER). 01, Created;
DT 01-NOV-1996 (TRENBLER). 01, Last sequence update;
DT 01-DEC-2001 (TRENBLER). 19, Last annotation update;
DE Mutant DNA polymerase beta (Fragment);
GN
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
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RX MEDLINE: 92220069; PubMed: 7548922;
RA Sadekane Y., Masda K., Kuroda Y., Hori K.;
RT "Identification of mutations in DNA polymerase beta (PNAS) from patients with Werner syndrome";
RL Gene 247:241-253(2000);
DR EMBL: AF076221; AAG21273.1;
DR NCBI: AF076221; AAG21273.1;
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QY 1 AGS 4
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DT 01-MAY-2000 (TRENBLER). 19, Created;
DT 01-MAY-2000 (TRENBLER). 19, Last sequence update;
DT 01-MAY-2000 (TRENBLER). 19, Last annotation update;
DE Transferrin (Fragment);
GN Equus caballus (Horse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus;
CX NCBI: TaxID 9746;
RN
RP
SEQUENCE FROM N.A.
RX Glifford M., Brandon R.B., Bell T.K.;
RT "Further identification of single nucleotide polymorphisms in the equine transferrin gene";
RL Submitted (Sep 1999) to the EMBL/GenBank/DBJ databases;
DR EMBL: AF185748; AAF05462.1;
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DR EMBL: AF185750; AAF05464.1;
DR EMBL: AF185751; AAF05465.1;
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CGM protein protein search, using SW mode.

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Post-processing: listing first 500 summaries

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	5	45.5	10	1	US-08-434-120-110	Sequence 129, App
2	5	45.5	10	4	US-09-115-737-127	Sequence 129, App
3	5	45.5	13	3	US-08-465-325-148	Sequence 47, App
4	5	45.5	13	3	US-08-465-325-148	Sequence 47, App
5	5	45.5	14	6	5304-01-9	Patent No. 5304531
6	4	36.4	8	1	US-08-193-521-1	Sequence 147, App
7	4	36.4	8	1	US-08-434-120-110	Sequence 108, App
8	4	36.4	8	2	US-08-465-325-127	Sequence 107, App
9	4	36.4	8	2	US-08-621-803-206	Sequence 257, App
10	4	36.4	8	2	US-08-621-803-206	Sequence 259, App
11	4	36.4	8	2	US-08-621-803-206	Sequence 243, App
12	4	36.4	8	2	US-08-928-958-17	Sequence 17, App
13	4	36.4	8	2	US-09-072-429-17	Sequence 17, App
14	4	36.4	8	3	US-09-217-352-206	Sequence 217, App
15	4	36.4	8	4	US-09-022-065A-11	Sequence 11, App
16	4	36.4	8	4	US-39-115-737-112	Sequence 11, App
17	4	36.4	9	1	US-08-193-521-1	Sequence 15, App
18	4	36.4	9	1	US-08-434-120-110	Sequence 109, App
19	4	36.4	9	1	US-08-465-325-128	Sequence 108, App
20	4	36.4	9	1	US-08-434-120-110	Sequence 11, App
21	4	36.4	9	1	US-08-434-120-110	Sequence 12, App
22	4	36.4	9	1	US-08-434-120-110	Sequence 13, App
23	4	36.4	9	1	US-08-434-120-110	Sequence 23, App
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25	4	36.4	9	1	US-08-434-120-110	Sequence 27, App
26	4	36.4	9	1	US-08-434-120-110	Sequence 138, App
27	4	36.4	10	1	US-08-193-521-1	Sequence 15, App

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30	4	36.4	10	1	US-08-465-325-148	Sequence 148, App
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34	4	36.4	10	2	US-08-653-632-39	Sequence 39, Appl
35	4	36.4	10	2	US-08-621-803-205	Sequence 205, App
36	4	36.4	10	2	US-08-621-803-205	Sequence 180, App
37	4	36.4	10	2	US-08-150-260A-437	Sequence 437, App
38	4	36.4	10	3	US-08-847-844A-38	Sequence 48, Appl
39	4	36.4	10	4	US-09-217-352-205	Sequence 205, App
40	4	36.4	10	4	US-09-020-065A-28	Sequence 28, Appl
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42	4	36.4	10	4	US-09-115-737-148	Sequence 148, App
43	4	36.4	10	4	US-09-104-137A-437	Sequence 437, App
44	4	36.4	10	4	US-08-983-157B-17	Sequence 17, Appl
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47	4	36.4	11	1	US-08-193-521-1	Sequence 1, Appl
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51	4	36.4	11	1	US-08-434-120-95	Sequence 95, Appl
52	4	36.4	11	1	US-08-434-120-111	Sequence 111, App
53	4	36.4	11	1	US-08-434-120-112	Sequence 112, App
54	4	36.4	11	1	US-08-465-325-94	Sequence 94, Appl
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56	4	36.4	11	1	US-08-465-325-111	Sequence 111, App
57	4	36.4	11	1	US-08-465-325-112	Sequence 112, App
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59	4	36.4	11	1	US-08-465-325-128	Sequence 128, App
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62	4	36.4	11	1	US-08-465-325-146	Sequence 146, App
63	4	36.4	11	1	US-08-343-882-11	Sequence 11, Appl
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65	4	36.4	11	2	US-08-621-803-206	Sequence 181, App
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84	4	36.4	12	1	US-08-434-120-96	Sequence 96, Appl
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165	4	36.4	14	1	US-08-465-125-114	Sequence 20, Appl	208	4	36.4	15	5	US-08-711-928-4	Sequence 4, Appl
166	4	36.4	14	1	US-08-465-125-114	Sequence 15, Appl	209	4	36.4	15	5	US-08-666-473-1	Sequence 1, Appl
167	4	36.4	14	2	US-08-688-675A-15	Sequence 15, Appl	210	4	36.4	15	5	US-08-701-124-1	Sequence 1, Appl
168	4	36.4	14	2	US-08-726-406A-189	Sequence 189, Appl	211	4	36.4	15	5	US-08-621-803-217	Sequence 217, Appl
169	4	36.4	14	4	US-09-115-737-115	Sequence 115, Appl	212	4	36.4	15	5	US-08-621-259A-157	Sequence 157, Appl
170	4	36.4	14	4	US-09-115-737-115	Sequence 117, Appl	213	4	36.4	15	5	US-08-621-259A-209	Sequence 209, Appl
171	4	36.4	14	4	US-09-115-737-115	Sequence 117, Appl	214	4	36.4	15	5	US-08-588-201-6	Sequence 6, Appl
172	4	36.4	14	4	US-09-115-737-117	Sequence 147, Appl	215	4	36.4	15	5	US-08-637-759B-453	Sequence 453, Appl
173	4	36.4	14	4	US-08-949-059A-1	Sequence 1, Appl	216	4	36.4	15	5	US-08-637-759B-496	Sequence 496, Appl
174	4	36.4	14	4	US-08-949-059A-6	Sequence 6, Appl	217	4	36.4	15	5	US-08-307-485A-2	Sequence 2, Appl
175	4	36.4	14	4	US-08-949-059A-6	Sequence 2, Appl	218	4	36.4	15	5	US-08-750-128-6	Sequence 6, Appl
176	4	36.4	14	4	US-08-949-059A-6	Sequence 8, Appl	219	4	36.4	15	5	US-08-595-043A-42	Sequence 42, Appl
177	4	36.4	14	4	US-08-949-059A-6	Sequence 9, Appl	220	4	36.4	15	5	US-08-669-284B-16	Sequence 16, Appl
178	4	36.4	14	4	US-08-949-059A-6	Sequence 1, Appl	221	4	36.4	15	5	US-08-894-339-2	Sequence 2, Appl
179	4	36.4	14	4	US-08-949-059A-6	Sequence 1, Appl	222	4	36.4	15	5	US-08-672-345C-48	Sequence 48, Appl
180	4	36.4	14	4	US-08-949-059A-6	Sequence 12, Appl	223	4	36.4	15	5	US-08-672-345C-51	Sequence 51, Appl
181	4	36.4	14	4	US-08-949-059A-6	Sequence 14, Appl	224	4	36.4	15	5	US-08-672-345C-57	Sequence 57, Appl
182	4	36.4	14	4	US-08-949-059A-6	Sequence 14, Appl	225	4	36.4	15	5	US-08-874-678-5	Sequence 5, Appl
183	4	36.4	14	4	US-08-949-059A-6	Sequence 15, Appl	226	4	36.4	15	5	US-09-016-368A-42	Sequence 42, Appl
184	4	36.4	14	4	US-08-949-059A-20	Sequence 20, Appl	227	4	36.4	15	5	US-08-563-368B-1	Sequence 1, Appl
185	4	36.4	14	4	US-08-949-059A-20	Sequence 27, Appl	228	4	36.4	15	5	US-09-169-605-6	Sequence 6, Appl
186	4	36.4	14	4	US-08-949-059A-20	Sequence 28, Appl	229	4	36.4	15	5	US-08-986-234-64	Sequence 64, Appl
187	4	36.4	14	4	US-08-949-059A-20	Sequence 3, Appl	230	4	36.4	15	5	US-08-477-860C-3	Sequence 3, Appl
188	4	36.4	14	5	PCT-US91-05047-1	Sequence 1, Appl	231	4	36.4	15	5	US-08-871-355A-453	Sequence 453, Appl
189	4	36.4	14	5	PCT-US91-05047-1	Sequence 2, Appl	232	4	36.4	15	5	US-08-871-355A-496	Sequence 496, Appl
190	4	36.4	14	5	PCT-US91-05047-1	Sequence 6, Appl	233	4	36.4	15	5	US-09-139-491-2	Sequence 2, Appl
191	4	36.4	14	5	PCT-US91-05047-1	Sequence 6, Appl	234	4	36.4	15	5	US-08-893-327-6	Sequence 6, Appl
192	4	36.4	14	5	PCT-US95-05062-20	Sequence 20, Appl	235	4	36.4	15	5	US-08-897-924A-13	Sequence 13, Appl
193	4	36.4	14	5	PCT-US95-05062-20	Sequence 5, Appl	236	4	36.4	15	5	US-08-897-924A-20	Sequence 20, Appl
194	4	36.4	15	1	US-07-725-331-58	Sequence 5, Appl	237	4	36.4	15	5	US-09-080-865-1	Sequence 1, Appl
195	4	36.4	15	1	US-08-194-921-7	Sequence 7, Appl	238	4	36.4	15	5	US-08-718-904-25	Sequence 25, Appl
196	4	36.4	15	1	US-08-194-921-7	Sequence 8, Appl	239	4	36.4	15	5	US-08-718-904-32	Sequence 32, Appl
197	4	36.4	15	1	US-08-434-120-161	Sequence 161, Appl	240	4	36.4	15	5	US-09-130-225-1	Sequence 1, Appl
198	4	36.4	15	1	US-08-434-120-162	Sequence 162, Appl	241	4	36.4	15	5	US-08-990-015-11	Sequence 11, Appl
199	4	36.4	15	1	US-08-434-120-162	Sequence 160, Appl	242	4	36.4	15	5	US-08-851-843A-223	Sequence 223, Appl
200	4	36.4	15	1	US-08-434-120-162	Sequence 101, Appl	243	4	36.4	15	5	US-08-643-839-5	Sequence 5, Appl
201	4	36.4	15	1	US-08-434-120-162	Sequence 116, Appl	244	4	36.4	15	5	US-08-974-549A-342	Sequence 342, Appl
202	4	36.4	15	1	US-08-434-120-162	Sequence 5, Appl	245	4	36.4	15	5	US-09-068-753B-2	Sequence 2, Appl
203	4	36.4	15	3	US-08-584-187-1	Sequence 1, Appl	246	4	36.4	15	5	US-09-142-078-32	Sequence 32, Appl


```

1 FILING DATE: 01-JUN-92
2 ATTORNEY/AGENT INFORMATION:
3 NAME: Fordis, Jean B
4 REGISTRATION NUMBER: 32,984
5 REFERENCE/DOCKET NUMBER: 05/48/129-443-440
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: (202) 408-4009
8 TELEFAX: (202) 408-4460
9 INFORMATION FOR SEQ ID NO: 129:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 10 amino acids
12 TYPE: amino acid
13 STRANDEDNESS: Single
14 TOPOLOGY: linear
15 MOLECULE TYPE: peptide
16 US-09-465-129-129
17
18 Query Match: 45.5%; Score 5; DB 1; Length 10;
19 Best Local Similarity: 100.0%; Pred. No. 0;
20 Matches: 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
21
22 QY 6 KLKKK 10
23 III
24 KLKKK 5
25
26 RESULT 2
27 US-09-115-737-129
28 Sequence 129, Application US/0915347
29 Patent No. 6348445
30 GENERAL INFORMATION:
31 APPLICANT: U. Prasad Kari
32 Jaffy J. Williams
33 Michael McNamee
34 TITLE OF INVENTION: Biologically Active Peptides With Reduced
35 Toxicity in Animals and a Method for Preparation Same
36 NUMBER OF SEQUENCES: 156
37 CORRESPONDENCE ADDRESS:
38 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
39 Dunner, L.L.P.
40 STREET: 1300 I Street, N.W. Suite 100
41 CITY: Washington
42 STATE: D.C.
43 COUNTRY: USA
44 ZIP: 20005-3315
45 COMPUTER READABLE FORM:
46 MEDIUM TYPE: Floppy disk
47 COMPUTER: IBM PC compatible
48 OPERATING SYSTEM: PC DOS/MS-DOS
49 SOFTWARE: Patent In Release #1.0, Version #1.30
50 CURRENT APPLICATION DATA:
51 APPLICATION NUMBER: US/09/115-737
52 FILING DATE: 15-Jul-1998
53 CLASSIFICATION: unknown
54 PRIOR APPLICATION DATA:
55 APPLICATION NUMBER: 08/465,129
56 FILING DATE: 05-JUN-1996
57 APPLICATION NUMBER: 08/184,462
58 FILING DATE: 18-JAN-94
59 APPLICATION NUMBER: 07/871,201
60 FILING DATE: 01-JUN-92
61 ATTORNEY/AGENT INFORMATION:
62 NAME: Fordis, Jean B
63 REGISTRATION NUMBER: 32,984
64 REFERENCE/DOCKET NUMBER: 05/48/129-443-440
65 TELEPHONE: (202) 408-4009
66 TELEFAX: (202) 408-4460
67 INFORMATION FOR SEQ ID NO: 129:
68 SEQUENCE CHARACTERISTICS:
69 LENGTH: 10 amino acids
70 TYPE: amino acid
71 STRANDEDNESS: single

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1 TOPOLOGY: linear
2 MOLECULE TYPE: peptide
3 SEQUENCE DESCRIPTION: SEQ ID NO: 129:
4 US-09-115-737-129
5
6 Query Match: 45.5%; Score 5; DB 4; Length 10;
7 Best Local Similarity: 100.0%; Pred. No. 38;
8 Matches: 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
9
10 QY 6 KLKKK 10
11 III
12 KLKKK 5
13
14 RESULT 3
15 US-08-855-531D-47
16 Sequence 47, Application US/08/855531D
17 Patent No. 6110467
18 GENERAL INFORMATION:
19 APPLICANT: PREK, PAUL S.
20 HALBUR, PATRICK G.
21 MENG, XIANGJIN
22 LUM, MELISSA A.
23 LYBO, YOUNG S.
24 TITLE OF INVENTION: VACCINES RAISING AN IMMUNOLOGICAL
25 RESPONSE AGAINST VIRUSES CAUSING PORCINE RESPIRATORY AND
26 REPRODUCTIVE DISEASES, METHODS OF PROTECTING A PIG AGAINST
27 A DISEASE CAUSED BY A RESPIRATORY AND REPRODUCTIVE
28 NUMBER OF SEQUENCES: 47
29 CORRESPONDENCE ADDRESS:
30 ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTALT,
31 P.C.
32 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
33 CITY: ARLINGTON
34 STATE: VA
35 COUNTRY: USA
36 ZIP: 22202
37 COMPUTER READABLE FORM:
38 MEDIUM TYPE: Floppy disk
39 COMPUTER: IBM PC compatible
40 OPERATING SYSTEM: PC DOS/MS-DOS
41 SOFTWARE: Patent In Release #1.0, Version #1.30
42 CURRENT APPLICATION DATA:
43 APPLICATION NUMBER: US/08/855,531D
44 FILING DATE: 13-May-1997
45 CLASSIFICATION: unknown
46 PRIOR APPLICATION DATA:
47 APPLICATION NUMBER: US 07/969,071
48 FILING DATE: 30-OCT-1992
49 ATTORNEY/AGENT INFORMATION:
50 NAME: LAVALLEYE, JEAN-PAUL M.P.
51 REGISTRATION NUMBER: 41,451
52 REFERENCE/DOCKET NUMBER: 4625-038-55X DIV
53 TELECOMMUNICATION INFORMATION:
54 TELEPHONE: 703-413-3000
55 TELEFAX: 703-413-2220
56 TELEX: 248855 SPAT GR
57 INFORMATION FOR SEQ ID NO: 47:
58 SEQUENCE CHARACTERISTICS:
59 LENGTH: 13 amino acids
60 TYPE: amino acid
61 TOPOLOGY: linear
62 MOLECULE TYPE: protein
63 SEQUENCE DESCRIPTION: SEQ ID NO: 47:
64 US-08-855-531D-47
65
66 Query Match: 45.5%; Score 5; DB 3; Length 13;
67 Best Local Similarity: 100.0%; Pred. No. 47;
68 Matches: 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
69
70 QY 6 KLKKK 10
71 III
72 KLKKK 12

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Query Match      35.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 KKKK 4
      III
IT      4 KKKK 7

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RESULT 7
US-08-444-120-108
: Sequence 107, Application US/08454120
: Patent No. 5635479
: GENERAL INFORMATION:
: APPLICANT: Baker, Margaret A.
: APPLICANT: Jacob, Leonard S.
: APPLICANT: Maloy, W. Lee
: TITLE OF INVENTION: Treatment of Gynecomastia
: TITLE OF INVENTION: Malinquinolactones with
: TITLE OF INVENTION: Biologically Active Peptides
: NUMBER OF SEQUENCES: 117
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Carelia, Byrne, Bain, Grilloham,
: ADDRESSEE: Cecchi & Stewart
: STREET: 6 Becker Farm Road
: CITY: Roseland
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07068
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch diskette
: COMPUTER: IBM PS/2
: OPERATING SYSTEM: PC-DOS
: SOFTWARE: DM4 V2
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/444,120
: FILING DATE:
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/297,990
: FILING DATE:
: APPLICATION NUMBER: US/08/226,105
: FILING DATE:
: APPLICATION NUMBER: US/07/937,462
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Gieseler, Elliot M.
: REGISTRATION NUMBER: 24,025
: REFERENCE/DACKET NUMBER: 421250 194
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201 994-1700
: TELEFAX: 201 994-1744
: INFORMATION FOR SEQ ID NO: 108:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS:
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-444-120-108

Query Match 36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9
Db 4 KLKK 7

RESULT 8
US-08-465-325-107
: Sequence 107, Application US/08455125
: Patent No. 5686563
: GENERAL INFORMATION:
: APPLICANT: Madalain Pharmaceuticals Inc.
: APPLICANT: 5110 Campus Drive
: APPLICANT: Plymouth Meeting, PA 19462
: TITLE OF INVENTION: Biologically Active Peptides Having
: TITLE OF INVENTION: N-Terminal Substitutions
: NUMBER OF SEQUENCES: 153

```

```

: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
: ADDRESSEE: Dunner
: STREET: 1400 L Street, N.W. Suite 700
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20005-3315
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/445,325
: FILING DATE: 05-JUN-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 04/184,462
: FILING DATE: 18-JAN-94
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/891,261
: FILING DATE: 01-JUN-92
: ATTORNEY/AGENT INFORMATION:
: NAME: Fordis, Jean R.
: REGISTRATION NUMBER: 42,984
: REFERENCE/DACKET NUMBER: 05387-0021 03000
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 408-4000
: TELEFAX: (202) 408-4400
: INFORMATION FOR SEQ ID NO: 107:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 8 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-465-325-107

Query Match 36.4%; Score 4; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9
Db 4 KLKK 7

RESULT 9
US-08-621-803-217
: Sequence 237, Application US/08521803
: Patent No. 5851802
: GENERAL INFORMATION:
: APPLICANT: Better, Marc D.
: TITLE OF INVENTION: Methods for Recombinant Microbial Production of
: TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
: NUMBER OF SEQUENCES: 265
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/621,803
: FILING DATE: 22-MAR-1996
: ATTORNEY/AGENT INFORMATION:

```



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1  GENERAL INFORMATION:
2  APPLICANT: NAUER, STEVEN G.
3  APPLICANT: CLEVELAND, JEFFREY S.
4  APPLICANT: BLAKE, JAMES K.
5  APPLICANT: HAFAR, OMAR K.
6  TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR P5 CTFN
7  TITLE OF INVENTION: TRANSLATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND
8  TITLE OF INVENTION: METHODS OF USE THEREOF
9  NUMBER OF SEQUENCES: 24
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: ROBINS & ASSOCIATES
12 STREET: 93 MIDDLEFIELD ROAD, SUITE 200
13 CITY: MENLO PARK
14 STATE: CA
15 COUNTRY: USA
16 ZIP: 94025
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: Floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: Patent In Release #1.0, Version #1.0
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/928,958
24 FILING DATE: 20-SEP-1996
25 ATTORNEY/AGENT INFORMATION:
26 NAME: ROBINS, ROBERTA L.
27 REGISTRATION NUMBER: 43,208
28 REFERENCE/Docket NUMBER: 59-08-0011
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: (650) 325-7812
31 TELEFAX: (650) 325-7823
32 INFORMATION FOR SEQ ID NO: 17:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 8 amino acids
35 TYPE: amino acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38 MOLECULE TYPE: peptide
39 US-08-928-958-17
40
41 Query Match: 36.4% Score 4: DB 2: Length 8:
42 Best Local Similarity 100.0%: Pref. No. 2.5e+05:
43 Matches 4: Conservative 0: Mismatches 0: Gaps 0:
44
45 QY 6 KLKK 9
46 IIII
47 2 KLKK 5
48
49 RESULT 15
50 US-09-772-429-17
51 Sequence 17: Application US/09/012429
52 Patent No. 5962415
53 GENERAL INFORMATION:
54 APPLICANT: NADIG, STEVEN J.
55 TITLE OF INVENTION: COMPOSITIONS COMPRISING A TETRAPEPTIDE
56 TITLE OF INVENTION: INHIBITOR OF NUCLEAR PROTEIN TRANSLATION AND AN
57 TITLE OF INVENTION: IMMUNOSUPPRESSANT AND METHODS OF USE THEREOF
58 NUMBER OF SEQUENCES: 24
59 CORRESPONDENCE ADDRESS:
60 ADDRESSEE: BRISTOL-MYERS Squibb Company
61 STREET: P.O. Box 4000
62 CITY: Princeton
63 STATE: New Jersey
64 COUNTRY: USA
65 ZIP: 08543-4000
66 COMPUTER READABLE FORM:
67 MEDIUM TYPE: Floppy disk
68 COMPUTER: IBM PC compatible

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1  OPERATING SYSTEM: PC-DOS/MS-DOS
2  SOFTWARE: Patent In Release #1.0, Version #1.30
3  CURRENT APPLICATION DATA:
4  APPLICATION NUMBER: US/09/012,429
5  FILING DATE: 04 MAY 1998
6  CLASSIFICATION: 514
7  ATTORNEY/AGENT INFORMATION:
8  NAME: Kiehl, Christopher A.
9  REGISTRATION NUMBER: 41,954
10 REFERENCE/Docket NUMBER: 090141b
11 TELECOMMUNICATION INFORMATION:
12 TELEPHONE: (609) 252-4714
13 TELEFAX: (609) 252-4926
14 INFORMATION FOR SEQ ID NO: 17:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 8 amino acids
17 TYPE: amino acid
18 STRANDEDNESS: single
19 TOPOLOGY: linear
20 MOLECULE TYPE: peptide
21 US-09-072-429-17
22
23 Query Match: 49.4% Score 4: DB 2: Length 8:
24 Best Local Similarity 100.0%: Pref. No. 2.5e+05:
25 Matches 4: Conservative 0: Mismatches 0: Gaps 0:
26
27 QY 6 KLKK 9
28 IIII
29 2 KLKK 5
30
31 RESULT 14
32 US-09-217-352-237
33 Sequence 237: Application US/09/217352
34 Patent No. 6274344
35 GENERAL INFORMATION:
36 APPLICANT: BOTTORF, MARK D.
37 TITLE OF INVENTION: METHODS FOR RECOMBINANT MICROBIAL PRODUCTION OF
38 TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
39 NUMBER OF SEQUENCES: 25
40 CORRESPONDENCE ADDRESS:
41 ADDRESSEE: Marshall J. O'Boyle, Gerstein, Murray & Borun
42 STREET: 606 Sears Tower, 233 South Wacker Drive
43 CITY: Chicago
44 STATE: Illinois
45 COUNTRY: United States of America
46 ZIP: 60605-6402
47 COMPUTER READABLE FORM:
48 MEDIUM TYPE: Floppy disk
49 COMPUTER: IBM PC compatible
50 OPERATING SYSTEM: PC-DOS/MS-DOS
51 SOFTWARE: Patent In Release #1.0, Version #1.25
52 CURRENT APPLICATION DATA:
53 APPLICATION NUMBER: US/09/217,352
54 FILING DATE:
55 PUBLICATION DATA:
56 APPLICATION NUMBER: US/621,853
57 FILING DATE: 22 MAR 1996
58 ATTORNEY/AGENT INFORMATION:
59 NAME: Borun, Michael F.
60 REGISTRATION NUMBER: 25,447
61 REFERENCE/Docket NUMBER: 27129/33199
62 TELECOMMUNICATION INFORMATION:
63 TELEPHONE: 312/474-6300
64 TELEFAX: 312/474-0448
65 TELEX: 253856
66 INFORMATION FOR SEQ ID NO: 237:
67 SEQUENCE CHARACTERISTICS:
68 LENGTH: 6 amino acids
69 TYPE: amino acid
70 TOPOLOGY: linear
71 MOLECULE TYPE: peptide
72 FEATURE:

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NAME/KEY: misc:feature
OTHER INFORMATION: "XMP 412"
US 09 217-62 247

Query Match 36.48% Score 4; DB 4; Length 8;
Best Local Similarity 100.00% Pred No 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Index 0; Gaps 0;

QY 7 LKXX 12
DB 1 LKXX 4

RESULT 15
US 09 220 365A-11
Sequence 11, Application US/0902205A
Patent No. 644602
GENERAL INFORMATION:
APPLICANT: Townsend, Robert M.
TITLE OF INVENTION: Peptide Methods of the Gamma Receptor Channel
TITLE OF INVENTION: Gamma Chain and Methods and Compositions for
TITLE OF INVENTION: Making and Using the Same
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washington K 112 9th Avenue S.W. #400-18 11P
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Windows NT
SOFTWARE: Wordperfect V. 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/20,000A
FILING DATE: 07-FEB-1997
PRIORITY APPLICATION DATA:
CLASSIFICATION: 530
REFERENCE/DOCKET NUMBER: 110 2101
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Belouch, Mark
REGISTRATION NUMBER: 35,204
TELEPHONE: 215 568-3439
TELEFAX: 215 568-3439
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: both
POPULACY: both

US 09 220 365A-11
Query Match 36.48% Score 4; DB 4; Length 8;
Best Local Similarity 100.00% Pred No 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Index 0; Gaps 0;

QY 1 AUSA 4
DB 3 AUSA 6

RESULT 16
US 09 115-737-107
Sequence 17, Application US/09115737
Patent No. 644645
GENERAL INFORMATION:
APPLICANT: J. Plasac K 111

NAME/KEY: misc:feature
OTHER INFORMATION: "XMP 412"
US 09 217-62 247

Query Match 36.48% Score 4; DB 4; Length 8;
Best Local Similarity 100.00% Pred No 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Index 0; Gaps 0;

QY 7 LKXX 12
DB 1 LKXX 4

RESULT 15
US 09 220 365A-11
Sequence 11, Application US/0902205A
Patent No. 644602
GENERAL INFORMATION:
APPLICANT: Townsend, Robert M.
TITLE OF INVENTION: Peptide Methods of the Gamma Receptor Channel
TITLE OF INVENTION: Gamma Chain and Methods and Compositions for
TITLE OF INVENTION: Making and Using the Same
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washington K 112 9th Avenue S.W. #400-18 11P
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Windows NT
SOFTWARE: Wordperfect V. 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/20,000A
FILING DATE: 07-FEB-1997
PRIORITY APPLICATION DATA:
CLASSIFICATION: 530
REFERENCE/DOCKET NUMBER: 110 2101
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Belouch, Mark
REGISTRATION NUMBER: 35,204
TELEPHONE: 215 568-3439
TELEFAX: 215 568-3439
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: both
POPULACY: both

US 09 220 365A-11
Query Match 36.48% Score 4; DB 4; Length 8;
Best Local Similarity 100.00% Pred No 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Index 0; Gaps 0;

QY 1 AUSA 4
DB 3 AUSA 6

RESULT 16
US 09 115-737-107
Sequence 17, Application US/09115737
Patent No. 644645
GENERAL INFORMATION:
APPLICANT: J. Plasac K 111

NAME/KEY: misc:feature
OTHER INFORMATION: "XMP 412"
US 09 217-62 247

Query Match 36.48% Score 4; DB 4; Length 8;
Best Local Similarity 100.00% Pred No 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Index 0; Gaps 0;

QY 7 LKXX 12
DB 1 LKXX 4

RESULT 15
US 09 220 365A-11
Sequence 11, Application US/0902205A
Patent No. 644602
GENERAL INFORMATION:
APPLICANT: Townsend, Robert M.
TITLE OF INVENTION: Peptide Methods of the Gamma Receptor Channel
TITLE OF INVENTION: Gamma Chain and Methods and Compositions for
TITLE OF INVENTION: Making and Using the Same
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washington K 112 9th Avenue S.W. #400-18 11P
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Windows NT
SOFTWARE: Wordperfect V. 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/20,000A
FILING DATE: 07-FEB-1997
PRIORITY APPLICATION DATA:
CLASSIFICATION: 530
REFERENCE/DOCKET NUMBER: 110 2101
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Belouch, Mark
REGISTRATION NUMBER: 35,204
TELEPHONE: 215 568-3439
TELEFAX: 215 568-3439
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: both
POPULACY: both

US 09 220 365A-11
Query Match 36.48% Score 4; DB 4; Length 8;
Best Local Similarity 100.00% Pred No 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Index 0; Gaps 0;

QY 1 AUSA 4
DB 3 AUSA 6

RESULT 16
US 09 115-737-107
Sequence 17, Application US/09115737
Patent No. 644645
GENERAL INFORMATION:
APPLICANT: J. Plasac K 111

NAME/KEY: misc:feature
OTHER INFORMATION: "XMP 412"
US 09 217-62 247

Query Match 36.48% Score 4; DB 4; Length 8;
Best Local Similarity 100.00% Pred No 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Index 0; Gaps 0;

QY 7 LKXX 12
DB 1 LKXX 4

RESULT 15
US 09 220 365A-11
Sequence 11, Application US/0902205A
Patent No. 644602
GENERAL INFORMATION:
APPLICANT: Townsend, Robert M.
TITLE OF INVENTION: Peptide Methods of the Gamma Receptor Channel
TITLE OF INVENTION: Gamma Chain and Methods and Compositions for
TITLE OF INVENTION: Making and Using the Same
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washington K 112 9th Avenue S.W. #400-18 11P
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Windows NT
SOFTWARE: Wordperfect V. 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/20,000A
FILING DATE: 07-FEB-1997
PRIORITY APPLICATION DATA:
CLASSIFICATION: 530
REFERENCE/DOCKET NUMBER: 110 2101
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Belouch, Mark
REGISTRATION NUMBER: 35,204
TELEPHONE: 215 568-3439
TELEFAX: 215 568-3439
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: both
POPULACY: both

US 09 220 365A-11
Query Match 36.48% Score 4; DB 4; Length 8;
Best Local Similarity 100.00% Pred No 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Index 0; Gaps 0;

QY 1 AUSA 4
DB 3 AUSA 6

RESULT 16
US 09 115-737-107
Sequence 17, Application US/09115737
Patent No. 644645
GENERAL INFORMATION:
APPLICANT: J. Plasac K 111

NAME/KEY: misc:feature
OTHER INFORMATION: "XMP 412"
US 09 217-62 247

Query Match 36.48% Score 4; DB 4; Length 8;
Best Local Similarity 100.00% Pred No 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Index 0; Gaps 0;

QY 7 LKXX 12
DB 1 LKXX 4

RESULT 15
US 09 220 365A-11
Sequence 11, Application US/0902205A
Patent No. 644602
GENERAL INFORMATION:
APPLICANT: Townsend, Robert M.
TITLE OF INVENTION: Peptide Methods of the Gamma Receptor Channel
TITLE OF INVENTION: Gamma Chain and Methods and Compositions for
TITLE OF INVENTION: Making and Using the Same
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washington K 112 9th Avenue S.W. #400-18 11P
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: Windows NT
SOFTWARE: Wordperfect V. 8
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/20,000A
FILING DATE: 07-FEB-1997
PRIORITY APPLICATION DATA:
CLASSIFICATION: 530
REFERENCE/DOCKET NUMBER: 110 2101
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Belouch, Mark
REGISTRATION NUMBER: 35,204
TELEPHONE: 215 568-3439
TELEFAX: 215 568-3439
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: both
POPULACY: both

US 09 220 365A-11
Query Match 36.48% Score 4; DB 4; Length 8;
Best Local Similarity 100.00% Pred No 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Index 0; Gaps 0;

QY 1 AUSA 4
DB 3 AUSA 6

RESULT 16
US 09 115-737-107
Sequence 17, Application US/09115737
Patent No. 644645
GENERAL INFORMATION:
APPLICANT: J. Plasac K 111

NAME/KEY: misc:feature
OTHER INFORMATION: "XMP 412"
US 09 217-62 247

Query Match 36.48% Score 4; DB 4; Length 8;
Best Local Similarity 100.00% Pred No 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Index 0; Gaps 0;

QY 7 LKXX 12
DB 1 LKXX 4

RESULT 15
US 09 220 365A-11
Sequence 11, Application US/0902205A
Patent No. 644602
GENERAL INFORMATION:
APPLICANT: Townsend, Robert M.
TITLE OF INVENTION:

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1  ZIP: 07068
2  COMPUTER READABLE FORM:
3  MEDIUM TYPE: 3.5 inch diskette
4  COMPUTER: IBM PS/2
5  OPERATING SYSTEM: PC-DOS
6  SOFTWARE: DWA V2
7  CURRENT APPLICATION DATA:
8  APPLICATION NUMBER: US/08/434,521
9  FILING DATE:
10 CLASSIFICATION: 514
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US/07/870,950
13 FILING DATE:
14 APPLICATION NUMBER: 07/760,354
15 FILING DATE: 11-SEP-1991
16 ATTORNEY/AGENT INFORMATION:
17 NAME: Gisteln, Elliot M.
18 REGISTRATION NUMBER: 24,025
19 REFERENCE/DOCKET NUMBER: 421250-161
20 TELECOMMUNICATION INFORMATION:
21 TELEPHONE: 201-994-1700
22 TELEFAX: 201-994-1744
23 INFORMATION FOR SEQ ID NO: 15:
24 SEQUENCE CHARACTERISTICS:
25 LENGTH: 9 amino acids
26 TYPE: amino acid
27 STRANDEDNESS:
28 TOPOLOGY: linear
29 MOLECULE TYPE: peptide
30 FEATURE:
31 OTHER INFORMATION: May be a terminal amide.
32 OTHER INFORMATION: and/or may be acetylated at
33 OTHER INFORMATION: N-terminus.
34 US-09-193-521-15

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Query Match 36.4% Score 4; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.5e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 6 KLKK 9
DB 1 11
5 KLKK 8

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RESULT 18
US-08-434 120-109
Sequence 109, Application US/08434120
Patent No. 5645479
GENERAL INFORMATION:
APPLICANT: Baker, Margaret A.
APPLICANT: Jacob, Leonard S.
TITLE OF INVENTION: Treatment of Oxytocin Deficiency
TITLE OF INVENTION: Malignancies with
TITLE OF INVENTION: Biologically Active Peptides
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bail, Ellington
ADDRESSEE: Cecchi & Stewart
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DWA V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,120
FILING DATE:
CLASSIFICATION: 514

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1  PRIOR APPLICATION DATA:
2  APPLICATION NUMBER: US/08/297,950
3  FILING DATE:
4  APPLICATION NUMBER: US/08/226,108
5  FILING DATE:
6  APPLICATION NUMBER: US/07/937,462
7  FILING DATE:
8  ATTORNEY/AGENT INFORMATION:
9  NAME: Gisteln, Elliot M.
10 REGISTRATION NUMBER: 24,025
11 REFERENCE/DOCKET NUMBER: 421250-194
12 TELECOMMUNICATION INFORMATION:
13 TELEPHONE: 201-994-1700
14 TELEFAX: 201-994-1744
15 INFORMATION FOR SEQ ID NO: 109:
16 SEQUENCE CHARACTERISTICS:
17 LENGTH: 9 amino acids
18 TYPE: amino acid
19 STRANDEDNESS:
20 TOPOLOGY: linear
21 MOLECULE TYPE: peptide
22 US 08-434-120-109
23
24 Query Match 36.4% Score 4; DB 1; Length 9;
25 Best Local Similarity 100.0%; Pred. No. 2.5e-05;
26 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
27
28 QY 6 KLKK 9
29 DB 1 11
30 5 KLKK 8
31
32 RESULT 19
33 US-08-465-425-138
34 Sequence 108, Application US/08465425
35 Patent No. 5886563
36 GENERAL INFORMATION:
37 APPLICANT: Megadin Pharmaceuticals Inc.
38 APPLICANT: 5110 Campus Drive
39 APPLICANT: Plymouth Meeting, PA 19462
40 TITLE OF INVENTION: Biologically Active Peptides Having
41 TITLE OF INVENTION: N-Terminal Substitutions
42 NUMBER OF SEQUENCES: 153
43 CORRESPONDENCE ADDRESS:
44 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
45 ADDRESSEE: Dunner
46 STREET: 1300 L Street, N.W. Suite 700
47 CITY: Washington
48 STATE: D.C.
49 COUNTRY: USA
50 ZIP: 20005-4415
51 COMPUTER READABLE FORM:
52 MEDIUM TYPE: Floppy disk
53 COMPUTER: IBM PC Compatible
54 OPERATING SYSTEM: PC-DOS/MS-DOS
55 SOFTWARE: Patent Release #1.0, Version #1.25
56 CURRENT APPLICATION DATA:
57 APPLICATION NUMBER: US/08/465,425
58 FILING DATE: 05-JUN-1995
59 CLASSIFICATION: 514
60 PRIOR APPLICATION DATA:
61 APPLICATION NUMBER: 08/184,462
62 FILING DATE: 18-JAN-94
63 PRIOR APPLICATION DATA:
64 APPLICATION NUMBER: 07/891,201
65 FILING DATE: 01-JUN-92
66 ATTORNEY/AGENT INFORMATION:
67 NAME: Fordis, Joac B
68 REGISTRATION NUMBER: 32,984
69 REFERENCE/DOCKET NUMBER: 05387-0021-03000
70 TELECOMMUNICATION INFORMATION:
71 TELEPHONE: (202) 408-4000
72 TELEFAX: (202) 408-4400

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1 INFORMATION FOR SEQ ID NO: 108:
 2 SEQUENCE CHARACTERISTICS:
 3 LENGTH: 9 amino acids
 4 TYPE: amino acid
 5 STANDARDNESS: single
 6 TOPOLOGY: linear
 7 MOLECULE TYPE: peptide
 8 US-08-454-207A:108

Query Match: 36.4% Score 4: DB 1: Length 9;
 Best Local Similarity: 100.0% Pred. No. 2.5e+05;
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

Q7 6 LKKK 3
 1 I
 2 KKK 4

RESULT 20
 US-08-454-207A:11

1 Sequence 11: Application US/08454207A
 2 Patent No. 5710123
 3 GENERAL INFORMATION:
 4 APPLICANT: Heavner, George A.
 5 APPLICANT: KRUSZYNSKI, Marian
 6 TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
 7 NUMBER OF SEQUENCES: 70
 8 CORRESPONDENCE ADDRESS:
 9 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123rls LLP
 10 STREET: One Liberty Place - 46th Floor
 11 CITY: Philadelphia
 12 STATE: PA
 13 COUNTRY: U.S.A.
 14 ZIP: 19103
 15 COMPUTER READABLE FORM:
 16 MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
 17 COMPUTER: IBM PC compatible
 18 OPERATING SYSTEM: PC-DOS/MS-DOS
 19 SOFTWARE: WordPerfect 6.1
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/08/454-207A
 22 FILING DATE: 09-JUN-1995
 23 CLASSIFICATION: 514
 24 PRIOR APPLICATION DATA:
 25 APPLICATION NUMBER: PCT/US99/12110
 26 FILING DATE: 13-DEC-1993
 27 PRIOR APPLICATION DATA:
 28 APPLICATION NUMBER: 07/997,771
 29 FILING DATE: 18-DEC-1992
 30 ATTORNEY/AGENT INFORMATION:
 31 NAME: Blum B. Elderkin
 32 REGISTRATION NUMBER: 28,598
 33 REFERENCE/DOCKET NUMBER: CO-R-0183
 34 TELECOMMUNICATION INFORMATION:
 35 TELEPHONE: 215-568-3100
 36 TELEFAX: 215-568-3439
 37 INFORMATION FOR SEQ ID NO: 11:
 38 SEQUENCE CHARACTERISTICS:
 39 LENGTH: 9 amino acids
 40 TYPE: amino acid
 41 TOPOLOGY: linear
 42 US-08-454-207A:11

Query Match: 36.4% Score 4: DB 1: Length 9;
 Best Local Similarity: 100.0% Pred. No. 2.5e+05;
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

Q7 7 LKKK 10
 1 I
 2 LKKK 4

RESULT 21
 US-08-454-207A:11

1 Sequence 11: Application US/08454207A
 2 Patent No. 5710123
 3 GENERAL INFORMATION:
 4 APPLICANT: Heavner, George A.
 5 APPLICANT: KRUSZYNSKI, Marian
 6 TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
 7 NUMBER OF SEQUENCES: 70
 8 CORRESPONDENCE ADDRESS:
 9 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123rls LLP
 10 STREET: One Liberty Place - 46th Floor
 11 CITY: Philadelphia
 12 STATE: PA
 13 COUNTRY: U.S.A.
 14 ZIP: 19103
 15 COMPUTER READABLE FORM:
 16 MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
 17 COMPUTER: IBM PC compatible
 18 OPERATING SYSTEM: PC-DOS/MS-DOS
 19 SOFTWARE: WordPerfect 6.1
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/08/454-207A
 22 FILING DATE: 09-JUN-1995
 23 CLASSIFICATION: 514
 24 PRIOR APPLICATION DATA:
 25 APPLICATION NUMBER: PCT/US99/12110
 26 FILING DATE: 13-DEC-1993
 27 PRIOR APPLICATION DATA:
 28 APPLICATION NUMBER: 07/997,771
 29 FILING DATE: 18-DEC-1992
 30 ATTORNEY/AGENT INFORMATION:
 31 NAME: Blum B. Elderkin
 32 REGISTRATION NUMBER: 28,598
 33 REFERENCE/DOCKET NUMBER: CO-R-0183
 34 TELECOMMUNICATION INFORMATION:
 35 TELEPHONE: 215-568-3100
 36 TELEFAX: 215-568-3439
 37 INFORMATION FOR SEQ ID NO: 11:
 38 SEQUENCE CHARACTERISTICS:
 39 LENGTH: 9 amino acids
 40 TYPE: amino acid
 41 TOPOLOGY: linear
 42 US-08-454-207A:11

Q7 7 LKKK 10
 1 I
 2 LKKK 4

RESULT 21

US-08-454-207A:12
 1 Sequence 12: Application US/08454207A
 2 Patent No. 5710123
 3 GENERAL INFORMATION:
 4 APPLICANT: Heavner, George A.
 5 APPLICANT: KRUSZYNSKI, Marian
 6 TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
 7 NUMBER OF SEQUENCES: 70
 8 CORRESPONDENCE ADDRESS:
 9 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123rls LLP
 10 STREET: One Liberty Place - 46th Floor
 11 CITY: Philadelphia
 12 STATE: PA
 13 COUNTRY: U.S.A.
 14 ZIP: 19103
 15 COMPUTER READABLE FORM:
 16 MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
 17 COMPUTER: IBM PC compatible
 18 OPERATING SYSTEM: PC-DOS/MS-DOS
 19 SOFTWARE: WordPerfect 6.1
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/08/454-207A
 22 FILING DATE: 09-JUN-1995
 23 CLASSIFICATION: 514
 24 PRIOR APPLICATION DATA:
 25 APPLICATION NUMBER: PCT/US99/12110
 26 FILING DATE: 13-DEC-1993
 27 PRIOR APPLICATION DATA:
 28 APPLICATION NUMBER: 07/997,771
 29 FILING DATE: 18-DEC-1992
 30 ATTORNEY/AGENT INFORMATION:
 31 NAME: Blum B. Elderkin
 32 REGISTRATION NUMBER: 28,598
 33 REFERENCE/DOCKET NUMBER: CO-R-0183
 34 TELECOMMUNICATION INFORMATION:
 35 TELEPHONE: 215-568-3100
 36 TELEFAX: 215-568-3439
 37 INFORMATION FOR SEQ ID NO: 12:
 38 SEQUENCE CHARACTERISTICS:
 39 LENGTH: 9 amino acids
 40 TYPE: amino acid
 41 TOPOLOGY: linear
 42 US-08-454-207A:12

Query Match: 36.4% Score 4: DB 1: Length 9;
 Best Local Similarity: 100.0% Pred. No. 2.5e+05;
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

Q7 7 LKKK 10
 1 I
 2 LKKK 4

RESULT 22
 US-08-454-207A:13

1 Sequence 13: Application US/08454207A
 2 Patent No. 5710123
 3 GENERAL INFORMATION:
 4 APPLICANT: Heavner, George A.
 5 APPLICANT: KRUSZYNSKI, Marian
 6 TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
 7 NUMBER OF SEQUENCES: 70
 8 CORRESPONDENCE ADDRESS:
 9 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123rls LLP
 10 STREET: One Liberty Place - 46th Floor
 11 CITY: Philadelphia
 12 STATE: PA
 13 COUNTRY: U.S.A.
 14 ZIP: 19103
 15 COMPUTER READABLE FORM:
 16 MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
 17 COMPUTER: IBM PC compatible
 18 OPERATING SYSTEM: PC-DOS/MS-DOS
 19 SOFTWARE: WordPerfect 6.1
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/08/454-207A
 22 FILING DATE: 09-JUN-1995
 23 CLASSIFICATION: 514
 24 PRIOR APPLICATION DATA:
 25 APPLICATION NUMBER: PCT/US99/12110
 26 FILING DATE: 13-DEC-1993
 27 PRIOR APPLICATION DATA:
 28 APPLICATION NUMBER: 07/997,771
 29 FILING DATE: 18-DEC-1992
 30 ATTORNEY/AGENT INFORMATION:
 31 NAME: Blum B. Elderkin
 32 REGISTRATION NUMBER: 28,598
 33 REFERENCE/DOCKET NUMBER: CO-R-0183
 34 TELECOMMUNICATION INFORMATION:
 35 TELEPHONE: 215-568-3100
 36 TELEFAX: 215-568-3439
 37 INFORMATION FOR SEQ ID NO: 13:
 38 SEQUENCE CHARACTERISTICS:
 39 LENGTH: 9 amino acids
 40 TYPE: amino acid
 41 TOPOLOGY: linear
 42 US-08-454-207A:13

Query Match: 36.4% Score 4: DB 1: Length 9;
 Best Local Similarity: 100.0% Pred. No. 2.5e+05;
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

Q7 7 LKKK 10
 1 I
 2 LKKK 4

RESULT 23
 US-08-454-207A:14

1 Sequence 14: Application US/08454207A
 2 Patent No. 5710123
 3 GENERAL INFORMATION:
 4 APPLICANT: Heavner, George A.
 5 APPLICANT: KRUSZYNSKI, Marian
 6 TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
 7 NUMBER OF SEQUENCES: 70
 8 CORRESPONDENCE ADDRESS:
 9 ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123rls LLP
 10 STREET: One Liberty Place - 46th Floor
 11 CITY: Philadelphia
 12 STATE: PA
 13 COUNTRY: U.S.A.
 14 ZIP: 19103
 15 COMPUTER READABLE FORM:
 16 MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
 17 COMPUTER: IBM PC compatible
 18 OPERATING SYSTEM: PC-DOS/MS-DOS
 19 SOFTWARE: WordPerfect 6.1
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/08/454-207A
 22 FILING DATE: 09-JUN-1995
 23 CLASSIFICATION: 514
 24 PRIOR APPLICATION DATA:
 25 APPLICATION NUMBER: PCT/US99/12110
 26 FILING DATE: 13-DEC-1993
 27 PRIOR APPLICATION DATA:
 28 APPLICATION NUMBER: 07/997,771
 29 FILING DATE: 18-DEC-1992
 30 ATTORNEY/AGENT INFORMATION:
 31 NAME: Blum B. Elderkin
 32 REGISTRATION NUMBER: 28,598
 33 REFERENCE/DOCKET NUMBER: CO-R-0183
 34 TELECOMMUNICATION INFORMATION:
 35 TELEPHONE: 215-568-3100
 36 TELEFAX: 215-568-3439
 37 INFORMATION FOR SEQ ID NO: 14:
 38 SEQUENCE CHARACTERISTICS:
 39 LENGTH: 9 amino acids
 40 TYPE: amino acid
 41 TOPOLOGY: linear
 42 US-08-454-207A:14

Q7 7 LKKK 10
 1 I
 2 LKKK 4

RESULT 24


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: SOFTWARE: Wordperfect 6.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/454,207A
: FILING DATE: 09-JUN-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US99/12110
: FILING DATE: 13-DEC-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/997,771
: FILING DATE: 18-DEC-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Dianne B. Elderkin
: REGISTRATION NUMBER: 28,598
: REFERENCE/DOCKET NUMBER: COAR 0183
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-568-3100
: TELEFAX: 215-568-3439
: INFORMATION FOR SEQ ID NO: 13:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-08 454-207A-13
:
: Query Match 36.4%; Score 4; DB 1; Length 9;
: Best Local Similarity 100.0%; Pred. No. 2.5e-05;
: Matches 4; Conservative 0; Mismatches 0; Gaps 0;
:
: QY 7 KKKK 10
: DB 1111
: 2 KKKK 4
:
: RESULT 25
: US-08 454-207A-24
: Sequence 24, Application US/08/454,207A
: Patent No. 5710123
: GENERAL INFORMATION:
: APPLICANT: Heavner, George A.
: TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
: NUMBER OF SEQUENCES: 70
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123 is LLP
: STREET: One Liberty Place - 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: U.S.A.
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch disk, 1.44 MB
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect 6.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 07/997,771
: FILING DATE: 18-DEC-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Dianne B. Elderkin
: REGISTRATION NUMBER: 28,598
: REFERENCE/DOCKET NUMBER: COAR-0183
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-568-3100
: TELEFAX: 215-568-3439
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-08 454-207A-24
:
: Query Match 36.4%; Score 4; DB 1; Length 9;
: Best Local Similarity 100.0%; Pred. No. 2.5e-05;
: Matches 4; Conservative 0; Mismatches 0; Gaps 0;
:
: QY 8 KKKK 11
: DB 1111
: 2 KKKK 5
:
: RESULT 25
: US-08 615-181-27
: Sequence 27, Application US/08/615181
: Patent No. 5756666
: INFORMATION FOR SEQ ID NO: 23:

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: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-08 454-207A-23
:
: Query Match 36.4%; Score 4; DB 1; Length 9;
: Best Local Similarity 100.0%; Pred. No. 2.5e-05;
: Matches 4; Conservative 0; Mismatches 0; Gaps 0;
:
: QY 8 KKKK 11
: DB 1111
: 2 KKKK 5
:
: RESULT 24
: US-08 454-207A-24
: Sequence 24, Application US/08/454,207A
: Patent No. 5710123
: GENERAL INFORMATION:
: APPLICANT: Heavner, George A.
: TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
: NUMBER OF SEQUENCES: 70
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5710123 is LLP
: STREET: One Liberty Place - 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: U.S.A.
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch disk, 1.44 MB
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect 6.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/454,207A
: FILING DATE: 09-JUN-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US99/12110
: FILING DATE: 13-DEC-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/997,771
: FILING DATE: 18-DEC-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Dianne B. Elderkin
: REGISTRATION NUMBER: 28,598
: REFERENCE/DOCKET NUMBER: COAR-0183
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-568-3100
: TELEFAX: 215-568-3439
: INFORMATION FOR SEQ ID NO: 24:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 9 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: US-08 454-207A-24
:
: Query Match 36.4%; Score 4; DB 1; Length 9;
: Best Local Similarity 100.0%; Pred. No. 2.5e-05;
: Matches 4; Conservative 0; Mismatches 0; Gaps 0;
:
: QY 8 KKKK 11
: DB 1111
: 2 KKKK 5
:
: RESULT 25
: US-08 615-181-27
: Sequence 27, Application US/08/615181
: Patent No. 5756666

```

GENERAL INFORMATION:
 APPLICANT: MASAFUMI, TAKIUCHI
 APPLICANT: MIWA, KIYOSHI
 TITLE OF INVENTION: PEPTIDES CAPABLE OF INHIBITING MURDER
 TITLE OF INVENTION: RESPONSE TO REV AND AGENT'S ADVISEMENT RE:
 NUMBER OF SEQUENCES: 114
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GELON, SPIVAK, MUGGELLANI, WELLS & ROUSHMAN
 ADDRESS: P.O.
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 110
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent In Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/615,196
 FILING DATE: 04-APR-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 101/1694/1296
 FILING DATE: 19-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 30-261362/1000
 FILING DATE: 19-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: DEON, NORMAN F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 16 94 104
 INFORMATION FOR SEQ ID NO: 1
 TELEPHONE: 703 413 3000
 TELEFAX: 703 413 2220
 INFORMATION FOR SEQ ID NO: 273
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide
 ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 US-07-615,196-27

Query Match: 36 19 Score 47 DB 4: Length 9:
 Best Local Similarity: 100.0%, Pct. Id: 2.5e-05;
 Matches: 4: Conservative 0: Mismatches 0: Gaps 0:

07 5 KKKR 9
 14 5 KKKR 9

RESULT 27
 US-07-615,196-27
 Sequence: 27 Application: US/07/615,196
 Patent No: 647097
 GENERAL INFORMATION:
 APPLICANT: MULLOY, WILLIAM
 APPLICANT: KATZ, J. PRASAD
 APPLICANT: WILLIAMS, TERRY J.
 TITLE OF INVENTION: Biochemically Active Peptide
 TITLE OF INVENTION: Compositions and Uses Thereof
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carolina, Pyron, Rana, Gilliland
 ADDRESS: Carolina, Pyron, Rana, Gilliland
 STREET: 6 Becker Field Road
 CITY: Rosemead
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch Diskette
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC DOS
 SOFTWARE: IBM V2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/99/100,141
 FILING DATE: 08/09/1999
 CLASSIFICATION: 04

GENERAL INFORMATION:
 APPLICANT: MASAFUMI, TAKIUCHI
 APPLICANT: MIWA, KIYOSHI
 TITLE OF INVENTION: PEPTIDES CAPABLE OF INHIBITING MURDER
 TITLE OF INVENTION: RESPONSE TO REV AND AGENT'S ADVISEMENT RE:
 NUMBER OF SEQUENCES: 114
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: GELON, SPIVAK, MUGGELLANI, WELLS & ROUSHMAN
 ADDRESS: P.O.
 STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 110
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent In Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/615,196
 FILING DATE: 04-APR-1996
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 101/1694/1296
 FILING DATE: 19-OCT-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 30-261362/1000
 FILING DATE: 19-OCT-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: DEON, NORMAN F.
 REGISTRATION NUMBER: 24,618
 REFERENCE/DOCKET NUMBER: 16 94 104
 INFORMATION FOR SEQ ID NO: 1
 TELEPHONE: 703 413 3000
 TELEFAX: 703 413 2220
 INFORMATION FOR SEQ ID NO: 273
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide
 ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 US-07-615,196-27

Query Match: 36 19 Score 47 DB 4: Length 9:
 Best Local Similarity: 100.0%, Pct. Id: 2.5e-05;
 Matches: 4: Conservative 0: Mismatches 0: Gaps 0:

07 5 KKKR 9
 14 5 KKKR 9

RESULT 27
 US-07-615,196-27
 Sequence: 27 Application: US/07/615,196
 Patent No: 647097
 GENERAL INFORMATION:
 APPLICANT: MULLOY, WILLIAM
 APPLICANT: KATZ, J. PRASAD
 APPLICANT: WILLIAMS, TERRY J.
 TITLE OF INVENTION: Biochemically Active Peptide
 TITLE OF INVENTION: Compositions and Uses Thereof
 NUMBER OF SEQUENCES: 19
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Carolina, Pyron, Rana, Gilliland
 ADDRESS: Carolina, Pyron, Rana, Gilliland
 STREET: 6 Becker Field Road
 CITY: Rosemead
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07068
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch Diskette
 COMPUTER: IBM PS/2
 OPERATING SYSTEM: PC DOS
 SOFTWARE: IBM V2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/99/100,141
 FILING DATE: 08/09/1999
 CLASSIFICATION: 04

1 PRIOR APPLICATION DATA: 36.4% Score 4: DB 1: Length 10:
 2 APPLICATION NUMBER: US/07/070,966
 3 FILING DATE: 13-SEP-1991
 4 FILING DATE: 13-SEP-1991
 5 FILING DATE: 13-SEP-1991
 6 FILING DATE: 13-SEP-1991
 7 FILING DATE: 13-SEP-1991
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 98 FILING DATE: 13-SEP-1991
 99 FILING DATE: 13-SEP-1991
 100 FILING DATE: 13-SEP-1991

1 REFERENCE/DOCKET NUMBER: 421250-134
 2 TELECOMMUNICATION INFORMATION:
 3 TELEPHONE: 201-994-1700
 4 TELEFAX: 201-994-1744
 5 INFORMATION FOR SEQ ID NO: 110:
 6 SEQUENCE CHARACTERISTICS:
 7 LENGTH: 10 amino acids
 8 TYPE: amino acid
 9 STRANDEDNESS:
 10 TOPOLOGY: linear
 11 MOLECULE TYPE: peptide
 12 US 09-443-443-4-120-110
 13 Query Match 36.4% Score 4: DB 1: Length 10:
 14 Best Local Similarity 100.0% Pred. No. 3.6e+02
 15 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

1 QY 6 KLKK 9
 2 DE 6 KLKK 9
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1 RESULT 29
 2 US 09-465-425-109
 3 Sequence 109: Application US/0845525
 4 Patent No. 565563
 5 GENERAL INFORMATION:
 6 APPLICANT: Mataslin Pharmaceuticals Inc.
 7 APPLICANT: 5110 Campus Drive
 8 APPLICANT: Plymouth Meeting, PA 19462
 9 TITLE OF INVENTION: Biologically Active Peptides Having
 10 TITLE OF INVENTION: N-Terminal Substitutions
 11 NUMBER OF SEQUENCES: 13
 12 CORRESPONDENCE ADDRESS:
 13 ADDRESSEE: Elinor, Henderson, Farabow, Garrett &
 14 STREET: 1400 L Street, N.W. Suite 700
 15 CITY: Washington
 16 STATE: D.C.
 17 ZIP: 20005-3475
 18 COUNTRY: USA
 19 COMPUTER READABLE FORM:
 20 COMPUTER: IBM PC compatible
 21 OPERATING SYSTEM: PC DOS/MS DOS
 22 SOFTWARE: Patent In Release #1.0, Version #1.25
 23 CURRENT APPLICATION DATA:
 24 APPLICATION NUMBER: US/08/465,425
 25 FILING DATE: 05 JUN 1995
 26 CLASSIFICATION: 514
 27 PRIOR APPLICATION DATA:
 28 APPLICATION NUMBER: US/184-462
 29 FILING DATE: 18 JAN 94
 30 PRIOR APPLICATION DATA:
 31 APPLICATION NUMBER: 07/891,261
 32 FILING DATE: 01-JUN-92
 33 ATTORNEY/AGENT INFORMATION:
 34 NAME: Forde, Sean R
 35 REGISTRATION NUMBER: 32,984
 36 REFERENCE/DOCKET NUMBER: 05387-0021-03000
 37 TELECOMMUNICATION INFORMATION:
 38 TELEPHONE: (202) 408-4000
 39 TELEFAX: (202) 408-4400
 40 INFORMATION FOR SEQ ID NO: 109:
 41 SEQUENCE CHARACTERISTICS:
 42 LENGTH: 10 amino acids
 43 TYPE: amino acid
 44 STRANDEDNESS: single
 45 TOPOLOGY: linear
 46 MOLECULE TYPE: peptide
 47 US 09-465-425-109
 48 Query Match 36.4% Score 4: DB 1: Length 10:
 49 Best Local Similarity 100.0% Pred. No. 3.6e+02
 50 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

1 QY 6 KLKK 9
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1 RESULT 28
 2 US 08-443-420-110
 3 Sequence 110: Application US/0844110
 4 Patent No. 565479
 5 GENERAL INFORMATION:
 6 APPLICANT: Baker, Margaret A.
 7 APPLICANT: Jacob, Leonard S.
 8 APPLICANT: Mayo, W. Lee
 9 TITLE OF INVENTION: Treatment of Osteoporosis
 10 TITLE OF INVENTION: Multimeric w/10
 11 TITLE OF INVENTION: Biologically Active Peptides
 12 NUMBER OF SEQUENCES: 11
 13 CORRESPONDENCE ADDRESS:
 14 ADDRESSEE: Carella, Byrne, Bunn, Gellman
 15 ADDRESSEE: Jacob, W. Stewart
 16 STREET: 6 Becker Farm Road
 17 CITY: Roseland
 18 STATE: New Jersey
 19 COUNTRY: USA
 20 ZIP: 07068
 21 COMPUTER READABLE FORM:
 22 MEDIUM TYPE: 3.5 inch diskette
 23 COMPUTER: IBM PS/2
 24 OPERATING SYSTEM: PC DOS
 25 SOFTWARE: DM4 V2
 26 CURRENT APPLICATION DATA:
 27 APPLICATION NUMBER: US/08/443,420
 28 FILING DATE:
 29 CLASSIFICATION: 514
 30 PRIOR APPLICATION DATA:
 31 APPLICATION NUMBER: US/08/297,450
 32 FILING DATE:
 33 APPLICATION NUMBER: US/08/220,108
 34 FILING DATE:
 35 APPLICATION NUMBER: US/07/070,966
 36 FILING DATE:
 37 ATTORNEY/AGENT INFORMATION:
 38 NAME: Cistead, Elliot M.
 39 REGISTRATION NUMBER: 26,525

1 QY 6 KLKK 9
 2 DE 6 KLKK 9
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1 Query Match 36.4% Score 4: DB 1: Length 10:
 2 Best Local Similarity 100.0% Pred. No. 3.6e+02
 3 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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Best Local Similarity 100.0%, Seq ID No. 148, Length 148
Matches 4: Conservative 0: Mismatches 0: Indels 0: Caps 0:

QY 1 KKK 7
DB 1 1
6 KKK 9

RESULT 30
US 08-454-207A-1
Sequence 4: Application US/08454207A
Patent No. 5710123
GENERAL INFORMATION:
APPLICANT: Kleszynski, Marian
TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kottitz Mackiewicz & No. 5710123rls LLP
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454-207A
FILING DATE: 09 JUN 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12110
FILING DATE: 15 DEC 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/497,771
FILING DATE: 16 DEC 1992
ATTORNEY/AGENT INFORMATION:
NAME: Diagne H. Elderkin
REGISTRATION NUMBER: 26,598
REFERENCE/DOCKET NUMBER: COIR 0164
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-4439
TELEFAX: 215-568-4439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLGY: linear
US 08-454-207A-1

Query Match 36.4%, Score 4; DB 1; Length 10;
Best Local Similarity 100.0%, Seq ID No. 148, Length 10;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Caps 0:

QY 1 KKK 10
DB 1 1
2 KKK 6

RESULT 32
US 08-454-207A-4
Sequence 4: Application US/08454207A
Patent No. 5710123
GENERAL INFORMATION:
APPLICANT: Kleszynski, Marian
TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kottitz Mackiewicz & No. 5710123rls LLP
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454-207A
FILING DATE: 09 JUN 1995
CLASSIFICATION: 514

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Best Local Similarity 100.0%, Seq ID No. 148, Length 148
Matches 4: Conservative 0: Mismatches 0: Indels 0: Caps 0:

QY 1 KKK 7
DB 1 1
6 KKK 9

RESULT 30
US 08-454-207A-1
Sequence 4: Application US/08454207A
Patent No. 5710123
GENERAL INFORMATION:
APPLICANT: Kleszynski, Marian
TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kottitz Mackiewicz & No. 5710123rls LLP
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454-207A
FILING DATE: 09 JUN 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/12110
FILING DATE: 15 DEC 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/497,771
FILING DATE: 16 DEC 1992
ATTORNEY/AGENT INFORMATION:
NAME: Diagne H. Elderkin
REGISTRATION NUMBER: 26,598
REFERENCE/DOCKET NUMBER: COIR 0164
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-4439
TELEFAX: 215-568-4439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLGY: linear
US 08-454-207A-1

Query Match 36.4%, Score 4; DB 1; Length 10;
Best Local Similarity 100.0%, Seq ID No. 148, Length 10;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Caps 0:

QY 1 KKK 10
DB 1 1
2 KKK 6

RESULT 32
US 08-454-207A-4
Sequence 4: Application US/08454207A
Patent No. 5710123
GENERAL INFORMATION:
APPLICANT: Kleszynski, Marian
TITLE OF INVENTION: PEPTIDE INHIBITORS OF SELECTIN BINDING
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kottitz Mackiewicz & No. 5710123rls LLP
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch disk, 1.44 MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454-207A
FILING DATE: 09 JUN 1995
CLASSIFICATION: 514

```

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PAPER APPLICATION DATA:
  APPLICATION NUMBER: PCT/US93/12110
  FILING DATE: 13-DEC-1993
  PAPER APPLICATION DATA:
  APPLICATION NUMBER: 07/997,771
  FILING DATE: 18-DEC-1992
  ATTORNEY/AGENT INFORMATION:
  NAME: Dianne B. Elderkin
  REGISTRATION NUMBER: 28,598
  REFERENCE/DOCKET NUMBER: CDR-1183
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: 215-568-3100
  TELEFAX: 215-568-3439
  INFORMATION FOR SEQ ID NO: 4:
  SEQUENCE CHARACTERISTICS:
  LENGTH: 10 amino acids
  TYPE: amino acid
  TOPOLOGY: circular
US-08-454-207A-4

Query Match: 36.4%; Score 4: DP 1: Length 10:
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 KKKK 10
DB 2 KKKK 5

RESULT 34
US-08-653-642-39
: Sequence 39, Application US/08653632
: Patent No. 5830860
: GENERAL INFORMATION:
: APPLICANT: GRAY, Judith R.
: APPLICANT: HASEMAN, Judith R.
: APPLICANT: MAYO, Kevin
: TITLE OF INVENTION: PEPTIDES WITH BACTERICIDAL AND ENDOOTOXIN NEUTRALIZING
: NUMBER OF SEQUENCES: 66
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
: STREET: 3100 No. 5830860 West Center, 90 South Seventh St
: CITY: Minneapolis
: STATE: MN
: COUNTRY: USA
: ZIP: 55402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/653,632
: FILING DATE: 24-MAY-1996
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/218026
: FILING DATE: 24-MAR-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: Kelleigh, Corliss M
: REGISTRATION NUMBER: 33,924
: REFERENCE/DOCKET NUMBER: 600,2860811
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 612/371-5268
: TELEFAX: 612/342 9081
: TELEX:
: INFORMATION FOR SEQ ID NO: 39:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: STRANDEDNESS: Single
: TOPOLOGY: Linear
: MOLECULE TYPE: peptide
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE: Internal
: ORIGINAL SOURCE:
US-08-653-642-39

Query Match: 36.4%; Score 4: DP 2: Length 10:
Best Local Similarity 100.0%; Pred. No. 3.6e+02;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 8 KKKK 11
DB 1 KKKK 4

RESULT 35
US-08-621-803-205
: Sequence 205, Application US/08621803
: Patent No. 5831802
: GENERAL INFORMATION:
: APPLICANT: Better, Marc E.

```

TITLE OF INVENTION: Methods for Recombinant Mammalian Produced Peptides
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago

STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/621,804

FILING DATE: 22-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Borun, Michael F.

REGISTRATION NUMBER: 25,447

REFERENCE/DACKET NUMBER: 27124/0199

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0446

TELEX: 25 4856

INFORMATION FOR SEQ ID NO: 265:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

Topology: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: misc-feature

OTHER INFORMATION: "XMP.349"

FEATURE:

NAME/KEY: Modified-site

LOCATION: C-Terminus

OTHER INFORMATION: /Label: Amidation

OTHER INFORMATION: /note- "The C-Terminus is Amidated."

US-08-621,804-265

Query Match 36.4% Score 47 DB 2 Length 10

Best Local Similarity 100.0% Pred. No. 3.6e+02

Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 7 LKKK 10

DB 7 LKKK 10

RESULT 36

US-08 621,259A-180

Sequence 180: Application US/08621259A

Patent No. 5898974

GENERAL INFORMATION:

APPLICANT: Little, J. Roger G

APPLICANT: Lem, Edward

APPLICANT: Padem, Mitchell B.

TITLE OF INVENTION: Anti-Fungal Peptides

NUMBER OF SEQUENCES: 252

CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Maltz, P.C.

STREET: 500 West Madison Street

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60661

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/621,259A

FILING DATE: 21-MAR-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/504,841

FILING DATE: 20-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Monicholas, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DACKET NUMBER: 110218502

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/767-8889

TELEFAX: 312/767-9155

TELEX:

INFORMATION FOR SEQ ID NO: 180:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

Topology: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: misc-feature

OTHER INFORMATION: "XMP.349"

FEATURE:

NAME/KEY: Modified-site

LOCATION: C-Terminus

OTHER INFORMATION: /Label: Amidation

OTHER INFORMATION: /note- "The C-Terminus is Amidated."

US-08-621-259A-180

Query Match 36.4% Score 47 DB 2 Length 10

Best Local Similarity 100.0% Pred. No. 3.6e+02

Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 7 LKKK 10

DB 7 LKKK 10

RESULT 37

US-08-350,260A-437

Sequence 437: Application US/08350260A

Patent No. 5962255

GENERAL INFORMATION:

APPLICANT: Winter, Gregory Paul

APPLICANT: Griffiths, Andrew David

APPLICANT: Williams, Samuel Cameron

APPLICANT: Waterhouse, Peter

APPLICANT: Nissim, Ahuva

APPLICANT: Johnson, Kevin Stuart

APPLICANT: Smith, Andrew John Hammond

TITLE OF INVENTION: Methods for producing members of specific

NUMBER OF SEQUENCES: 602

CORRESPONDENCE ADDRESS:

ADDRESSEE: David W. Clough

STREET: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/350,260A

FILING DATE: 05-DEC-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9110549.4

1 FILING DATE: 15-MAY-1991
 2 PRIOR APPLICATION DATA:
 3 APPLICATION NUMBER: US 08/426,418
 4 FILING DATE: 24-MAR-1992
 5 PRIOR APPLICATION DATA:
 6 APPLICATION NUMBER: PCT/JP91/01174
 7 FILING DATE: 10-JUL-1991
 8 PRIOR APPLICATION DATA:
 9 APPLICATION NUMBER: PCT/JP92/00894
 10 FILING DATE: 15-MAY-1992
 11 PRIOR APPLICATION DATA:
 12 APPLICATION NUMBER: PCT/JP93/00175
 13 FILING DATE: 24-MAR-1993
 14 PRIOR APPLICATION DATA:
 15 APPLICATION NUMBER: US 08/150,162
 16 FILING DATE: 31-MAR-1994
 17 PRIOR APPLICATION DATA:
 18 APPLICATION NUMBER: US 08/407,419
 19 FILING DATE: 16-SEP-1994
 20 ATTORNEY/AGENT INFORMATION:
 21 NAME: CLOUAT, David W
 22 REGISTRATION NUMBER: 16,107
 23 REFERENCE/DOCKET NUMBER: 251,174,672
 24 TELECOMMUNICATION INFORMATION:
 25 TELEPHONE: 312 474-5400
 26 INFORMATION FOR SEQ ID NO: 447:
 27 SEQUENCE CHARACTERISTICS:
 28 LENGTH: 10 amino acids
 29 TYPE: amino acid
 30 STRANDEDNESS: single
 31 FEATURE: linear
 32 US 08-459 260A 447

Query Match 35.4% Score 4.05 4 Length 10
 Best Local Similarity 100.0% Prod. No. 3.6e+02
 Matches 4 Conservative 0 Mismatches 0 Gaps 0

QY 2 USAV 5
 LB 111
 7 USAV 10

RES 11 47
 US 08 847 844A 48
 1 Sequence 48 Application US/08547844A
 2 Patent No. 6274544
 3 GENERAL INFORMATION:
 4 APPLICANT: KAZAKIAN JR., DAVID B
 5 APPLICANT: BEKE, GREG D
 6 APPLICANT: MURAN, JOHN V
 7 APPLICANT: DOMGROSKI, BETH A
 8 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT OF
 9 NUMBER OF SEQUENCES: 137
 10 CORRESPONDENT ADDRESS:
 11 ADDRESSEE: PANICH SCHWARTZ JACOBS & MULLER
 12 CITY: PHILADELPHIA
 13 STATE: PA
 14 COUNTRY: U.S.A.
 15 ZIP: 19103 7086
 16 COMPUTER READABLE FORM:
 17 MEDIUM TYPE: Floppy disk
 18 OPERATING SYSTEM: PC DOS/MS DOS
 19 SOFTWARE: Patent In Release #10, Version # 1
 20 CURRENT APPLICATION DATA:
 21 APPLICATION NUMBER: US/08/647,844A
 22 FILING DATE: 28-APR-1997
 23 CLASSIFICATION: 950
 24 PRIOR APPLICATION DATA:
 25 APPLICATION NUMBER: US 08/749,800
 26 FILING DATE: 16-NOV-1996

1 PRIOR APPLICATION DATA:
 2 APPLICATION NUMBER: US 09/305,841
 3 FILING DATE: 12-NOV-1996
 4 ATTORNEY/AGENT INFORMATION:
 5 NAME: BOYLE LEARY PH.D., KATHRYN
 6 REGISTRATION NUMBER: 36,417
 7 REFERENCE/DOCKET NUMBER: 9596 2402
 8 TELECOMMUNICATION INFORMATION:
 9 TELEPHONE: 213-567 4520
 10 TELEFAX: 213-567-2497
 11 INFORMATION FOR SEQ ID NO: 448:
 12 SEQUENCE CHARACTERISTICS:
 13 LENGTH: 10 amino acids
 14 TYPE: amino acid
 15 STRANDEDNESS: single
 16 FEATURE: linear
 17 MOLECULE TYPE: protein
 18 US 08 847-844A-48

Query Match 66.4% Score 4.05 4 Length 10
 Best Local Similarity 100.0% Prod. No. 3.6e+02
 Matches 4 Conservative 0 Mismatches 0 Gaps 0

QY 2 USAV 5
 LB 3 USAV 6

RES 11 49
 US 09 217 305 205
 1 Sequence 205 Application US/9273052
 2 Patent No. 6274544
 3 GENERAL INFORMATION:
 4 APPLICANT: Better, Marc B
 5 TITLE OF INVENTION: Methods for Recombinant Microbial Production of
 6 NUMBER OF SEQUENCES: 265
 7 CORRESPONDENT ADDRESS:
 8 ADDRESSEE: Marshall, Thomas, Gotschell, Murray & Burns
 9 STREET: 6400 Sears Tower, 24th South Wacker Drive
 10 CITY: Chicago
 11 STATE: Illinois
 12 COUNTRY: United States of America
 13 ZIP: 60606 6402
 14 COMPUTER READABLE FORM:
 15 MEDIUM TYPE: Floppy disk
 16 OPERATING SYSTEM: PC DOS/MS DOS
 17 SOFTWARE: Patent In Release #10, Version #1.25
 18 CURRENT APPLICATION DATA:
 19 APPLICATION NUMBER: US/09/217,452
 20 FILING DATE:
 21 PRIOR APPLICATION DATA:
 22 APPLICATION NUMBER: 08/621,803
 23 FILING DATE: 22-MAR-1996
 24 ATTORNEY/AGENT INFORMATION:
 25 NAME: Borou, Michael E
 26 REGISTRATION NUMBER: 25,447
 27 REFERENCE/DOCKET NUMBER: 2712974099
 28 TELECOMMUNICATION INFORMATION:
 29 TELEPHONE: 312/474-6400
 30 TELEFAX: 312/474-6448
 31 TELEX: 254856
 32 INFORMATION FOR SEQ ID NO: 205:
 33 SEQUENCE CHARACTERISTICS:
 34 LENGTH: 10 amino acids
 35 TYPE: amino acid
 36 STRANDEDNESS: single
 37 FEATURE: linear
 38 NAME/KEY: 205 205 10
 39 C-TERM: 205 10 10 10 10 10 10 10 10 10
 40 ORF: 205 10 10 10 10 10 10 10 10 10

NAME/KEY: Modified site
 LOCATION: 3 Regions
 OTHER INFORMATION: /label: Activated
 OTHER INFORMATION: /note: "The 3 Regions of Activated"
 US-09-787-443-4.205

Query Match: 96.4% Score 47, DB 47, Length 107
 Best Local Similarity: 100.0% Pat. No. 6,454,445
 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 7 KLKK 10
 IIII
 DC 7 KLKK 10

RESULT 4:
 US-09-787-443-4.205A-20
 Sequence 28: Application US/09/020,556
 Patent No. 6,454,502
 GENERAL INFORMATION:
 APPLICANT: Townsend, Robert M.
 TITLE OF INVENTION: Peptide Methods of the Tyrosine Receptor Domain
 TITLE OF INVENTION: Gamma Chain and Methods and Compositions for
 TITLE OF INVENTION: Making and Using the Same
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Washburn Kari Markiewicz & Co. 645020112, LLP
 STREET: One Liberty Place, 40th Floor
 CITY: Philadelphia
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Wordperfect V. 8
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/020,556A
 FILING DATE: 07 FEB 1997
 PRIORITY APPLICATION NUMBER: US 63/030,541
 FILING DATE: 07 FEB 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Richard, Mark
 REGISTRATION NUMBER: 530
 REFERENCE/CKET NUMBER: 100,429
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215 568-3100
 TELEFAX: 215 568-3439
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: circular
 N-TERMINUS: peptide
 US-09-787-443-4-205A-20

Query Match: 36.4% Score 47, DB 47, Length 107
 Best Local Similarity: 100.0% Pat. No. 6,454,445
 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 1 AGSA 4
 IIII
 DC 4 AGSA 7

RESULT 4:
 US-09-787-443-4.205A-20
 Sequence 109: Application US/09/020,556A
 Patent No. 6,454,445
 GENERAL INFORMATION:
 APPLICANT: U. Prasad Kari
 Tally J. Williams
 Michael McNamee
 TITLE OF INVENTION: Biologically Active Peptides With Reduced
 NUMBER OF SEQUENCES: 109
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 STREET: 1300 I Street, N.W. Suite 700
 CITY: Washington

GENERAL INFORMATION:
 APPLICANT: U. Prasad Kari
 Tally J. Williams
 Michael McNamee
 TITLE OF INVENTION: Biologically Active Peptides With Reduced
 NUMBER OF SEQUENCES: 109
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 STREET: 1300 I Street, N.W. Suite 700
 CITY: Washington

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: PC DOS/MS DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/115,737
 FILING DATE: 15-JUL-1995
 CLASSIFICATION: Unknown
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 06/265,530
 FILING DATE: 05-JUN-1995
 APPLICATION NUMBER: 06/184,462
 FILING DATE: 18 JAN 94
 APPLICATION NUMBER: 07/891,201
 FILING DATE: 01 JUN 92
 ATTORNEY/AGENT INFORMATION:
 NAME: Fardis, Joan P.
 REGISTRATION NUMBER: 12,984
 REFERENCE/CKET NUMBER: 05387,0021-06000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 408-4000
 TELEFAX: (202) 408-4400
 INFORMATION FOR SEQ ID NO: 109:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 N-TERMINUS: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 109:
 US-09-787-443-4.205A-20

Query Match: 36.4% Score 47, DB 47, Length 107
 Best Local Similarity: 100.0% Pat. No. 6,454,445
 Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0

QY 6 KLKK 9
 IIII
 DC 6 KLKK 9

RESULT 4:
 US-09-787-443-4.205A-20
 Sequence 148: Application US/09/115,737
 Patent No. 6,454,445
 GENERAL INFORMATION:
 APPLICANT: U. Prasad Kari
 Tally J. Williams
 Michael McNamee
 TITLE OF INVENTION: Biologically Active Peptides With Reduced
 NUMBER OF SEQUENCES: 148
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
 STREET: 1300 I Street, N.W. Suite 700
 CITY: Washington


```

1  STATE: D.C.
2  COUNTRY: USA
3  ZIP: 20005-3515
4  COMPUTER READABLE FORM:
5  MEDIUM TYPE: Floppy disk
6  COMPUTER: IBM PC compatible
7  OPERATING SYSTEM: PC DOS/MS DOS
8  SOFTWARE: Patent in Release #1.0, Version #1.30
9
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: US/09/115 147
12 FILING DATE: 15-JUN-1998
13 CLASSIFICATION: Unknown
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: 08/445,443
16 FILING DATE: 05-JUN-1995
17 APPLICATION NUMBER: 08/144,462
18 FILING DATE: 18-JAN '94
19 APPLICATION NUMBER: 07/441,201
20 FILING DATE: 01-JUN '92
21 ATTORNEY/AGENT INFORMATION:
22 NAME: Fordis, Jean B
23 REGISTRATION NUMBER: 42,494
24 REFERENCE/DOCKET NUMBER: 05/06/0021 Patent
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: (202) 408 4300
27 TELEFAX: (202) 408 4400
28 INFORMATION FOR SEQ ID NO: 148:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 10 amino acids
31 TYPE: amino acid
32 STRANDEDNESS: single
33 TOPOLOGY: linear
34 NUCLEOTIDE TYPE: peptide
35 SEQUENCE DESCRIPTION: SEQ ID NO: 148:
36 US 09-115 147 148
37
38 Query Match 36.4% Score 41 DB 4 Length 10
39 Best Local Similarity 100.0% Pref No. 3,6e+02
40 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
41
42 QY 6 KKKK 4
43 LL 1 1
44 : KKKK 4
45
46 RESULT 44
47 US 09-114 437A 437
48 Sequence 147, Application US/09/04437A
49 Patent No. 6492160
50 GENERAL INFORMATION:
51 APPLICANT: Winter, Gregory Paul
52 Griffiths, Andrew David
53 Williams, Samuel Cameron
54 Waterhouse, Peter
55 Nissim, Abaya
56 Johnson, Kevin Stuart
57 Smith, Andrew John Hammond
58 TITLE OF INVENTION: Methods for predicting members of species
59 binding pairs
60 NUMBER OF SEQUENCES: 600
61 CORRESPONDENCE ADDRESS:
62 ADDRESSEE: Audrey L. Bartnicki
63 STREET: Marshall, Gerstein & Board
64 6300 Sears Tower, 23rd South Wacker Drive
65 CITY: Chicago
66 STATE: Illinois
67 COUNTRY: USA
68 ZIP: 60606-8402
69 COMPUTER READABLE FORM:
70 MEDIUM TYPE: Floppy disk
71 COMPUTER: IBM PC compatible
72 OPERATING SYSTEM: PC DOS/MS DOS
73 SOFTWARE: Patent in Release #1.0, Version #1.30

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1  CURRENT APPLICATION DATA:
2  APPLICATION NUMBER: US/09/104,337A
3  FILING DATE: 25-JUN-1998
4  PRIOR APPLICATION DATA:
5  APPLICATION NUMBER: US 08/350,260
6  FILING DATE: 05-DEC-1994
7  APPLICATION NUMBER: 08 411,054 9.4
8  FILING DATE: 15 MAY 1991
9  APPLICATION NUMBER: 08 420,618 9
10 FILING DATE: 24 MAR 1992
11 APPLICATION NUMBER: PCI/3894/C08B3
12 FILING DATE: 15 MAY-1992
13 APPLICATION NUMBER: PCI/3894/C0605
14 FILING DATE: 28-MAR-1994
15 APPLICATION NUMBER: US 08/156,002
16 FILING DATE: 31-MAR-1994
17 APPLICATION NUMBER: US 08/307,619
18 FILING DATE: 16-SEP-1994
19 ATTORNEY/AGENT INFORMATION:
20 NAME: Bartnicki, Audrey L.
21 REGISTRATION NUMBER: 40,499
22 REFERENCE/DOCKET NUMBER: 28111/32372A
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: 312-474-6300
25 INFORMATION FOR SEQ ID NO: 437:
26 SEQUENCE CHARACTERISTICS:
27 LENGTH: 10 amino acids
28 TYPE: amino acid
29 STRANDEDNESS: single
30 TOPOLOGY: linear
31 SEQUENCE DESCRIPTION: SEQ ID NO: 437:
32 US 09 104 437A 437
33
34 Query Match 36.4% Score 41 DB 4 Length 10
35 Best Local Similarity 100.0% Pref No. 3,6e+02
36 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
37
38 QY 2 GSAY 5
39 LL 1 1
40 DB 7 GSAY 10
41
42 RESULT 44
43 US 08 983-157B 17
44 Sequence 17, Application US/08983157B
45 Patent No. 6579848
46 GENERAL INFORMATION:
47 APPLICANT: HEARING, Vincent J., Jr.
48 TITLE OF INVENTION: Protein and Peptides Thereof
49 NUMBER OF SEQUENCES: 28
50 CORRESPONDENCE ADDRESS:
51 ADDRESSEE: Needle & Rosenberg, P.C.
52 STREET: 127 Peachtree St., N.E.
53 CITY: Atlanta
54 STATE: GA
55 COUNTRY: USA
56 ZIP: 30303-1811
57 COMPUTER READABLE FORM:
58 MEDIUM TYPE: Floppy disk
59 COMPUTER: IBM PC compatible
60 OPERATING SYSTEM: PC-DOS/MS-DOS
61 SOFTWARE: Patent in Release #1.0, Version #1.30
62 CURRENT APPLICATION DATA:
63 APPLICATION NUMBER: US/08/983,157B
64 FILING DATE: 22-Dec-1997
65 CLASSIFICATION: Unknown
66 PRIOR APPLICATION DATA:
67 APPLICATION NUMBER: PCI/US96/10695
68 FILING DATE: 21 JUN 1996
69 APPLICATION NUMBER: 60/ 000,436
70 FILING DATE: 23 JUN 1995
71 ATTORNEY/AGENT INFORMATION:

```

1 NAME: Spratt, Gwendolyn D.
 2 REGISTRATION NUMBER: 36,316
 3 REFERENCE/DOCKET NUMBER: 14014, 6, 195
 4 TELECOMMUNICATION INFORMATION:
 5 TELEPHONE: (404) 688-0770
 6 TELEFAX: (404) 688-9869
 7 INFORMATION FOR SEQ ID NO: 17:
 8 SEQUENCE CHARACTERISTICS:
 9 LENGTH: 10 amino acids
 10 TYPE: amino acid
 11 TOPOLOGY: linear
 12 STRAIGHTNESS: not relevant
 13 MOLECULE TYPE: peptide
 14 SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 15
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OTHER INFORMATION: C-terminal amide, may be
OTHER INFORMATION: acetylated at N terminus
US-07-725-931-67

Query Match: 36.4%, Score 4, DB 1, Length 11;
Best Local Similarity 100.0%, Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 5 KLKK 9
III
LB 3 KLKK 6

RESULT 47
US-08-193-521-17
Sequence 1, Application US/08193521
Patent No. 5470950
GENERAL INFORMATION:
APPLICANT: Maloy, W. Lee
APPLICANT: Williams, Jon I.
TITLE OF INVENTION: Biologically Active Peptide
TITLE OF INVENTION: Compositions and Uses Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carolyn, Byrne, Bain, Gilligan,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DM4 V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08193521
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/870,960
FILING DATE:
APPLICATION NUMBER: 07/760,054
FILING DATE: 13 SEP 1991
ATTORNEY/AGENT INFORMATION:
NAME: Glstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 421250-161
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide,
OTHER INFORMATION: and/or may be acetylated at
OTHER INFORMATION: N-terminus.

Query Match: 36.4%, Score 4, DB 1, Length 11;
Best Local Similarity 100.0%, Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 6 KLKK 9
III
LB 3 KLKK 6

US-08-193-521-17
Sequence 1, Application US/08193521
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GENERAL INFORMATION:
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QY 6 KLKK 9
III
LB 3 KLKK 6

US-08-193-521-17
Sequence 1, Application US/08193521
Patent No. 5470950
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Query Match: 36.4%, Score 4, DB 1, Length 11;
Best Local Similarity 100.0%, Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 6 KLKK 9
III
LB 3 KLKK 6

RESULT 48
US-08-193-521-17
Sequence 1, Application US/08193521
Patent No. 5470950
GENERAL INFORMATION:
APPLICANT: Maloy, W. Lee
APPLICANT: Williams, Jon I.
TITLE OF INVENTION: Biologically Active Peptide
TITLE OF INVENTION: Compositions and Uses Thereof
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Query Match: 36.4%, Score 4, DB 1, Length 11;
Best Local Similarity 100.0%, Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 6 KLKK 9
III
LB 7 KLKK 10

US-08-193-521-18
Sequence 1, Application US/08193521
Patent No. 5470950
GENERAL INFORMATION:
APPLICANT: Maloy, W. Lee
APPLICANT: Williams, Jon I.
TITLE OF INVENTION: Biologically Active Peptide
TITLE OF INVENTION: Compositions and Uses Thereof
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
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STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DM4 V2
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APPLICATION NUMBER: US/08193521
FILING DATE:
CLASSIFICATION: 514
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APPLICATION NUMBER: US/07/870,960
FILING DATE:
APPLICATION NUMBER: 07/760,054
FILING DATE: 13 SEP 1991
ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 421250-161
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TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide,
OTHER INFORMATION: and/or may be acetylated at
OTHER INFORMATION: N-terminus.

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QY 6 KLKK 9
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LB 7 KLKK 10

US-08-193-521-17
Sequence 1, Application US/08193521
Patent No. 5470950
GENERAL INFORMATION:
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APPLICANT: Williams, Jon I.
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US-08-193-521-18
Sequence 1, Application US/08193521
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CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DM4 V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08193521
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/870,960
FILING DATE:
APPLICATION NUMBER: 07/760,054
FILING DATE: 13 SEP 1991
ATTORNEY/AGENT INFORMATION:
NAME: Glstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 421250-161
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: May be a C-terminal amide,
OTHER INFORMATION: and/or may be acetylated at
OTHER INFORMATION: N-terminus.

Query Match: 36.4%, Score 4, DB 1, Length 11;
Best Local Similarity 100.0%, Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 6 KLKK 9
III
LB 7 KLKK 10

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1 TITLE OF INVENTION: Compositions and Uses Involving
2 NUMBER OF SEQUENCES: 19
3 CORRESPONDENCE ADDRESS:
4 ADDRESSEE: Carrell, Byrne, Bach, Sullivan,
5 ADDRESSEE: Carrell & Stewart
6 STREET: 6 Hooker Farm Road
7 CITY: Roseland
8 STATE: New Jersey
9 COUNTRY: USA
10 ZIP: 07068
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: 3.5 inch diskette
13 COMPUTER: IBM PS/2
14 OPERATING SYSTEM: PC-DOS
15 SOFTWARE: DM4 V2
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/06/143,521
18 FILING DATE:
19 CLASSIFICATION: 514
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: US/91/870,319
22 FILING DATE:
23 ATTACHMENT NUMBER: 07/760,054
24 FILING DATE: 13-SEP-1991
25 ATTORNEY/AGENT INFORMATION:
26 NAME: OLSTEIN, ELLIOT M.
27 REGISTRATION NUMBER: 24,025
28 REFERENCE/DCKET NUMBER: 42,200-10,
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 201-994-1700
31 TELEFAX: 201-994-1744
32 INFORMATION FOR SEQ ID NO: 1:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 11 amino acids
35 TYPE: amino acid
36 STRANDEDNESS:
37 NUCLEIC ACID: linear
38 MOLECULE TYPE: peptide
39 FEATURES:
40 OTHER INFORMATION: May be a C-terminal amino,
41 OTHER INFORMATION: and/or may be acetylated at
42 OTHER INFORMATION: N-terminus.
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44 US 06/143,521-19
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1 SOFTWARE: ASCII text
2 CURRENT APPLICATION DATA:
3 APPLICATION NUMBER: US/91/8,570
4 FILING DATE: JANUARY 7, 1994
5 CLASSIFICATION: 435
6 ATTORNEY/AGENT INFORMATION:
7 NAME: DEGGRELL, GILBERT A., JR.
8 REGISTRATION NUMBER: 61,505
9 REFERENCE/DCKET NUMBER: HRI 104
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (617) 427-7400
12 TELEFAX: (617) 427-5941
13 INFORMATION FOR SEQ ID NO: 75:
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 11 amino acids
16 TYPE: amino acid
17 TOPOLOGY: linear
18 MOLECULE TYPE: peptide
19 FRAGMENT TYPE: internal
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21 US-06 178-570-75
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Best Local Similarity: 100.0%, Pred. No. 3.9e+02;
Matches: 47, Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

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Q7: 8 KKKK 11
    111
DB: 8 KKKK 11

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Search completed: September 30, 2003, 10:28:38
Job time: 14.9167 secs

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Matches: 47, Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

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Q7: 6 KKKK 9
    111
DB: 7 KKKK 10

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1 RESUME 50
2 US 8 178 570-75
3 Sequence 75, Application US/06178570
4 Patent No. 552187
5
6 GENERAL INFORMATION:
7 APPLICANT: Lewis C. Cantley
8 APPLICANT: Zhou Song Yang
9 TITLE OF INVENTION: Substrate Specificity of Protein Kinases
10 NUMBER OF SEQUENCES: 77
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: LARIVE & CROCKFELD
13 STREET: 60 STATE STREET, Suite 510
14 CITY: Boston
15 STATE: MASSACHUSETTS
16 COUNTRY: USA
17 ZIP: 02109-1875
18
19 COMPUTER READABLE FORM:
20 MEDIUM TYPE: Floppy disk
21 COMPUTER: IBM PC compatible
22 OPERATING SYSTEM: PC-DOS/MS-DOS

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GenBank version 1.1
Copyright (c) 1994-2003 by the NCBI

1M protein: protein search, using sw-motif

Run on: September 30, 2003, 10:16:07, Search time 21.5 seconds
(without a database)
72.4 x 60.0 x 11.0 bp data/sec

Title: US-09-787-443-4

Perfect score: 11

Sequence: 1 ASNAVKKKKA 11

Scoring table: 61135

Gapop: 60.0 x Gapext: 60.0

Searched: 556894 seqs, 15137600 residues

Word size: 3

Total number of hits satisfying chosen parameters: 6487

Minimum hit seq length: 8

Maximum hit seq length: 15

Post-processing: listing first 500 summaries

Database: 1 Published Applications AA

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2 /can2_6/prodata/2/pdata/US09-787-443-4-oli.rapb
3 /can2_6/prodata/2/pdata/US09-787-443-4-oli.rapb
4 /can2_6/prodata/2/pdata/US09-787-443-4-oli.rapb
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7 /can2_6/prodata/2/pdata/US09-787-443-4-oli.rapb
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18 /can2_6/prodata/2/pdata/US09-787-443-4-oli.rapb

Used: 60 is the number of residues in the hit sequence. The score is greater than or equal to the score of the result found. The score is derived by analysis of the total score distribution.

SUMMARIES

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2	5	45.5	10	12	US-10-244-125-5	Sequence 6, Appl
3	5	45.5	10	15	US-10-100-100A-10	Sequence 15, Appl
4	5	45.5	13	11	US-09-902-902-27	Sequence 23, Appl
5	5	45.5	15	12	US-10-100-100A-10	Sequence 23, Appl
6	4	46.4	8	9	US-09-787-443-4-oli.rapb	Sequence 237, App
7	4	46.4	8	10	US-09-142-142-2	Sequence 2, Appl
8	4	46.4	8	12	US-10-100-100A-10	Sequence 96, Appl
9	4	46.4	8	15	US-10-100-100A-10	Sequence 14, Appl
10	4	46.4	8	15	US-10-100-100A-10	Sequence 14, Appl
11	4	46.4	8	15	US-10-100-100A-10	Sequence 14, Appl
12	4	46.4	8	15	US-10-100-100A-10	Sequence 14, Appl
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Sequence 46, Appl
Sequence 48, Appl
Sequence 52, Appl
Sequence 54, Appl
Sequence 62, Appl
Sequence 21, Appl
Sequence 588, App
Sequence 136, App
Sequence 205, App
Sequence 4, Appl
Sequence 180, App
Sequence 145, App
Sequence 504, App
Sequence 506, App
Sequence 508, App
Sequence 510, App
Sequence 2516, App
Sequence 2676, App
Sequence 2676, App
Sequence 2706, App
Sequence 2908, App
Sequence 3280, App
Sequence 142, App
Sequence 318, App
Sequence 320, App
Sequence 629, App
Sequence 631, App
Sequence 840, App
Sequence 842, App
Sequence 4, Appl
Sequence 46, Appl
Sequence 406, App
Sequence 11, Appl
Sequence 42, Appl
Sequence 21, Appl
Sequence 78, Appl
Sequence 142, App
Sequence 38, Appl
Sequence 10, Appl
Sequence 206, App
Sequence 181, App
Sequence 274, App
Sequence 246, App
Sequence 434, App
Sequence 544, App
Sequence 597, App
Sequence 162, App
Sequence 251, App
Sequence 89, Appl
Sequence 127, App
Sequence 1, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 134, App
Sequence 54, Appl
Sequence 3, Appl
Sequence 2, Appl
Sequence 24, Appl
Sequence 54, Appl
Sequence 6, Appl
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Sequence 34, Appl
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Sequence 420, App
Sequence 422, App
Sequence 6, Appl
Sequence 11, Appl
Sequence 34, App

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238	3	27.3	8	15	US-10-054-295-225	Sequence 223, Appl	311	3	27.3	9	7	US-09-881-490-160	Sequence 160, Appl
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247	3	27.3	8	15	US-10-211-048-262	Sequence 262, Appl	320	3	27.3	9	7	US-09-881-490-178	Sequence 178, Appl
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249	3	27.3	8	15	US-10-109-171-107	Sequence 107, Appl	322	3	27.3	9	7	US-09-780-053-56	Sequence 56, Appl
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271	3	27.3	9	9	US-09-765-527-222	Sequence 229, Appl	344	3	27.3	9	7	US-09-918-243-47	Sequence 47, Appl
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273	3	27.3	9	9	US-09-765-527-222	Sequence 223, Appl	346	3	27.3	9	7	US-09-918-243-74	Sequence 74, Appl
274	3	27.3	9	9	US-09-765-527-222	Sequence 224, Appl	347	3	27.3	9	7	US-09-918-243-75	Sequence 75, Appl
275	3	27.3	9	9	US-09-765-527-222	Sequence 225, Appl	348	3	27.3	9	7	US-09-918-243-128	Sequence 128, Appl
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883	3	27.3	9	11	US 09-882-291-73	Sequence 73, Appl	456	9	12	US-10-022-066-534	Sequence 534, App
884	3	27.3	9	11	US 09-883-748-118	Sequence 118, Ap	457	9	12	US-10-022-066-570	Sequence 570, App
885	3	27.3	9	11	US 09-883-864-49	Sequence 49, Appl	458	9	12	US-10-022-066-616	Sequence 616, App
886	3	27.3	9	11	US 09-918-864-42	Sequence 42, Appl	459	9	12	US-10-062-109A-269	Sequence 269, App
887	3	27.3	9	11	US 09-918-864-10	Sequence 10, Appl	460	9	12	US-10-062-109A-284	Sequence 284, App
888	3	27.3	9	11	US 09-938-604-26	Sequence 26, Appl	461	9	12	US-10-062-109A-662	Sequence 662, App
889	3	27.3	9	11	US 09-875-904A-260	Sequence 260, App	462	9	12	US-10-077-106-11	Sequence 11, Appl
890	3	27.3	9	11	US 09-875-904A-271	Sequence 271, App	463	9	12	US-10-077-106-11	Sequence 11, Appl
891	3	27.3	9	11	US 09-875-904A-272	Sequence 272, App	464	9	12	US-10-077-106-13	Sequence 13, Appl
892	3	27.3	9	11	US 09-875-904A-273	Sequence 273, App	465	9	12	US-10-077-106-13	Sequence 13, Appl
893	3	27.3	9	11	US 09-875-904A-435	Sequence 435, App	466	9	12	US-10-077-106-15	Sequence 15, Appl
894	3	27.3	9	11	US 09-875-904A-436	Sequence 436, App	467	9	12	US-10-077-106-16	Sequence 16, Appl
895	3	27.3	9	11	US 09-875-904A-444	Sequence 444, App	468	9	12	US-10-077-106-17	Sequence 17, Appl
896	3	27.3	9	11	US 09-875-904A-576	Sequence 576, App	469	9	12	US-10-077-106-18	Sequence 18, Appl
897	3	27.3	9	11	US 09-875-904A-589	Sequence 589, App	470	9	12	US-10-184-708-3	Sequence 3, Appl
898	3	27.3	9	11	US 09-876-904A-596	Sequence 596, App	471	9	12	US-10-144-188-33	Sequence 33, Appl
899	3	27.3	9	11	US 09-876-904A-615	Sequence 615, App	472	9	12	US-10-144-188-42	Sequence 42, Appl
900	3	27.3	9	11	US 09-753-427-6	Sequence 6, Appl	473	9	12	US-10-210-148-64	Sequence 64, Appl
901	3	27.3	9	11	US 09-791-477-26	Sequence 26, Appl	474	9	12	US-10-293-580-8	Sequence 8, Appl
902	3	27.3	9	11	US 09-791-477-72	Sequence 72, Appl	475	9	12	US-10-395-541-3	Sequence 3, Appl
903	3	27.3	9	11	US 09-791-477-75	Sequence 75, Appl	476	9	12	US-09-854-248-1	Sequence 1, Appl
904	3	27.3	9	11	US 09-791-477-236	Sequence 236, App	477	9	12	US-10-083-259-9	Sequence 9, Appl
905	3	27.3	9	11	US 09-785-319-24	Sequence 24, Appl	478	9	12	US-10-239-313A-83	Sequence 83, Appl
906	3	27.3	9	11	US 09-785-319-72	Sequence 72, Appl	479	9	12	US-10-239-313A-205	Sequence 205, App
907	3	27.3	9	11	US 09-785-319-75	Sequence 75, App	480	9	12	US-10-239-313A-208	Sequence 208, App
908	3	27.3	9	11	US 09-785-319-246	Sequence 246, App	481	9	12	US-10-239-313A-368	Sequence 368, App
909	3	27.3	9	11	US 09-865-548A-70	Sequence 70, Appl	482	9	12	US-10-239-313A-650	Sequence 650, App
910	3	27.3	9	11	US 09-865-548A-81	Sequence 81, Appl	483	9	12	US-10-353-929-141	Sequence 141, App
911	3	27.3	9	11	US 09-865-548A-104	Sequence 104, App	484	9	12	US-10-353-929-153	Sequence 153, App
912	3	27.3	9	11	US 09-924-656-24	Sequence 24, Appl	485	9	12	US-10-353-929-190	Sequence 190, App
913	3	27.3	9	11	US 09-924-656A-45	Sequence 45, Appl	486	9	14	US-10-011-321-4	Sequence 4, Appl
914	3	27.3	9	11	US 09-791-524A-29	Sequence 29, Appl	487	9	14	US-10-042-202-13	Sequence 13, Appl
915	3	27.3	9	12	US 09-791-524-145	Sequence 145, App	488	9	14	US-10-042-202-14	Sequence 14, Appl
916	3	27.3	9	12	US 09-942-165-93	Sequence 93, App	489	9	14	US-10-039-645-12	Sequence 12, Appl
917	3	27.3	9	12	US 09-942-165-106	Sequence 106, Ap	490	9	14	US-10-046-922-42	Sequence 42, Appl
918	3	27.3	9	12	US 09-942-165-107	Sequence 107, App	491	9	14	US-10-057-505-9	Sequence 9, Appl
919	3	27.3	9	12	US 09-942-165-124	Sequence 124, Ap	492	9	14	US-10-106-487-19	Sequence 19, Appl
920	3	27.3	9	12	US 10-039-177-42	Sequence 42, Appl	493	9	14	US-10-106-487-33	Sequence 33, Appl
921	3	27.3	9	12	US 10-164-043-8	Sequence 43, Appl	494	9	14	US-10-131-965-6	Sequence 6, Appl
922	3	27.3	9	12	US 10-169-031-26	Sequence 26, Appl	495	9	14	US-10-211-207-11	Sequence 11, Appl
923	3	27.3	9	12	US 10-169-031-26	Sequence 16, Appl	496	9	15	US-10-211-207-11	Sequence 11, Appl
924	3	27.3	9	12	US 10-169-031-26	Sequence 16, Appl	497	9	15	US 10-211-207-12	Sequence 12, Appl
925	3	27.3	9	12	US 10-169-031-26	Sequence 16, Appl	498	9	15	US 10-211-207-13	Sequence 13, Appl
926	3	27.3	9	12	US 10-169-031-26	Sequence 16, Appl	499	9	15	US 10-211-207-15	Sequence 15, Appl
927	3	27.3	9	12	US 10-169-031-26	Sequence 16, Appl	500	9	15	US-10-211-088-284	Sequence 284, App
928	3	27.3	9	12	US 09-791-524-145	Sequence 145, App					
929	3	27.3	9	12	US 09-791-524-145	Sequence 145, App					
930	3	27.3	9	12	US 09-791-524-145	Sequence 145, App					
931	3	27.3	9	12	US 09-791-524-145	Sequence 145, App					
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966	3	27.3	9	12	US 09-791-524-145	Sequence 145, App					
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978	3	27.3	9	12	US 09-791-524-145	Sequence 145, App					
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991	3	27.3	9	12	US 09-791-524-145	Sequence 145, App					
992	3	27.3	9	12	US 09-791-524-145	Sequence 145, App					
993	3	27.3	9	12	US 09-791-524-145	Sequence 145, App					
994	3	27.3	9	12	US 09-791-524-145	Sequence 145, App					
995	3	27.3	9	12	US 09-791-524-145	Sequence 145, App					
996	3	27.3	9	12	US 09-791-52						

Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 AGSAV 5
11111
11 2 AGSAV 6

RESULT 2
US-10-424 125 6
Sequence 5, Application US/10224125
Publication No. US2003016184A1
GENERAL INFORMATION:
APPLICANT: REID, ROBERT H.
APPLICANT: BOELEKER, EUGEN C.
APPLICANT: VAN HAMONT, JOHN
APPLICANT: SETTERSTROM, JEAN A.
APPLICANT: MCCUEEN, CHARLES
APPLICANT: CASSELS, FREDERICK
TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROBACTERIACEAE
TITLE OF INVENTION: ORGANISMS USING ANTIGENS FROM ENTEROBACTERIACEAE WITHIN
TITLE OF INVENTION: B-CELL-ADAPTABLE HYPOCOMPATIBLE MULTISPECIES
FILE REFERENCE: Army 108
CURRENT APPLICATION NUMBER: US/10/224,125
CURRENT FILING DATE: 2002-08-20
PRIOR APPLICATION NUMBER: 08/789,734
PRIOR FILING DATE: 1997-01-27
PRIOR APPLICATION NUMBER: 08/452,944
PRIOR FILING DATE: 1994-12-09
PRIOR APPLICATION NUMBER: 06/034,947
PRIOR FILING DATE: 1993-03-22
PRIOR APPLICATION NUMBER: 07/467,403
PRIOR FILING DATE: 1992-04-10
PRIOR APPLICATION NUMBER: 07/805,724
PRIOR FILING DATE: 1991-11-21
PRIOR APPLICATION NUMBER: 07/690,495
PRIOR FILING DATE: 1991-04-24
PRIOR APPLICATION NUMBER: 07/521,445
PRIOR FILING DATE: 1990-05-11
PRIOR APPLICATION NUMBER: 07/495,547
PRIOR FILING DATE: 1990-03-15
PRIOR APPLICATION NUMBER: 06/640,608
PRIOR FILING DATE: 1984-03-16
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO 5
LENGTH: 10
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthesized
US 10-224 125 6

Query Match 45.5% Score 5: 11111 Length 10:
Best Local Similarity 100.0%, Pred. No. 11111
Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 1 SAVKL 7
11111
11 2 SAVKL 6

RESULT 3
US-10-156-570A-15
Sequence 15, Application US/10156570A
Publication No. US20030125242A1
GENERAL INFORMATION:
APPLICANT: ROSENECKER, JOSEPH
APPLICANT: RUTTER, WOLFGANG
APPLICANT: KUCLEPH, CARSTEN MARTIN
APPLICANT: FRANK, CHRISTIAN
TITLE OF INVENTION: COMBINING MOLECULES OF NOCTUID
TITLE OF INVENTION: LOCALIZATION SIGNALS FOR PROTEIN TRANSLOCATION DOMAINS

1 TITLE OF INVENTION: ANTI-HERPES USE FOR TRANSFERRING NUCLEIC ACID MOLECULES
2 FILE REFERENCE: VOS-16
3 CURRENT APPLICATION NUMBER: US/10/156,570A
4 CURRENT FILING DATE: 2002-09-24
5 PRIOR APPLICATION NUMBER: 09/4700/11690
6 PRIOR FILING DATE: 2000-11-23
7 NUMBER OF SEQ ID NOS: 32
8 SOFTWARE: FASTSEQ FOR Windows Version 4.0
9 SEQ ID NO 15
10 LENGTH: 10
11 TYPE: PRI
12 ORGANISM: Artificial Sequence
13 FEATURE:
14 OTHER INFORMATION: Description of Artificial Sequence: hepatitis virus
15 OTHER INFORMATION: Delta antigen nuclear localization sequence
16 US 10-156-570A-15

Query Match 45.5% Score 5: 6 KKKKK 10:
Best Local Similarity 100.0%, Pred. No. 6
Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 6 KKKKK 10
11111
11 2 KKKKK 6

RESULT 4
US-09-992 665-27
Sequence 27, Application US/09992665
Publication No. US200303092009A1
GENERAL INFORMATION:
APPLICANT: KALP, PAUL
TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: GENES-002A
CURRENT APPLICATION NUMBER: US/09/992,665
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 09/249,508
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO 27
LENGTH: 15
TYPE: PRI
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Probe
US 09-992-665 27

Query Match 45.5% Score 5: 6 KKKKK 10:
Best Local Similarity 100.0%, Pred. No. 11111 Length 13:
Matches 5: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 6 KKKKK 10
11111
11 5 KKKKK 9

RESULT 5
US-10-014-322A 92
Sequence 92, Application US/10014322A
Publication No. US20030162129A1
GENERAL INFORMATION:
APPLICANT: NESTOR, JR., JOHN
APPLICANT: WILSON, CAROL
APPLICANT: TAN BEHR, CHRISTINE
APPLICANT: KATES, STEVEN
APPLICANT: KISTENBERG, JOHN
TITLE OF INVENTION: BINDING COMPOUNDS AND METHODS FOR IDENTIFYING BINDING COMPOUNDS
FILE REFERENCE: CNS 008
CURRENT APPLICATION NUMBER: US/10/014,322A
CURRENT FILING DATE: 2002-07-09

PRIOR APPLICATION NUMBER: US 62/243,142
 PRIOR FILING DATE: 2000-10-27
 PRIOR APPLICATION NUMBER: US 09/816,663
 PRIOR FILING DATE: 2001-03-29
 PRIOR APPLICATION NUMBER: US 09/816,665
 PRIOR FILING DATE: 2001-03-29
 PRIOR APPLICATION NUMBER: US 09/816,646
 PRIOR FILING DATE: 2001-03-29
 NUMBER OF SEQ ID NOS: 126
 SOFTWARE: Patent In version 3.0
 SEQ ID NO 92
 LENGTH: 15
 TYPE: PRT
 ORGANISM: Artificial sequence
 FEATURE:
 OTHER INFORMATION: CXC84 binding peptide
 US 10 014 922A 92

Query Match 45.5% Score 54 DB 10 Length 15
 Best Local Similarity 100.0% Pred. No. 5.1e+05
 Matches 57 Conservative 0 Mismatches 0 Indels 0 Gaps 0

CY 6 KK88 10
 111
 IL 1 KK88 15

RESULT 1
 US-09 142 043 2
 Sequence 27 Application US/09142043
 Patent No. US2002014232A
 GENERAL INFORMATION:
 APPLICANT: SMITH, Richard Anthony Godwin
 TITLE OF INVENTION: FRAGMENTS OF CRL AND THEIR USE
 FILE REFERENCE: B6162/104
 CURRENT APPLICATION NUMBER: US/09/142,043
 EARLIER FILING DATE: 1998-12-01
 EARLIER FILING DATE: 1997-02-26
 EARLIER APPLICATION NUMBER: JP 95-5162.2
 EARLIER FILING DATE: 1996-03-02
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: Patent In Ver. 3.0
 SEQ ID NO 2
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: peptide
 US-09 142 043 2

Query Match 96.4% Score 41 DB 10 Length 8
 Best Local Similarity 100.0% Pred. No. 5.1e+05
 Matches 41 Conservative 0 Mismatches 0 Indels 0 Gaps 0
 CY 8 KK8A 11
 111
 IL 5 KK8A 6
 RESULT 2
 US-09 142 043 96
 Sequence 27 Application US/09142043
 Patent No. US2002014232A
 GENERAL INFORMATION:
 APPLICANT: SMITH, Richard Anthony Godwin
 TITLE OF INVENTION: FRAGMENTS OF CRL AND THEIR USE
 FILE REFERENCE: B6162/104
 CURRENT APPLICATION NUMBER: US/09/142,043
 EARLIER FILING DATE: 1998-12-01
 EARLIER FILING DATE: 1997-02-26
 EARLIER APPLICATION NUMBER: JP 95-5162.2
 EARLIER FILING DATE: 1996-03-02
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: Patent In Ver. 3.0
 SEQ ID NO 2
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: peptide
 US-09 142 043 96

Query Match 96.4% Score 41 DB 10 Length 8
 Best Local Similarity 100.0% Pred. No. 5.1e+05
 Matches 41 Conservative 0 Mismatches 0 Indels 0 Gaps 0
 CY 8 KK8A 11
 111
 IL 5 KK8A 6
 RESULT 3
 US-09 142 043 96
 Sequence 27 Application US/09142043
 Patent No. US2002014232A
 GENERAL INFORMATION:
 APPLICANT: SMITH, Richard Anthony Godwin
 TITLE OF INVENTION: FRAGMENTS OF CRL AND THEIR USE
 FILE REFERENCE: B6162/104
 CURRENT APPLICATION NUMBER: US/09/142,043
 EARLIER FILING DATE: 1998-12-01
 EARLIER FILING DATE: 1997-02-26
 EARLIER APPLICATION NUMBER: JP 95-5162.2
 EARLIER FILING DATE: 1996-03-02
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: Patent In Ver. 3.0
 SEQ ID NO 2
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: peptide
 US-09 142 043 96

Query Match 96.4% Score 41 DB 10 Length 8
 Best Local Similarity 100.0% Pred. No. 5.1e+05
 Matches 41 Conservative 0 Mismatches 0 Indels 0 Gaps 0
 CY 8 KK8A 11
 111
 IL 5 KK8A 6
 RESULT 4
 US-09 142 043 96
 Sequence 27 Application US/09142043
 Patent No. US2002014232A
 GENERAL INFORMATION:
 APPLICANT: SMITH, Richard Anthony Godwin
 TITLE OF INVENTION: FRAGMENTS OF CRL AND THEIR USE
 FILE REFERENCE: B6162/104
 CURRENT APPLICATION NUMBER: US/09/142,043
 EARLIER FILING DATE: 1998-12-01
 EARLIER FILING DATE: 1997-02-26
 EARLIER APPLICATION NUMBER: JP 95-5162.2
 EARLIER FILING DATE: 1996-03-02
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: Patent In Ver. 3.0
 SEQ ID NO 2
 LENGTH: 8
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: peptide
 US-09 142 043 96

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Best Local Similarity 100.0%  Score 4: DB 15: Length 8;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

CY 7 LKXX 10
DB 2 LKXX 5

RESULT 9
US-10-133-210-174
? Sequence 174, Application US/10/133-210
? Publication No. US20040175809A1
? GENERAL INFORMATION:
? APPLICANT: Fedorov, Arcady Fedorovich
? APPLICANT: Fedorov, Alexey
? TITLE OF INVENTION: FLUORESCENT LIMER PROTEINS AND METHODS
? TITLE OF INVENTION: FOR THEIR USE
? FILE REFERENCE: CLON-077CIP
? CURRENT APPLICATION NUMBER: US/10/133-210
? CURRENT FILING DATE: 2002-02-09
? PRIOR APPLICATION NUMBER: 60/211,667
? PRIOR FILING DATE: 2000-06-14
? PRIOR APPLICATION NUMBER: PCT/US01/14697
? PRIOR FILING DATE: 2001-06-14
? NUMBER OF SEQ ID NOS: 22
? SOFTWARE: FastSeq for Windows Version 1.1
? SEQ ID NO 14
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-174

Query Match 36.4%  Score 4: DB 15: Length 8;
Best Local Similarity 100.0%  Score 4: DB 15: Length 8;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

CY 7 LKXX 10
DB 2 LKXX 5

RESULT 10
US-10-133-210-174
? Sequence 174, Application US/10/133-210
? Publication No. US20040175809A1
? GENERAL INFORMATION:
? APPLICANT: Fedorov, Arcady Fedorovich
? APPLICANT: Fedorov, Alexey
? TITLE OF INVENTION: FLUORESCENT LIMER PROTEINS AND METHODS
? TITLE OF INVENTION: FOR THEIR USE
? FILE REFERENCE: CLON-077CIP
? CURRENT APPLICATION NUMBER: US/10/133-210
? CURRENT FILING DATE: 2002-02-09
? PRIOR APPLICATION NUMBER: 60/211,667
? PRIOR FILING DATE: 2000-06-14
? PRIOR APPLICATION NUMBER: PCT/US01/14697
? PRIOR FILING DATE: 2001-06-14
? NUMBER OF SEQ ID NOS: 22
? SOFTWARE: FastSeq for Windows Version 1.1
? SEQ ID NO 14
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-174

Query Match 36.4%  Score 4: DB 15: Length 8;
Best Local Similarity 100.0%  Score 4: DB 15: Length 8;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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CY 5 VKKK 8
DB 2 VKKK 5

RESULT 11
US-10-133-210-172
? Sequence 172, Application US/10/133-210
? Publication No. US2004016964A1
? GENERAL INFORMATION:
? APPLICANT: Belitsky, Charles
? APPLICANT: Belitsky, Jay
? APPLICANT: Gilukota, Kamalakat
? APPLICANT: Vaccaro, Dennis
? APPLICANT: Wong, Zhiping
? APPLICANT: Zhang, Chao
? TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
? TITLE OF INVENTION: COMPOSITIONS THEREOF
? FILE REFERENCE: HQ-035AX
? CURRENT APPLICATION NUMBER: US/10/133-210
? CURRENT FILING DATE: 2002-04-26
? NUMBER OF SEQ ID NOS: 281
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 172
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-172

Query Match 36.4%  Score 4: DB 15: Length 8;
Best Local Similarity 100.0%  Score 4: DB 15: Length 8;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

CY 7 LKXX 10
DB 2 LKXX 5

RESULT 12
US-10-133-210-174
? Sequence 173, Application US/10/133-210
? Publication No. US2004016964A1
? GENERAL INFORMATION:
? APPLICANT: Belitsky, Charles
? APPLICANT: Belitsky, Jay
? APPLICANT: Gilukota, Kamalakat
? APPLICANT: Vaccaro, Dennis
? APPLICANT: Wong, Zhiping
? APPLICANT: Zhang, Chao
? TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
? TITLE OF INVENTION: COMPOSITIONS THEREOF
? FILE REFERENCE: HQ-035AX
? CURRENT APPLICATION NUMBER: US/10/133-210
? CURRENT FILING DATE: 2002-04-26
? NUMBER OF SEQ ID NOS: 281
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 173
? LENGTH: 8
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-174

Query Match 36.4%  Score 4: DB 15: Length 8;
Best Local Similarity 100.0%  Score 4: DB 15: Length 8;
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

CY 7 LKXX 10
DB 2 LKXX 5

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1  TYPE: PVI
2  ORGANISM: N. rustica
3  US-09 826 177 12

Query Match
4 4 AVKL 7
5 111
6 2 AVKL 5

Best Local Similarity 100.0%, Score 4, DB 9, Length 9,
Matches 4, Conservative 0, Mismatches 0, Gaps 0;

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RESULT 14
US-09 826 177 14
1 Sequence 14, Application US/09/826177
2 Patent No. US2002022024A1
3 GENERAL INFORMATION:
4 APPLICANT: BAIG, Salim
5 TITLE OF INVENTION: Homologase Inhibitors and Methods of Use
6 FILE REFERENCE: 245,0038 0101
7 CURRENT APPLICATION NUMBER: US/09/826,177
8 CURRENT FILING DATE: 2001-09-18
9 PRIOR APPLICATION NUMBER: US 60/144,426
10 PRIOR FILING DATE: 2000-04-14
11 NUMBER OF SEQ ID NOS: 97
12 SOFTWARE: Patent in version 3.1
13 SEQ ID NO 14
14 LENGTH: 9
15 TYPE: PVI
16 ORGANISM: N. rusticum
17 US-09 826 177 14

Query Match
4 4 AVKL 7
5 111
6 2 AVKL 5

Best Local Similarity 100.0%, Score 4, DB 9, Length 9,
Matches 4, Conservative 0, Mismatches 0, Gaps 0;

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RESULT 16
US-09 826 177 36
1 Sequence 16, Application US/09/826177
2 Patent No. US2002022024A1
3 GENERAL INFORMATION:
4 APPLICANT: BAIG, Salim
5 TITLE OF INVENTION: Homologase Inhibitors and Methods of Use
6 FILE REFERENCE: 245,0038 0101
7 CURRENT APPLICATION NUMBER: US/09/826,177
8 CURRENT FILING DATE: 2001-09-18
9 PRIOR APPLICATION NUMBER: US 60/144,426
10 PRIOR FILING DATE: 2000-04-14
11 NUMBER OF SEQ ID NOS: 97
12 SOFTWARE: Patent in version 3.1
13 SEQ ID NO 16
14 LENGTH: 9
15 TYPE: PVI
16 ORGANISM: A. thaliana
17 US-09 826 177 36

Query Match
4 4 AVKL 7
5 111
6 2 AVKL 5

Best Local Similarity 100.0%, Score 4, DB 9, Length 9,
Matches 4, Conservative 0, Mismatches 0, Gaps 0;

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RESULT 18
US-09 826 177 42
1 Sequence 18, Application US/09/826177
2 Patent No. US2002022024A1
3 GENERAL INFORMATION:
4 APPLICANT: BAIG, Salim
5 TITLE OF INVENTION: Homologase Inhibitors and Methods of Use
6 FILE REFERENCE: 245,0038 0101
7 CURRENT APPLICATION NUMBER: US/09/826,177
8 CURRENT FILING DATE: 2001-09-18
9 PRIOR APPLICATION NUMBER: US 60/144,426
10 PRIOR FILING DATE: 2000-04-14
11 NUMBER OF SEQ ID NOS: 97
12 SOFTWARE: Patent in version 3.1
13 SEQ ID NO 18
14 LENGTH: 9
15 TYPE: PVI
16 ORGANISM: N. rustica
17 US-09 826 177 42

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RESULT 17
US-09-826-177-46
; Sequence 46, Application US/09826177
; Patent No. US2002022024A1
; GENERAL INFORMATION:
; APPLICANT: BAIG, Salman
; APPLICANT: PETERSON, David
; TITLE OF INVENTION: Hemoglobinase Inhibitors and Methods of Use
; FILE REFERENCE: 235,0038,0101
; CURRENT APPLICATION NUMBER: US/09/826,177
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/194,426
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 9
; TYPE: PRT
; ORGANISM: C. elodans
US-09-826-177-46

Query Match
Best Local Similarity 36.4%, Score 4; DB 9; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 4 AVKL 7
DB 2 AVKL 5

RESULT 18
US-09-826-177-44
; Sequence 48, Application US/09826177
; Patent No. US2002022024A1
; GENERAL INFORMATION:
; APPLICANT: BAIG, Salman
; APPLICANT: PETERSON, David
; TITLE OF INVENTION: Hemoglobinase Inhibitors and Methods of Use
; FILE REFERENCE: 235,0038,0101
; CURRENT APPLICATION NUMBER: US/09/826,177
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/194,426
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 9
; TYPE: PRT
; ORGANISM: C. elodans
US-09-826-177-48

Query Match
Best Local Similarity 36.4%, Score 4; DB 9; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 4 AVKL 7
DB 2 AVKL 5

RESULT 19
US-09-826-177-52
; Sequence 54, Application US/09826177
; Patent No. US2002022024A1
; GENERAL INFORMATION:
; APPLICANT: BAIG, Salman
; APPLICANT: PETERSON, David
; TITLE OF INVENTION: Hemoglobinase Inhibitors and Methods of Use
; FILE REFERENCE: 235,0038,0101
; CURRENT APPLICATION NUMBER: US/09/826,177
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/194,426
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Aedes aegypti
US-09-826-177-52

Query Match
Best Local Similarity 36.4%, Score 4; DB 9; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 4 AVKL 7
DB 2 AVKL 5

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; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: L. mexicana
US-09-826-177-52

Query Match
Best Local Similarity 36.4%, Score 4; DB 9; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 4 AVKL 7
DB 2 AVKL 5

RESULT 20
US-09-826-177-54
; Sequence 54, Application US/09826177
; Patent No. US2002022024A1
; GENERAL INFORMATION:
; APPLICANT: BAIG, Salman
; APPLICANT: PETERSON, David
; TITLE OF INVENTION: Hemoglobinase Inhibitors and Methods of Use
; FILE REFERENCE: 235,0038,0101
; CURRENT APPLICATION NUMBER: US/09/826,177
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/194,426
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 9
; TYPE: PRT
; ORGANISM: L. major
US-09-826-177-54

Query Match
Best Local Similarity 36.4%, Score 4; DB 9; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 4 AVKL 7
DB 2 AVKL 5

RESULT 21
US-09-826-177-62
; Sequence 62, Application US/09826177
; Patent No. US2002022024A1
; GENERAL INFORMATION:
; APPLICANT: BAIG, Salman
; APPLICANT: PETERSON, David
; TITLE OF INVENTION: Hemoglobinase Inhibitors and Methods of Use
; FILE REFERENCE: 235,0038,0101
; CURRENT APPLICATION NUMBER: US/09/826,177
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/194,426
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Aedes aegypti
US-09-826-177-62

Query Match
Best Local Similarity 36.4%, Score 4; DB 9; Length 9;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 4 AVKL 7
DB 2 AVKL 5

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LP 111
2 AVKE 5

RESULT 22

US-09-878-603-21

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1 Sequence 21: Application US/09878603
2 Patent No. US20020365138A
3 GENERAL INFORMATION:
4 APPLICANT: Ward, Peter A.
5 APPLICANT: Haber, Jacq. Markus
6 APPLICANT: Sarna, Vidya
7 APPLICANT: Csernak, Boris
8 TITLE OF INVENTION: Compositions and Methods for the Treatment of Seters
9 FILE REFERENCE: DN-03783
10 CURRENT APPLICATION NUMBER: US/09/878,603
11 CURRENT FILING DATE: 2001-06-11
12 PRIOR APPLICATION NUMBER: 09/487,471
13 PRIOR FILING DATE: 1999-08-31
14 NUMBER OF SEQ ID NOS: 74
15 SOFTWARE: Patent In Ver. 2.0
16 SEQ ID NO 21
17 LENGTH: 9
18 TYPE: PRT
19 ORGANISM: Artificial. Sequence
20 FEATURE:
21 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
22 US-09-878-603-21

```

Query Match: 36.4%, Score 41, DB 11, Length 9;
Best Local Similarity: 100.0%; Pred. No. 5, 1e-05;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 SAVK 5
LE 1 SAVK 8

RESULT 23

US-09-876-904A-586

```

1 Sequence 586: Application US/09876904A
2 Patent No. US20040072794A1
3 GENERAL INFORMATION:
4 APPLICANT: BOLLIGAS, TENI
5 TITLE OF INVENTION: ENCAPSULATION OF PLASMA AND CELL GENES IN AN IMPROVED...
6 TITLE OF INVENTION: AGENTS WITH NO CLEARLY DEFINED...
7 TITLE OF INVENTION: COMBUSTIBLES AND TARGETED...
8 FILE REFERENCE: JP 2002-00
9 CURRENT APPLICATION NUMBER: US/09/876,904A
10 CURRENT FILING DATE: 2001-06-09
11 PRIOR APPLICATION NUMBER: US 60/210,963
12 PRIOR FILING DATE: 2000-06-09
13 NUMBER OF SEQ ID NOS: 629
14 SOFTWARE: Patent In Ver. 2.1
15 SEQ ID NO 586
16 LENGTH: 9
17 TYPE: PRT
18 ORGANISM: Unknown Organism
19 FEATURE:
20 OTHER INFORMATION: Description of Unknown Organism: Testis H (194 day)
21 US-09-876-904A-586

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Query Match: 36.4%, Score 41, DB 11, Length 9;
Best Local Similarity: 100.0%; Pred. No. 5, 1e-05;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 KKKK 11
LE 6 KKKK 9

RESULT 24

US-09-995-529-136

```

1 Sequence 136: Application US/09995529
2 Patent No. US20040099659A1
3 GENERAL INFORMATION:
4 APPLICANT: Watkins, Jeffery L.
5 APPLICANT: Buse, William L.
6 APPLICANT: Tang, Yung
7 TITLE OF INVENTION: Humanized Celladen Antibodies and
8 TITLE OF INVENTION: Related Methods
9 FILE REFERENCE: P IX 4576
10 CURRENT APPLICATION NUMBER: US/09/995,529
11 CURRENT FILING DATE: 2001-11-26
12 NUMBER OF SEQ ID NOS: 456
13 SOFTWARE: FastSeq for Windows Version 4.0
14 SEQ ID NO 136
15 LENGTH: 9
16 TYPE: PRT
17 ORGANISM: Artificial. Sequence
18 FEATURE:
19 OTHER INFORMATION: Synthetic antibody mutation
20 US-09-995-529-136

```

Query Match: 36.4%, Score 41, DB 11, Length 9;
Best Local Similarity: 100.0%; Pred. No. 5, 1e-05;
Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 GSAY 5
LE 3 GSAY 6

RESULT 25

US-09-715-527-265

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1 Sequence 265: Application US/09765527
2 Patent No. US20020066638A
3 GENERAL INFORMATION:
4 APPLICANT: Better, Marc L.
5 TITLE OF INVENTION: Methods for Recombinant Microbial Production of
6 TITLE OF INVENTION: Fusion Proteins and BPI-Derived Peptides
7 NUMBER OF SEQUENCES: 265
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: Marsden, O'Toole, Gerstein, Murray & Horan
10 STREET: 6400 Sears Tower, 233 South Wacker Drive
11 CITY: Chicago
12 STATE: Illinois
13 COUNTRY: United States of America
14 ZIP: 60606-6432
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent In Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/09/765,527
22 FILING DATE: 18 Jan-2001
23 PRIORITY APPLICATION DATA:
24 APPLICATION NUMBER: 08/621,803
25 FILING DATE: <UNKNOWN>
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Borum, Michael E.
28 REGISTRATION NUMBER: 25,447
29 REFERENCE/DOCKET NUMBER: 27129/33199
30 TELECOMMUNICATION INFORMATION:
31 TELEPHONE: 312/474-6100
32 TELEFAX: 312/474-0448
33 TELEX: 25-4856
34 INFORMATION FOR SEQ ID NO: 205:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 10 amino acids
37 TYPE: amino acid
38 TOPOLOGY: linear
39 MOLECULE TYPE: peptide
40 FEATURE:
41 NAME/KEY: misc_feature

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1 1746 987
2 ORGANISM: Homo Sapiens
3 US-09-572-404B-508
4
5 Query Match: 36.4% Score 47 DB 11: Length 10;
6 Best Local Similarity: 100.0% Pident No: 8e+02;
7 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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1 LENGTH: 10
2 TYPE: PRT
3 ORGANISM: Homo Sapiens
4 PEA:09B
5 OTHER INFORMATION: sequence located in RefSeq at 29-37 and may interact with Sequence
6 OTHER INFORMATION: in this patent.
US-09-572-404B-2515

Query Match: 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. Re-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGSA 4
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3 AGSA 9
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RESULT 34
US-09-572-404B-2674
1 Sequence 2674; Application: US/09/572404B
2 Publication No.: US20030078474A1
3 GENERAL INFORMATION:
4 APPLICANT: Proteom Ltd
5 TITLE OF INVENTION: Complementary peptide ligands from the human genome
6 FILE REFERENCE: Human patent
7 CURRENT APPLICATION NUMBER: US/09/572,404B
8 CURRENT FILING DATE: 2000-05-17
9 NUMBER OF SEQ ID NOS: 4203
10 SOFTWARE: ProPatent version 1.0
11 SEQ ID NO 2674
12 LENGTH: 10
13 TYPE: PRT
14 ORGANISM: Homo Sapiens
15 FEATURE:
16 OTHER INFORMATION: sequence located in RefSeq at 168-177 and may interact with S
17 OTHER INFORMATION: in this patent.
US-09-572-404B-2674

Query Match: 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. Re-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGSA 4
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3 AGSA 9
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RESULT 35
US-09-572-404B-2676
1 Sequence 2676; Application: US/09/572404B
2 Publication No.: US20030078474A1
3 GENERAL INFORMATION:
4 APPLICANT: Proteom Ltd
5 TITLE OF INVENTION: Complementary peptide ligands from the human genome
6 FILE REFERENCE: Human patent
7 CURRENT APPLICATION NUMBER: US/09/572,404B
8 CURRENT FILING DATE: 2000-05-17
9 NUMBER OF SEQ ID NOS: 4203
10 SOFTWARE: ProPatent version 1.0
11 SEQ ID NO 2676
12 LENGTH: 10
13 TYPE: PRT
14 ORGANISM: Homo Sapiens
15 FEATURE:
16 OTHER INFORMATION: sequence located in RefSeq at 168-177 and may interact with Sequen
17 OTHER INFORMATION: in this patent.
US-09-572-404B-2676

Query Match: 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. Re-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGSA 4
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3 AGSA 9
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RESULT 36
US-09-572-404B-2677
1 Sequence 2677; Application: US/09/572404B
2 Publication No.: US20030078474A1
3 GENERAL INFORMATION:
4 APPLICANT: Proteom Ltd
5 TITLE OF INVENTION: Complementary peptide ligands from the human genome
6 FILE REFERENCE: Human patent
7 CURRENT APPLICATION NUMBER: US/09/572,404B
8 CURRENT FILING DATE: 2000-05-17
9 NUMBER OF SEQ ID NOS: 4203
10 SOFTWARE: ProPatent version 1.0
11 SEQ ID NO 2677
12 LENGTH: 10
13 TYPE: PRT
14 ORGANISM: Homo Sapiens
15 FEATURE:
16 OTHER INFORMATION: sequence located in RefSeq at 168-177 and may interact with S
17 OTHER INFORMATION: in this patent.
US-09-572-404B-2677

Query Match: 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. Re-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGSA 4
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3 AGSA 9
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RESULT 37
US-09-572-404B-2706
1 Sequence 2706; Application: US/09/572404B
2 Publication No.: US20030078474A1
3 GENERAL INFORMATION:
4 APPLICANT: Proteom Ltd
5 TITLE OF INVENTION: Complementary peptide ligands from the human genome
6 FILE REFERENCE: Human patent
7 CURRENT APPLICATION NUMBER: US/09/572,404B
8 CURRENT FILING DATE: 2000-05-17
9 NUMBER OF SEQ ID NOS: 4203
10 SOFTWARE: ProPatent version 1.0
11 SEQ ID NO 2706
12 LENGTH: 10
13 TYPE: PRT
14 ORGANISM: Homo Sapiens
15 FEATURE:
16 OTHER INFORMATION: sequence located in RefSeq at 365-374 and may interact with Se
17 OTHER INFORMATION: in this patent.
US-09-572-404B-2706

Query Match: 36.4%; Score 4; DB 11; Length 10;
Best Local Similarity 100.0%; Pred. No. Re-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 AGSA 4
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3 AGSA 9
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RESULT 38
US-09-572-404B-2908
1 Sequence 2908; Application: US/09/572404B
2 Publication No.: US20030078474A1
3 GENERAL INFORMATION:
4 APPLICANT: Proteom Ltd
5 TITLE OF INVENTION: Complementary peptide ligands from the human genome
6 FILE REFERENCE: Human patent
7 CURRENT APPLICATION NUMBER: US/09/572,404B

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: CURRENT FILING DATE: 2000-05-17
 : NUMBER OF SEQ ID NOS: 4203
 : SOFTWARE: ProtPatent version 1.0
 : SEQ ID NO 2908
 : LENGTH: 10
 : TYPE: PRT
 : ORGANISM: Homo Sapiens
 : FEATURES:
 : OTHER INFORMATION: Sequence located in MYK or MUK at 1354-1467 and may interact with
 : OTHER INFORMATION: Sequence 2907 in this patent
 US-09-572-404B-2908

Query Match 36.4% Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Prod. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSAV 5
 DB 3 GSAV 6

RESULT 49
 US-09-572-434P-4280
 : Sequence 4280, Application US/09/572404B
 : Publication No. US20030078374A1
 : GENERAL INFORMATION:
 : APPLICANT: Proteom Ltd
 : TITLE OF INVENTION: Complementary peptide fragments from the human genome
 : FILE REFERENCE: Human patent
 : CURRENT APPLICATION NUMBER: US/09/572-404B
 : CURRENT FILING DATE: 2000-05-17
 : NUMBER OF SEQ ID NOS: 4203
 : SOFTWARE: ProtPatent version 1.0
 : SEQ ID NO 4280
 : LENGTH: 10
 : TYPE: PRT
 : ORGANISM: Homo Sapiens
 : FEATURES:
 : OTHER INFORMATION: Sequence located in 02882 at 12801 at 16-17aa and may interact with
 : OTHER INFORMATION: Sequence 4279 in this patent
 US-09-572-404B-4280

Query Match 36.4% Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Prod. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AISA 4
 DB 5 AISA 6

RESULT 40
 US-09-572-405A-142
 : Sequence 142, Application US/09/572-05A
 : Publication No. US20030083243A1
 : GENERAL INFORMATION:
 : APPLICANT: Owen, Donald K.
 : TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
 : FILE REFERENCE: HELX027
 : CURRENT APPLICATION NUMBER: US/09/572-05A
 : CURRENT FILING DATE: 2001-03-28
 : NUMBER OF SEQ ID NOS: 165
 : SOFTWARE: PatentIn Ver. 2.1
 : SEQ ID NO 142
 : LENGTH: 10
 : TYPE: PRT
 : ORGANISM: ARTIFICIAL SEQUENCE
 : FEATURES:
 : OTHER INFORMATION: SYNTHETIC SEQUENCE
 : NAME/KEY: MOD-RES
 : LOCATION: (10)
 : OTHER INFORMATION: AMIDATION
 US-09-572-05A-142

Query Match 36.4% Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Prod. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKKK 9
 DB 6 KKKK 9

RESULT 41
 US-09-572-270A-318
 : Sequence 318, Application US/09/572270A
 : Publication No. US20030148368A1
 : GENERAL INFORMATION:
 : APPLICANT: Proteom Ltd
 : TITLE OF INVENTION: Inter complementary peptide listing
 : FILE REFERENCE:
 : CURRENT APPLICATION NUMBER: US/09/572,270A
 : CURRENT FILING DATE: 2000-05-17
 : NUMBER OF SEQ ID NOS: 1144
 : SOFTWARE: ProtPatent version 1.0
 : SEQ ID NO 318
 : LENGTH: 10
 : TYPE: PRT
 : ORGANISM: Arabidopsis thaliana
 : OTHER INFORMATION: Sequence located in TOP2, at 1249-1258 and may interact with
 US-09-572-270A-318

Query Match 36.4% Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Prod. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KKKK 11
 DB 2 KKKK 5

RESULT 42
 US-09-572-270A-320
 : Sequence 320, Application US/09/572270A
 : Publication No. US20030148368A1
 : GENERAL INFORMATION:
 : APPLICANT: Proteom Ltd
 : TITLE OF INVENTION: Inter complementary peptide listing
 : FILE REFERENCE:
 : CURRENT APPLICATION NUMBER: US/09/572,270A
 : CURRENT FILING DATE: 2000-05-17
 : NUMBER OF SEQ ID NOS: 1144
 : SOFTWARE: ProtPatent version 1.0
 : SEQ ID NO 320
 : LENGTH: 10
 : TYPE: PRT
 : ORGANISM: Arabidopsis thaliana
 : OTHER INFORMATION: Sequence located in TOP2, at 1248-1257 and may interact with
 US-09-572-270A-320

Query Match 36.4% Score 4; DB 12; Length 10;
 Best Local Similarity 100.0%; Prod. No. 8e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KKKK 11
 DB 3 KKKK 6

RESULT 43
 US-09-572-270A-629
 : Sequence 629, Application US/09/572270A
 : Publication No. US20030148368A1
 : GENERAL INFORMATION:
 : APPLICANT: Proteom Ltd
 : TITLE OF INVENTION: Inter complementary peptide listing

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1 FILE REFERENCE:
2 CURRENT APPLICATION NUMBER: US/09/572,270A
3 CURRENT FILING DATE: 2000-05-17
4 NUMBER OF SEQ ID NOS: 1144
5 SOFTWARE: ProtPatent version 1.0
6 SEQ ID NO 629
7 LENGTH: 10
8 TYPE: PRT
9 ORGANISM: Arabidopsis Thaliana
10 OTHER INFORMATION: Sequence located in Genbank at 76,85 and may interact with
US 09 572 270A-629

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSAY 5
DB 1 GSAY 4

RESULT 44
US-09-572-270A-631
1 Sequence 631, Application US/09/572,270A
2 Publication No. US20030148368A1
3 GENERAL INFORMATION:
4 APPLICANT: Proteom Ltd
5 TITLE OF INVENTION: Inter complementary peptide listing
6 FILE REFERENCE:
7 CURRENT APPLICATION NUMBER: US/09/572,270A
8 CURRENT FILING DATE: 2000-05-17
9 NUMBER OF SEQ ID NOS: 1144
10 SOFTWARE: ProtPatent version 1.0
11 SEQ ID NO 631
12 LENGTH: 10
13 TYPE: PRT
14 ORGANISM: Arabidopsis Thaliana
15 OTHER INFORMATION: Sequence located in Unknown at 76,84 and may interact with
US-09-572-270A-631

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSAY 5
DB 2 GSAY 5

RESULT 45
US-09-572-270A-840
1 Sequence 840, Application US/09/572,270A
2 Publication No. US20030148368A1
3 GENERAL INFORMATION:
4 APPLICANT: Proteom Ltd
5 TITLE OF INVENTION: Inter complementary peptide listing
6 FILE REFERENCE:
7 CURRENT APPLICATION NUMBER: US/09/572,270A
8 CURRENT FILING DATE: 2000-05-17
9 NUMBER OF SEQ ID NOS: 1144
10 SOFTWARE: ProtPatent version 1.0
11 SEQ ID NO 840
12 LENGTH: 10
13 TYPE: PRT
14 ORGANISM: Arabidopsis Thaliana
15 OTHER INFORMATION: Sequence located in RPL14 at 79,89 and may interact with
US-09-572-270A-840

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSAY 5
DB 1 GSAY 4

```

```

11
12 5 GSAY 8
13
14
15 RESULT 46
16 US-09-572-270A-842
17 1 Sequence 842, Application US/09/572,270A
18 2 Publication No. US20030148368A1
19 3 GENERAL INFORMATION:
20 4 APPLICANT: Proteom Ltd
21 5 TITLE OF INVENTION: Inter complementary peptide listing
22 6 FILE REFERENCE:
23 7 CURRENT APPLICATION NUMBER: US/09/572,270A
24 8 CURRENT FILING DATE: 2000-05-17
25 9 NUMBER OF SEQ ID NOS: 1144
26 10 SOFTWARE: ProtPatent version 1.0
27 11 SEQ ID NO 842
28 12 LENGTH: 10
29 13 TYPE: PRT
30 14 ORGANISM: Arabidopsis Thaliana
31 15 OTHER INFORMATION: Sequence located in RPL14 at 79-88 and may interact with
US 09-572-270A-842

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GSAY 5
DB 6 GSAY 9

RESULT 47
US-10-172-425B-4
1 Sequence 4, Application US/10172425B
2 Publication No. US20030147908A1
3 GENERAL INFORMATION:
4 APPLICANT: Kaempfer, Raymond
5 APPLICANT: Arad, Gila
6 TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
7 TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
8 FILE REFERENCE: A31957-PCT-USA-A 066031.0164
9 CURRENT APPLICATION NUMBER: US/10/172-425B
10 CURRENT FILING DATE: 2002-06-13
11 PRIOR APPLICATION NUMBER: 09/150,947
12 PRIOR FILING DATE: 1998-09-10
13 PRIOR APPLICATION NUMBER: 407/1197/064 18
14 PRIOR FILING DATE: 1997-12-40
15 PRIOR APPLICATION NUMBER: ISRAEL 119938
16 PRIOR FILING DATE: 1996-12-30
17 NUMBER OF SEQ ID NOS: 57
18 SOFTWARE: FastSeq for Windows Version 4.0
19 SEQ ID NO 4
20 LENGTH: 10
21 TYPE: PRT
22 ORGANISM: Staphylococcus aureus
23 OTHER INFORMATION:
US-10-172-425B-4

Query Match 36.4% Score 4; DB 12; Length 10;
Best Local Similarity 100.0%; Pred. No. 8e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KKKA 11
DB 1 KKKA 4

RESULT 48
US-09-833-203-46
1 Sequence 46, Application US/09833203
2 Publication No. US2003/166277A1
3 GENERAL INFORMATION:
4 APPLICANT: Zaidore, Maurice

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1 APPLICANT: Smith, Ernest S.
 2 TITLE OF INVENTION: Targeted Vaccine Delivery Systems
 3 FILE REFERENCE: 1821-0020001
 4 CURRENT APPLICATION NUMBER: US/09/336,233
 5 CURRENT FILING DATE: 2001-04-12
 6 PRIOR APPLICATION NUMBER: US/00/196,572
 7 PRIOR FILING DATE: 2000-04-12
 8 NUMBER OF SEQ ID NOS: 6
 9 SOFTWARE: Patent in version 4.0
 10 SEQ ID NO 46
 11 LENGTH: 10
 12 TYPE: PRT
 13 ORGANISM: Artificial Sequence
 14 NAME/KEY: misc_feature
 15 OTHER INFORMATION: 635 peptides
 16 US-09-533-203-46

Query Match: 36.4%, Score 47, DB 12, Length 10;
 Best Local Similarity: 100.0%, Pred. No. 86-02;
 Matches: 4; Conservative: 0; Mismatches: 0; Gaps: 0;

QY 4 SAVK 6
 11
 1 SAVK 4

RESULT 49
 1 Sequence 406: Application US/10/22003
 2 Patent ID No. US20030166057A1
 3 GENERAL INFORMATION:
 4 APPLICANT: PRILLMAN, KILEY RAE
 5 TITLE OF INVENTION: METHOD AND APPARATUS FOR THE DELIVERY OF ANTIGENS AND
 6 FILE REFERENCE: 6680-034
 7 CURRENT APPLICATION NUMBER: US/10/22003
 8 CURRENT FILING DATE: 2002-09-09
 9 PRIOR APPLICATION NUMBER: 69/256,413
 10 PRIOR FILING DATE: 2000-12-18
 11 PRIOR APPLICATION NUMBER: 69/256,413
 12 PRIOR FILING DATE: 2000-12-18
 13 PRIOR APPLICATION NUMBER: 69/256,413
 14 PRIOR FILING DATE: 2000-12-18
 15 NUMBER OF SEQ ID NOS: 548
 16 SOFTWARE: Patent in Ver. 2.1
 17 SEQ ID NO 466
 18 LENGTH: 10
 19 TYPE: PRT
 20 ORGANISM: Artificial Sequence
 21 NAME/KEY: N-TERMINUS
 22 LOCATION: (27-113)
 23 OTHER INFORMATION: Unknown amino acid
 24 US-10-022-060-406

Query Match: 36.4%, Score 47, DB 12, Length 10;
 Best Local Similarity: 100.0%, Pred. No. 86-02;
 Matches: 4; Conservative: 0; Mismatches: 0; Gaps: 0;

QY 1 AGSA 4
 1111
 6 AGSA 9

RESULT 50
 1 Sequence 406: Application US/10/168185

2 Publication No. US20030175802A1
 3 GENERAL INFORMATION:
 4 APPLICANT: Ambruster, Edgar Paul
 5 APPLICANT: Mussbacher, Albert
 6 APPLICANT: Schmidt Gayk, Reinhold
 7 TITLE OF INVENTION: Method for Determining Parathormone
 8 TITLE OF INVENTION: Activity in a Human Sample
 9 FILE REFERENCE: HLZ 00408
 10 CURRENT APPLICATION NUMBER: US/10/168,185
 11 CURRENT FILING DATE: 2002-06-17
 12 PRIOR APPLICATION NUMBER: PCT/EP02/12911
 13 PRIOR FILING DATE: 2000-12-18
 14 PRIOR APPLICATION NUMBER: DE 19961550
 15 PRIOR FILING DATE: 1999-12-17
 16 NUMBER OF SEQ ID NOS: 11
 17 SOFTWARE: FastSeq for Windows Version 4.0
 18 SEQ ID NO 11
 19 LENGTH: 10
 20 TYPE: PRT
 21 ORGANISM: Homo Sapiens
 22 US-10-168-185-11

Query Match: 36.4%, Score 47, DB 12, Length 10;
 Best Local Similarity: 100.0%, Pred. No. 86-02;
 Matches: 4; Conservative: 0; Mismatches: 0; Gaps: 0;

QY 4 KKKA 11
 1111
 7 KKKA 10

Search completed: September 30, 2003, 10:32:56
 Job Time: 1:25.5 secs

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10M Protein - Protein search, using SW-FLD

Run on: September 30, 2003, 10:07:14 Search File: 10m03 Sequences
(with local alignments)
A: 459 With local cell updates/sec

Title: US-09-787-443-4

Perfect score: 15

Sequence: 1 AGSAVKKKKA 11

Scoring table: GAPDP

GAPDP 60 9 - GAPDP 60 0

Searched: 1167863 seqs, 15872537 residues

Word size: 3

Total number of hits satisfying chosen parameters: 273822

Minimum hit seq length: 8

Maximum hit seq length: 15

Post processing: Listing first 500 summaries

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Prod. No. is the number of results produced by BLAST to have a score greater than or equal to the score of the best hit being printed, and is derived by analysis of the total score distribution.

SUMMARY

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1	11	100.0	11	21	AA988542
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4	5	45.5	10	15	AAE28320
5	5	45.5	10	15	AAE28320
6	5	45.5	10	20	AAE10706
7	5	45.5	10	22	AAE28320
8	5	45.5	10	22	AAE28320
9	5	45.5	10	22	AAE28320

Biologically active
Human En-1 transcr
Human peptide #887
Human gene 1 encod
Dendritic branched
Peptide forming a
Beta-sheet structu
CXK chemokine rece
Amino acid pendant
Amphiphilic peptid
Amphiphilic peptid
C-terminal substo
Amphiphilic peptid
Ion channel formi
Amphiphilic pepti
Amphiphilic pepti
Amphiphilic pepti
Peptide which neut
Cancer treating, a
Ion channel formi
Bactericidal/perme
Anti-fungal peptid
Anti-fungal peptid
Amphiphilic peptid
Peptide mimetic of
Nuclear localisati
Antifungal peptide
Peptide used to ma
Human or rat andro
HLA-B8-binding HIV
HLA-B8-binding HIV
HIV A02 super moti
HIV A02 super moti
HIV A03 super moti
HIV A03 super moti
HIV A24 super moti
HIV B62 super moti
HIV A03 motif pol
HIV A03 motif pol
HIV A11 motif pol
HIV A11 motif pol
Human peptide #204
Human C15 peptide
Human C15 peptide
Vaccine related MH
Anti-fungal peptid
Anti-fungal peptid
Anti-fungal peptid
Human leukocyte an
Recombinase domain
Biologically active
Fluorescent timer
NLS peptide SEQ ID
Sequence encoded b
Amphiphilic peptid
Amphiphilic peptid
C-terminal substo
Amphiphilic peptid
Hyaluronan recepto
Peptide inhibitor
Peptide inhibitor
Peptide inhibitor
Peptide inhibitor
Ion channel formi
Amphiphilic pepti
Amphiphilic peptid
Peptide which neut
Cancer treating, a
Antigen fragment, a
Ion channel formi
HIV peptide fragme

83	4	46.4	9	17	AAW49273	Human, leukocyte ad-	156	4	46.4	9	24	ABR08450	Human cancer-relat
84	4	46.4	9	17	AAW49274	Human, leukocyte ad-	157	4	46.4	9	24	ABR08552	Human cancer-relat
85	4	46.4	9	17	AAW07474	Anti-bacterial, anti-	158	4	46.4	9	24	ABR08684	Human cancer-relat
86	4	46.4	9	17	AAW07475	Anti-bacterial, anti-	159	4	46.4	9	24	ABR08705	Human cancer-relat
87	4	46.4	9	19	AAW07476	Amphiphilic peptid	160	4	46.4	9	24	ABR16054	Human cancer-relat
88	4	46.4	9	20	AAW46464	Chemokine peptid	161	4	46.4	9	24	ABR16471	Human cancer-relat
89	4	46.4	9	20	AAW47471	Chemokine peptid	162	4	46.4	9	24	ABR16403	Human cancer-relat
90	4	46.4	9	20	AAW47472	Peptide used to ma	163	4	46.4	9	24	ABR16569	Human cancer-relat
91	4	46.4	9	21	AAW47473	Peptide used to ma	164	4	46.4	9	24	ABR16586	Human cancer-relat
92	4	46.4	9	21	AAW47474	Peptide used to ma	165	4	46.4	9	24	ABR16629	Human cancer-relat
93	4	46.4	9	22	ABR12670	Peptide used to ma	166	4	46.4	9	24	ABR16991	Human cancer-relat
94	4	46.4	9	22	ABR12671	HIV A02 super moti	167	4	46.4	9	24	ABR17058	Human cancer-relat
95	4	46.4	9	22	ABR16847	HIV B02 super moti	168	4	46.4	9	24	ABR17215	Human cancer-relat
96	4	46.4	9	22	ABR19477	HIV B02 super moti	169	4	46.4	9	24	ABR17220	Human cancer-relat
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108	4	46.4	9	22	ABR27258	Human C05 peptid	181	4	46.4	9	24	ABR28444	Human cancer-relat
109	4	46.4	9	22	ABR27259	Human C05 peptid	182	4	46.4	9	24	ABR28447	Human cancer-relat
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113	4	46.4	9	22	ABR27263	Human C05 peptid	186	4	46.4	9	24	ABR28459	Human cancer-relat
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115	4	46.4	9	22	ABR27265	Human C05 peptid	188	4	46.4	9	24	ABR28465	Human cancer-relat
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117	4	46.4	9	22	ABR27267	Human C05 peptid	190	4	46.4	9	24	ABR28471	Human cancer-relat
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119	4	46.4	9	22	ABR27269	Human C05 peptid	192	4	46.4	9	24	ABR28477	Human cancer-relat
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121	4	46.4	9	22	ABR27271	Human C05 peptid	194	4	46.4	9	24	ABR28483	Human cancer-relat
122	4	46.4	9	22	ABR27272	Human C05 peptid	195	4	46.4	9	24	ABR28486	Human cancer-relat
123	4	46.4	9	22	ABR27273	Human C05 peptid	196	4	46.4	9	24	ABR28489	Human cancer-relat
124	4	46.4	9	22	ABR27274	Human C05 peptid	197	4	46.4	9	24	ABR28492	Human cancer-relat
125	4	46.4	9	22	ABR27275	Human C05 peptid	198	4	46.4	9	24	ABR28495	Human cancer-relat
126	4	46.4	9	22	ABR27276	Human C05 peptid	199	4	46.4	9	24	ABR28498	Human cancer-relat
127	4	46.4	9	22	ABR27277	Human C05 peptid	200	4	46.4	9	24	ABR28501	Human cancer-relat
128	4	46.4	9	22	ABR27278	Human C05 peptid	201	4	46.4	9	24	ABR28504	Human cancer-relat
129	4	46.4	9	22	ABR27279	Human C05 peptid	202	4	46.4	9	24	ABR28507	Human cancer-relat
130	4	46.4	9	22	ABR27280	Human C05 peptid	203	4	46.4	9	24	ABR28510	Human cancer-relat
131	4	46.4	9	22	ABR27281	Human C05 peptid	204	4	46.4	9	24	ABR28513	Human cancer-relat
132	4	46.4	9	22	ABR27282	Human C05 peptid	205	4	46.4	9	24	ABR28516	Human cancer-relat
133	4	46.4	9	22	ABR27283	Human C05 peptid	206	4	46.4	9	24	ABR28519	Human cancer-relat
134	4	46.4	9	22	ABR27284	Human C05 peptid	207	4	46.4	9	24	ABR28522	Human cancer-relat
135	4	46.4	9	22	ABR27285	Human C05 peptid	208	4	46.4	9	24	ABR28525	Human cancer-relat
136	4	46.4	9	22	ABR27286	Human C05 peptid	209	4	46.4	9	24	ABR28528	Human cancer-relat
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138	4	46.4	9	22	ABR27288	Human C05 peptid	211	4	46.4	9	24	ABR28534	Human cancer-relat
139	4	46.4	9	22	ABR27289	Human C05 peptid	212	4	46.4	9	24	ABR28537	Human cancer-relat
140	4	46.4	9	22	ABR27290	Human C05 peptid	213	4	46.4	9	24	ABR28540	Human cancer-relat
141	4	46.4	9	23	ABR15771	Peptide used to ma	214	4	46.4	9	24	ABR15774	Human cancer-relat
142	4	46.4	9	23	ABR15772	Peptide used to ma	215	4	46.4	9	24	ABR15777	Human cancer-relat
143	4	46.4	9	23	ABR15773	Peptide used to ma	216	4	46.4	9	24	ABR15780	Human cancer-relat
144	4	46.4	9	23	ABR15774	Peptide used to ma	217	4	46.4	9	24	ABR15783	Human cancer-relat
145	4	46.4	9	23	ABR15775	Peptide used to ma	218	4	46.4	9	24	ABR15786	Human cancer-relat
146	4	46.4	9	23	ABR15776	Peptide used to ma	219	4	46.4	9	24	ABR15789	Human cancer-relat
147	4	46.4	9	23	ABR15777	Peptide used to ma	220	4	46.4	9	24	ABR15792	Human cancer-relat
148	4	46.4	9	23	ABR15778	Peptide used to ma	221	4	46.4	9	24	ABR15795	Human cancer-relat
149	4	46.4	9	23	ABR15779	Peptide used to ma	222	4	46.4	9	24	ABR15798	Human cancer-relat
150	4	46.4	9	23	ABR15780	Peptide used to ma	223	4	46.4	9	24	ABR15801	Human cancer-relat
151	4	46.4	9	23	ABR15781	Peptide used to ma	224	4	46.4	9	24	ABR15804	Human cancer-relat
152	4	46.4	9	23	ABR15782	Peptide used to ma	225	4	46.4	9	24	ABR15807	Human cancer-relat
153	4	46.4	9	23	ABR15783	Peptide used to ma	226	4	46.4	9	24	ABR15810	Human cancer-relat
154	4	46.4	9	23	ABR15784	Peptide used to ma	227	4	46.4	9	24	ABR15813	Human cancer-relat
155	4	46.4	9	23	ABR15785	Peptide used to ma	228	4	46.4	9	24	ABR15816	Human cancer-relat

376	4	45.4	10	24	ABR27509	Human cancer-relat	448	4	36.4	11	20	AAV0733	Peptide used to ma
377	4	46.4	10	24	ABR27521	Human cancer-relat	449	4	46.4	11	21	ABR26808	Phosphoryl group a
378	4	46.4	10	24	ABR27961	Human cancer-relat	450	4	36.4	11	21	AAV5530	Transactivator of
379	4	36.4	10	24	ABR28117	Human cancer-relat	451	4	36.4	11	21	ABR8559	NCAM Igl binding p
380	4	46.4	10	24	ABR28249	Human cancer-relat	452	4	36.4	11	21	AAV7919	Cyclin containing
381	4	46.4	10	24	ABR28418	Human cancer-relat	453	4	46.4	11	22	ABR34031	Human DNA derived
382	4	46.4	10	24	ABR28508	Human cancer-relat	454	4	36.4	11	22	ABP13794	HIV A02 super moti
383	4	46.4	10	24	ABR28509	Human cancer-relat	455	4	46.4	11	22	ABP13804	HIV A02 super moti
384	4	46.4	11	5	AAV52439	Biactive synteti	456	4	36.4	11	22	ABP1805	HIV B02 super moti
385	4	46.4	11	13	AAV23494	Sequence of peptid	457	4	36.4	11	22	ABP18275	HIV B02 super moti
386	4	46.4	11	14	AAV45115	Amphiphilic peptid	458	4	46.4	11	22	ABP19373	Thymosin beta fami
387	4	46.4	11	14	AAV45131	Amphiphilic peptid	459	4	36.4	11	22	AAU0690	Anti-fungal peptid
388	4	46.4	11	14	AAV45132	Amphiphilic peptid	460	4	36.4	11	23	ABP55000	Cyclin dependent p
389	4	46.4	11	14	AAV45133	Amphiphilic peptid	461	4	36.4	11	23	AAE24225	Human HIF-1 protei
390	4	46.4	11	14	AAV45371	Amphiphilic ion ch	462	4	36.4	11	23	AAE23798	Peptide encoded by
391	4	46.4	11	14	AAV45396	Amphiphilic peptid	463	4	36.4	11	23	AAU97241	Thymosin-beta-10-1
392	4	46.4	11	14	AAV45972	Amphiphilic peptid	464	4	36.4	11	23	ABE50826	Hyaluronan (HA) b
393	4	46.4	11	14	AAV45973	Amphiphilic peptid	465	4	36.4	11	23	AAE22446	Biologically activ
394	4	46.4	11	14	AAV47156	C-terminal subst.	466	4	36.4	11	23	AAE22462	Biologically activ
395	4	46.4	11	14	AAV47157	C-terminal subst.	467	4	36.4	11	23	AAE22463	Biologically activ
396	4	46.4	11	14	AAV47163	C-terminal subst.	468	4	36.4	11	23	AAE22464	Biologically activ
397	4	46.4	11	14	AAV45384	Amphiphilic peptid	469	4	36.4	11	23	AAE22479	Biologically activ
398	4	46.4	11	14	AAV45385	Amphiphilic peptid	470	4	36.4	11	23	AAE22480	Biologically activ
399	4	46.4	11	14	AAV45387	Amphiphilic peptid	471	4	36.4	11	23	AAE22482	Biologically activ
400	4	46.4	11	14	AAV45392	Biologically activ	472	4	36.4	11	23	AAE22493	Biologically activ
401	4	46.4	11	15	AAV50970	Ion channel formi	473	4	36.4	11	23	AAE22498	Biologically activ
402	4	46.4	11	15	AAV50985	Ion channel formi	474	4	36.4	11	23	AAU75185	Amino acid sequenc
403	4	46.4	11	15	AAV50987	Ion channel formi	475	4	36.4	11	23	ABR74482	DNA repair protein
404	4	46.4	11	15	AAV50988	Peptide which neut	476	4	36.4	11	23	ABR74670	Transcription fact
405	4	46.4	11	15	AAV50989	Peptide which neut	477	4	36.4	11	23	ABR74780	Nuclear protein nu
406	4	46.4	11	15	AAV50992	Cancer treating, a	478	4	36.4	11	23	ABR74833	Nuclear protein nu
407	4	46.4	11	15	AAV50994	Cancer treating, a	479	4	36.4	11	23	ABR74833	Human opsin recept
408	4	46.4	11	15	AAV50995	Cancer treating, a	480	4	36.4	11	24	AAE54316	G protein coupled
409	4	46.4	11	15	AAV50996	Peptide used as ph	481	4	36.4	11	24	ABJ36811	G protein coupled
410	4	46.4	11	15	AAV50997	Peptide used as ph	482	4	36.4	11	24	ABJ36897	Peptide used as ph
411	4	46.4	11	15	AAV50998	Peptide which neut	483	4	36.4	11	24	ABJ36897	Cyclin dependent p
412	4	46.4	11	15	AAV50999	Peptide which neut	484	4	36.4	11	24	ABJ36897	Phosphoryl group a
413	4	46.4	11	15	AAV50999	Cancer treating, a	485	4	36.4	11	24	ABP56629	Cyclin dependent p
414	4	46.4	11	15	AAV50999	Cancer treating, a	486	4	36.4	11	24	ABP56629	Peptide stabilised
415	4	46.4	11	15	AAV50999	Cancer treating, a	487	4	36.4	12	10	AAV92222	Sequence of amphip
416	4	46.4	11	15	AAV50999	Peptide used as ph	488	4	36.4	12	13	AAE23396	Amphiphilic peptid
417	4	46.4	11	16	AAV2792	Ion channel formi	489	4	36.4	12	14	AAE5116	Amphiphilic peptid
418	4	46.4	11	16	AAV2792	Ion channel formi	490	4	36.4	12	14	AAE5116	Amphiphilic peptid
419	4	46.4	11	16	AAV2792	Ion channel formi	491	4	36.4	12	14	AAE5116	Amphiphilic ion ch
420	4	46.4	11	16	AAV2792	Ion channel formi	492	4	36.4	12	14	AAE5116	Amphiphilic peptid
421	4	46.4	11	16	AAV2792	Ion channel formi	493	4	36.4	12	14	AAE5116	C-terminal subst.
422	4	46.4	11	16	AAV2792	Ion channel formi	494	4	36.4	12	14	AAE5116	Amphiphilic peptid
423	4	46.4	11	16	AAV2792	Ion channel formi	495	4	36.4	12	14	AAE5116	Biologically activ
424	4	46.4	11	16	AAV2792	Ion channel formi	496	4	36.4	12	14	AAE5116	Ion channel formi
425	4	46.4	11	16	AAV2792	Ion channel formi	497	4	36.4	12	15	AAE5116	Amphiphilic peptid
426	4	46.4	11	16	AAV2792	Ion channel formi	498	4	36.4	12	15	AAE5116	Amphiphilic peptid
427	4	46.4	11	16	AAV2792	Ion channel formi	499	4	36.4	12	15	AAE5116	Peptide which neut
428	4	46.4	11	17	AAV2792	Ion channel formi	500	4	36.4	12	15	AAE5116	N-terminal a.a. of

ALIGNMENTS

RESULT :

ID AAY88532 standard: peptide; 11 AA.

XX AAY88532:

XX AAY88532:

XX 07-AUG-2000 (first entry)

XX NCAM Igl binding peptide #4.

XX NCAM: neural cell adhesion molecule; Igl: immunoglobulin domain 1;

XX neurite outgrowth promoter; proliferation: nerve damage; sclerosis;

XX impaired myelination; stroke; Parkinson's disease; memory; schizophrenia;

XX Alzheimer's disease; diabetes mellitus; circadian clock; nephrosis;

XX treatment: prosthetic nerve guide; treatment: nervous system.

XX Synthesis.
 XX WO200018601-A2.
 XX 06 APR 2000.
 XX 24 SEP 1999; 99WO-DK00500.
 XX 29 SEP 1998; 98DK-0001252.
 XX 29 APR 1999; 99DK-0000592.
 XX (BORN/) KENN L C B.
 XX (BECK/) BECK E.
 XX (HOLM/) HOLM A.
 XX (OLSE/) OLSEN M.
 XX (OLSE/) OLSEN M.
 XX (JENSE/) JENSEN P H.
 XX (POUL/) POULSEN F M.
 XX (SØRK/) SØRKA V.
 XX (RALE/) RALETS I.
 XX (BERE/) BEREZIN V.
 XX
 XX Poulson FM, Soroka V, Ralets I, Berezin V.
 XX WO 2000 293112/25.
 XX Compositions that bind neural cell adhesion molecules, useful for
 XX treatment disorders of the nervous system and muscles (e.g. Alzheimer's
 XX and Parkinson's diseases)
 XX
 XX Example 4: Page 25; 119pp; English.
 XX
 XX Neural cell adhesion molecule (NCAM) is a cell-cell adhesion molecule.
 XX NCAM is found in three forms, two of which are transmembrane forms, while
 XX the third is attached via a lipid anchor to the cell membrane. All three
 XX NCAM forms have an extracellular structure consisting of five immunoglobulin
 XX domains (Ig domains). The Ig domains are numbered 1 to 5 from the
 XX N terminal. The present sequence represents a peptide which binds to the
 XX NCAM Ig1 domain. The peptide can be used in a compound which binds to
 XX NCAM Ig1/Ig2 domains, and is capable of stimulation or promotion of neurite
 XX outgrowth from NCAM presenting cells, and is also capable of promoting
 XX the proliferation of NCAM presenting cells. The compound may be used in
 XX the treatment of normal, degenerated or injured NCAM presenting cells.
 XX The compound may in particular be used to treat diseases of the central,
 XX and peripheral nervous systems such as postoperative nerve damage,
 XX traumatic nerve damage, impaired myelination of nerve fibres, conditions
 XX resulting from a stroke, Parkinson's disease, Alzheimer's disease,
 XX dementia, sclerosis, nerve degeneration, associated with diabetes,
 XX cellitis, disorders affecting the contraction of skeletal muscle,
 XX transaxation and schizophrenia. Conditions affecting the muscles may also
 XX be treated with the compound, such as conditions associated with impaired
 XX function of neuromuscular connections (e.g. denervation of traumatic shock or
 XX traumatic atrophic muscle disorders), conditions of the glands, pancreas
 XX (e.g. diabetes mellitus types I and II), kidney (e.g. nephrosis), heart,
 XX liver and bowel may also be treated using the compound. The compound is
 XX used in a prosthetic nerve guide, and also to stimulate the ability to
 XX learn, and to stimulate the memory of a subject.

XX
 XX ARG59332 Standard; peptide; 11 AA.
 XX ARG59332:
 XX 21 OCT 2002 (first entry)
 XX
 XX Human neural cell adhesion molecule (NCAM) peptide 44.
 XX
 XX Human; neural cell adhesion molecule; NCAM; heart muscle cell survival;
 XX acute myocardial infarction; central nervous system disorder; stroke;
 XX peripheral nervous system disorder; postoperative nerve damage;
 XX traumatic nerve damage; spinal cord injury; nerve fibre; schizophrenia;
 XX postischaemic damage; multifactor dementia; multiple sclerosis;
 XX nerve degeneration; diabetes mellitus; neuro-muscular degeneration;
 XX Alzheimer's disease; Parkinson's disease; Huntington's disease;
 XX atrophic muscle disorder; gonad degeneration; nephrosis.
 XX
 XX Homo sapiens.
 XX
 XX WO200247719-A2.
 XX 20 JUN 2002.
 XX
 XX 12 DEC 2001; 2001WO-DK00822.
 XX 12 DEC 2000; 2000DK-0001854.
 XX (ENKA-) ENKAM PHARM AS.
 XX Beck E, Berezin V, Koller LB;
 XX WPI: 2002-583473/62.
 XX Use of a compound comprising a peptide of neural cell adhesion
 XX molecule, in the preparation of medicament for preventing death of
 XX cells presenting NCAM or NCAM ligand and treating central nervous
 XX system diseases
 XX
 XX Disclosure; Page 15; 57pp; English.
 XX
 XX The invention relates to use of a compound (I) comprising a peptide
 XX which comprises at least 5 contiguous amino acid residues of a sequence
 XX of the neural cell adhesion molecule (NCAM), its fragment, variant or its
 XX mimic, for the preparation of a medicament for preventing death of cells
 XX presenting the NCAM or an NCAM ligand. (I) is useful in the preparation
 XX of a medicament for preventing death of cells presenting the NCAM or an
 XX NCAM ligand. The medicament is for the stimulation of the survival of
 XX heart muscle cells, such as survival after acute myocardial infarction.
 XX The medicament is for the treatment of diseases or conditions of the
 XX central and peripheral nervous system, such as postoperative nerve
 XX damage, traumatic nerve damage, e.g. resulting from spinal cord injury,
 XX impaired myelination of nerve fibres, postischaemic damage, e.g.
 XX resulting from a stroke, multifactor dementia, multiple sclerosis, nerve
 XX degeneration associated with diabetes mellitus, neuro-muscular
 XX degeneration, schizophrenia, Alzheimer's disease, Parkinson's disease
 XX and Huntington's disease. The medicament is for the treatment of diseases
 XX or conditions of the muscles including conditions with impaired function
 XX of neuromuscular connections, such as genetic or traumatic atrophic
 XX muscle disorders, and for the treatment of diseases or conditions of
 XX various organs, such as degenerative conditions of the gonads, pancreas
 XX (e.g. diabetes mellitus type I and II) and kidney (e.g. nephrosis).
 XX ARG59329-ARG59352 represent human NCAM peptides of the invention.
 XX
 XX Sequence 11 AA:
 XX
 XX Query Match 100.0%; Score 11; DB 23; Length 11;
 XX Best Local Similarity 100.0%; Pred. No. 0.00011;
 XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 AGSAVKLRKKA 11
 XX 1111111111
 XX ; AGSAVKLRKKA 11

DE 11-SEP-2001 (first entry)
 DE Arabidopsis thaliana peptide library #434
 XX Plant peptide pesticides: peptide-bioinsecticides and related research
 XX Arabidopsis thaliana
 XX WJ200142279-A2
 XX 14-JUN-2001
 XX 11-SEP-2001: 2000WO-GB04751
 XX 13-DEC-1999: 99GB-0029469
 XX (PROT) PROTEAM LTD.
 XX ROBERTS GW, Heat Jk;
 XX WPI: 2001-983629/40
 XX A set of peptide ligands for antigenic and research and development of
 PT therapeutic agents comprise specific complementary peptides to proteins
 PT encoded by genes of plant genomes
 XX Example 4: Page 92; 20pp; English
 XX The present invention relates to a set of peptide ligands consisting of
 CC specific complementary peptides to proteins encoded by genes of plant
 CC genomes. The present sequence is one such peptide from Arabidopsis
 CC thaliana. The peptides of the present invention are useful in an assay to
 CC identify a peptide, especially a peptide polypeptide or heterodimer. The
 CC peptides are also useful for studies for antigenic and research and
 CC development.
 XX Sequence: 10 AA:
 XX Query Match: 45.0%; Score 5; DB 22; Length 10;
 XX Best Local Similarity: 100.0%; Pred. No. 1e-02;
 XX Matches: 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 1 ANSAV 5
 XX III
 XX 2 ANSAV 6
 XX
 XX RESULT #
 XX AA02429
 XX AA02429 standard; Peptide: 10 AA
 XX AA02429
 XX 11-SEP-2001 (first entry)
 XX Saccharomyces cerevisiae peptide, SEQ ID NO: 1074
 XX Saccharomyces cerevisiae complementary peptide: drug design
 XX Saccharomyces cerevisiae
 XX WJ200142276-A1
 XX 14-JUN-2001
 XX 13-DEC-2000: 2000WO-GB04773
 XX 13-DEC-1999: 99GB-0029471
 XX (PROT) PROTEAM LTD.
 XX ROBERTS GW, Heat Jk;
 XX WPI: 2001-983629/38
 XX Novel polypeptides comprising at least two monomers which comprise a
 PT nuclear localization sequence and protein transduction domain,
 PT respectively useful for transferring nucleic acid molecules into
 PT eukaryotic cells
 XX Disclosure: Page 4; 6pp; English
 XX The present invention relates to a polypeptide comprising at least two
 CC peptide monomers, in which each peptide monomer comprises an amino acid
 CC sequence which serves as a nuclear localisation sequence (NLS) or an
 CC amino acid sequence which serves as protein transduction domain (PTD) in
 CC eukaryotic cells. The polypeptide of the invention is used for
 CC transferring a molecule into eukaryotic cells. The use of a polypeptide

XX WPI: 2001-983629/38
 XX Identify complementary peptides by analysis of protein and
 XX nucleotide sequence databases, useful in drug design -
 XX Example 4: Page 247; 448pp; English
 XX The invention relates to the identification of complementary peptides
 CC by analysis of protein and nucleotide sequence databases from higher
 CC eukaryotic genomes, excluding human and plants. The specific
 CC complementary peptides interact with their relevant target proteins
 CC encoded in the eukaryotic genome. The peptides may be used as reagents
 CC and drugs for drug discovery and as lead ligands for drug design and
 CC development. The present sequence is a complementary peptide from
 CC Saccharomyces cerevisiae.
 XX Sequence: 10 AA:
 XX Query Match: 45.0%; Score 5; DB 22; Length 10;
 XX Best Local Similarity: 100.0%; Pred. No. 1e-02;
 XX Matches: 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX 7 LKKKA 11
 XX I L I I
 XX 5 LKKKA 9
 XX
 XX RESULT #
 XX AA02468
 XX AA02468 standard; Peptide: 10 AA
 XX AA02468
 XX 10-AUG-2001 (first entry)
 XX Nucleic acid localisation sequence #14 of hepatitis virus delta antigen
 XX Peptide monomer, nuclear localisation sequence; NLS;
 XX protein transduction domain; PTD; molecule transfer; delta antigen
 XX Hepatitis virus
 XX WJ200142277-A2
 XX 11-MAY-2001
 XX 24-NOV-2000: 2000WO-GB11690
 XX 24-NOV-1999: 99EP-GB23423
 XX (ROSE/) ROSENHECKER J
 XX (RUT/) RUTTER W
 XX (RUB/) RUBINOFF C M
 XX (PLAN/) PLANK C
 XX ROSENHECKER J, RUTTER W, RUBINOFF CM, PLANK C;
 XX WPI: 2001-983629/38
 XX Novel polypeptides comprising at least two monomers which comprise a
 PT nuclear localization sequence and protein transduction domain,
 PT respectively useful for transferring nucleic acid molecules into
 PT eukaryotic cells
 XX Disclosure: Page 4; 6pp; English
 XX The present invention relates to a polypeptide comprising at least two
 CC peptide monomers, in which each peptide monomer comprises an amino acid
 CC sequence which serves as a nuclear localisation sequence (NLS) or an
 CC amino acid sequence which serves as protein transduction domain (PTD) in
 CC eukaryotic cells. The polypeptide of the invention is used for
 CC transferring a molecule into eukaryotic cells. The use of a polypeptide

CC comprising NLS or PTD drastically increases the efficiency of the transfer of attached molecules, preferably negatively charged molecules into the nucleus or cytoplasm of a eukaryotic cell. The present sequence is NLS of the hepatitis virus delta antigen.

XX Sequence 10 AA:

SQ Query Match 45.5% Score 5; DB 23; Length 10;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKKK 10

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2 KLKKK 5

RESULT 10

AAE2248:

LD AAE2248: standard; peptide: 10 AA;

XX AAE2248:

AC AAE2248:

DT 25 JUL 2002 (first entry)

DE Biologically active peptide #13

XX

KW Biologically active peptide; toxicity; antitumoral; anti-tumor; methan sulphonic derivative; wound healing; burn therapy; sepsis; eye infection; cyst; spore; trophozoite; tumor; lung infection; cystic fibrosis; septic shock; bacterial endotoxin; cytostatic; antibacterial; immunosuppressive;

XX Unidentified.

CS

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KE Key location/qualifiers

FE Modified site 1

FI Modified site 10 /note "Linked to octanoyl group"

FI Modified site 10 /note "N-terminal amino"

XX US644845-B1

PN 19 FEB 2002

EP

XX 15 JUL 1996; 94US-0115747

XX 18 JAN 1994; 94US-0144462

XX 01 JUN 1992; 92US-0591207

XX 05 JUN 1995; 95US-0465330

XX 15 JUL 1997; 97US-0891096

XX (MAGNA) MAGNANIN PHARM INC.

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CC caused by bacteria or fungi, in killing cysts, spores, or trophozoites of infection-causing organisms, and may also be employed in the treatment of attached molecules, preferably negatively charged molecules into the nucleus or cytoplasm of a eukaryotic cell. The present sequence is NLS of the hepatitis virus delta antigen.

XX Sequence 10 AA:

SQ Query Match 45.5% Score 5; DB 23; Length 10;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKKK 10

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1 KLKKK 5

RESULT 11

ABJ01182

ID ABJ01182 standard; peptide: 13 AA;

XX ABJ01182:

AC ABJ01182:

DT 13 SEP 2002 (first entry)

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CC comprising NLS or PTD drastically increases the efficiency of the transfer of attached molecules, preferably negatively charged molecules into the nucleus or cytoplasm of a eukaryotic cell. The present sequence is NLS of the hepatitis virus delta antigen.

XX Sequence 10 AA:

SQ Query Match 45.5% Score 5; DB 23; Length 10;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKKK 10

1111

2 KLKKK 5

RESULT 10

AAE2248:

LD AAE2248: standard; peptide: 10 AA;

XX AAE2248:

AC AAE2248:

DT 25 JUL 2002 (first entry)

DE Biologically active peptide #13

XX

KW Biologically active peptide; toxicity; antitumoral; anti-tumor; methan sulphonic derivative; wound healing; burn therapy; sepsis; eye infection; cyst; spore; trophozoite; tumor; lung infection; cystic fibrosis; septic shock; bacterial endotoxin; cytostatic; antibacterial; immunosuppressive;

XX Unidentified.

CS

XX

KE Key location/qualifiers

FE Modified site 1

FI Modified site 10 /note "Linked to octanoyl group"

FI Modified site 10 /note "N-terminal amino"

XX US644845-B1

PN 19 FEB 2002

EP

XX 15 JUL 1996; 94US-0115747

XX 18 JAN 1994; 94US-0144462

XX 01 JUN 1992; 92US-0591207

XX 05 JUN 1995; 95US-0465330

XX 15 JUL 1997; 97US-0891096

XX (MAGNA) MAGNANIN PHARM INC.

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CC comprising NLS or PTD drastically increases the efficiency of the transfer of attached molecules, preferably negatively charged molecules into the nucleus or cytoplasm of a eukaryotic cell. The present sequence is NLS of the hepatitis virus delta antigen.

XX Sequence 10 AA:

SQ Query Match 45.5% Score 5; DB 23; Length 10;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKKK 10

1111

2 KLKKK 5

RESULT 10

AAE2248:

LD AAE2248: standard; peptide: 10 AA;

XX AAE2248:

AC AAE2248:

DT 25 JUL 2002 (first entry)

DE Biologically active peptide #13

XX

KW Biologically active peptide; toxicity; antitumoral; anti-tumor; methan sulphonic derivative; wound healing; burn therapy; sepsis; eye infection; cyst; spore; trophozoite; tumor; lung infection; cystic fibrosis; septic shock; bacterial endotoxin; cytostatic; antibacterial; immunosuppressive;

XX Unidentified.

CS

XX

KE Key location/qualifiers

FE Modified site 1

FI Modified site 10 /note "Linked to octanoyl group"

FI Modified site 10 /note "N-terminal amino"

XX US644845-B1

PN 19 FEB 2002

EP

XX 15 JUL 1996; 94US-0115747

XX 18 JAN 1994; 94US-0144462

XX 01 JUN 1992; 92US-0591207

XX 05 JUN 1995; 95US-0465330

XX 15 JUL 1997; 97US-0891096

XX (MAGNA) MAGNANIN PHARM INC.

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XX

CC comprising NLS or PTD drastically increases the efficiency of the transfer of attached molecules, preferably negatively charged molecules into the nucleus or cytoplasm of a eukaryotic cell. The present sequence is NLS of the hepatitis virus delta antigen.

XX Sequence 10 AA:

SQ Query Match 45.5% Score 5; DB 23; Length 10;

Best Local Similarity 100.0%; Pred. No. 1e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKKK 10

1111

2 KLKKK 5

RESULT 10

AAE2248:

LD AAE2248: standard; peptide: 10 AA;

XX AAE2248:

AC AAE2248:

DT 25 JUL 2002 (first entry)

DE Biologically active peptide #13

XX

KW Biologically active peptide; toxicity; antitumoral; anti-tumor; methan sulphonic derivative; wound healing; burn therapy; sepsis; eye infection; cyst; spore; trophozoite; tumor; lung infection; cystic fibrosis; septic shock; bacterial endotoxin; cytostatic; antibacterial; immunosuppressive;

XX Unidentified.

CS

XX

KE Key location/qualifiers

FE Modified site 1

FI Modified site 10 /note "Linked to octanoyl group"

FI Modified site 10 /note "N-terminal amino"

XX US644845-B1

PN 19 FEB 2002

REFSEQ 14	AAE01147 standard; peptide: 14 AA.	ID	AAE01147 standard; peptide: 14 AA.
AA097612		XX	AAE01137;
10	AA097612 standard; Peptide: 14 AA.	AC	AAE01137;
XX		XX	17-JUL-2001 (first entry)
AC	AA097612;	XX	Human gene 1 encoded secreted protein fragment, SEQ ID NO:91.
XX		DE	XX
XX	24-JAN-2002 (first entry)	XX	Human secreted protein; proliferative disorder; cancer; tumour;
XX	Human peptide #887 encoded by a SNT orthologous gene.	XX	tissue abnormality; developmental abnormality; haematopoietic disorder;
XX		KW	immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
XX	Immunosuppressive; immunoregulatory; anti-infective; cytostatic;	KW	inflammation; allergy; neurological disorder; Alzheimer's disease;
XX	neuroprotective; antimicrobial; gene therapy; vaccine; enzyme; cancer;	KW	Parkinson's disease; cognitive disorder; schizophrenia; asthma;
XX	amyloid protein; angiopoietin; apoptosis related protein; cadherin;	KW	skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
XX	Cyclic; polymerase; oncogene; histone; kinase; colony stimulating factor;	KW	cardiovascular disorder; angioecic disorder; kidney disorder;
XX	complement related protein; cytokine; kinase; colony stimulating factor;	KW	gastrointestinal disorder; pregnancy-related disorder; gene therapy;
XX	interleukin; G-protein coupled receptor; histone; kinase; colony stimulating factor;	KW	endocrine disorder; infection; wound healing; vulvovaginal;
XX	multifactorial; disease; autoimmune disease; infection;	KW	cell culture; chemotaxis; food additive;
XX	nervous system disease.	KW	binding partner identification.
XX		XX	
OS	Homo sapiens.	OS	Homo sapiens.
XX		XX	
XX	W02001347944 A2.	XX	W02001347944 A2.
PN		PN	
XX		XX	
XX	05-JUL-2001.	XX	17-MAY-2001.
XX		XX	
XX	28-DEC-2001; 2000W0-US45498.	XX	05-NOV-2000; 2000W0-US40657.
XX		XX	
XX	28-DEC-1999; 9905-0164741.	XX	12-NOV-1999; 9905-0164741.
XX	27-DEC-2000; 2000US-017443.	XX	30-JUN-2000; 2000US-025132.
XX		XX	
XX	(CRA) CRYGEN CORP.	XX	(CRA) HUMAN GENOME SCI INC.
XX		XX	
XX	Shinkels SA. Leach M.	XX	Rubio SM. Katzsonis GA. Ni J. Soppet DR.
XX		XX	WPI: 2001-016494/33.
XX		XX	New nucleic acid molecules encoding human secreted proteins, used in
XX	Pre-synthetic nucleic acids identified via amyloses, cyclins, polymerases,	XX	preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
XX	amyloses and histones, useful for diagnosing and treating, e.g.	XX	Parkinson's diseases and cancers
XX	cancer, autoimmune diseases and infectious.	XX	
XX		XX	
XX	Disclosures: Page 3862; 414pp; English.	XX	Disclosures: Page 7; 95pp; English.
XX		XX	
XX	The present invention relates to oligonucleotides (see AAE01147) encoding	XX	AA04898-AA04914 represent cDNAs corresponding to 6 human secreted
XX	polymorphic variants of proteins related to amyloses, amyloid	XX	protein genes, and AAE01147-AAE01148 represent the proteins they encode.
XX	proteins, angiopoietin, angiostatin, angiostatin-related proteins, angiostatin,	XX	AAE01147-AAE01148 represent human secreted protein fragments/variants.
XX	polymerase, oncogenes, histones, kinases, colony stimulating factors,	XX	The secreted proteins and their genes are useful for preventing,
XX	complement related proteins, cytokines, colony stimulating factors,	XX	treatment or ameliorating medical conditions, e.g., by protein or gene
XX	interleukins, interleukins, G-protein coupled receptors and histone kinases.	XX	therapy. Pathological conditions can be diagnosed by determining the
XX	The present sequence is a peptide encoded by one such oligonucleotide,	XX	amount of the new protein in a sample or by determining the presence of
XX	the oligonucleotides and the peptides encoded by them may be used in the	XX	mutations in the new genes. Specific uses are described for each of the
XX	prevention, diagnosis and treatment of diseases associated with,	XX	6 genes, based on the tissues in which they are most highly expressed,
XX	inappropriate expression of the proteins listed above. Disorders that may	XX	and include developing products for the diagnosis or treatment of
XX	be prevented, diagnosed and/or treated include multi-factorial diseases	XX	proliferative disorders, cancer, tumours, foetal and developmental
XX	with a genetic component, such as autoimmune diseases (e.g. rheumatoid	XX	abnormalities, haematopoietic disorders, diseases of the immune system,
XX	arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus	XX	allergies, neurological disorders (e.g., Alzheimer's disease,
XX	and Grave's disease), inflammatory cancer (e.g. cancers of the bladder,	XX	Parkinson's disease), cognitive disorders, schizophrenia, asthma,
XX	brain, breast, colon and kidney, leukaemia), diseases of the nervous	XX	skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
XX	system, and an infection of pathogenic organisms	XX	cardiovascular disorders, angioecic disorders, kidney disorders,
XX		XX	gastrointestinal disorders, pregnancy-related disorders, endocrine
XX	Sequence 14 AA:	XX	disorders, and infections. The proteins can also be used to aid wound
XX		XX	healing and epithelial cell proliferation, to prevent skin aging due to
XX	Query Match 45.5% Score 6; 16 P2; 2000W0; 14	XX	sunburn, to maintain cells before transplantation, for supporting cell
XX	Best Local Similarity 100.0% E-Val: 1e-14; 40-22	XX	culture of primary tissues, to regenerate tissues, to identify their
XX	Matches 5; Conservative 6; Mismatches 0; Indels 0; Gaps 0;	XX	cognate ligands or binding partners, and in chemotaxis, and can be used
XX		XX	as a food additive or preservative to modify storage properties.
XX	QY 6 KKKK 10	XX	Antibodies specific for a protein of the invention can be used in
XX	III	XX	diagnosing symptoms associated with the disorders mentioned above, and
XX	IC KKKK 14	XX	in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
XX		XX	immunosorbent assay (ELISA). The present disclosure represents a human
XX		XX	secreted protein fragment referred to in the disclosure of the invention.
XX		XX	

SQ Sequence 14 AA:
 Query Match 45.5%; Score 5; DB 220; length 14;
 Best Local Similarity 100.0%; Fred. No. 1.4e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 AKSAV 5
 I I I I
 DE 4 AKSAV 8

RESUL 14
 AAW76704
 ID AAW76704 standard; peptide: 15 AA;
 XX
 AC AAW76704;
 XX
 DE 01 JAN 1996 (first entry)
 XX
 DE dendritic branched signal peptide, (ppv);
 XX
 KW dendritic branched; membrane, signal, peptide, dendritic hormones;
 XX polylysine core; drug delivery;
 XX
 GS Synthetic;

XX Key location/qualifiers
 FT Modified site 5 /label branch site
 FT /note "omiga amino group in the signal chain of
 Lys(5) forms a peptide bond with the
 C-terminus of the peptide"
 FT Arg located between C-terminus and
 of Lys(5) and forming peptide bond of
 peptide bond with C-terminus of the
 tetrapeptide Arg-Lan-Leu-Leu

FT Modified site 6 /label branch site
 FT /note "omiga amino group in the signal chain of
 Lys(6) forms a peptide bond with the
 C-terminus of the peptide"
 FT Arg located between C-terminus and
 of Lys(6) and forming peptide bond of
 peptide bond with C-terminus of the
 tetrapeptide Arg-Lan-Leu-Leu

FT Modified site 7 /label branch site
 FT /note "omiga amino group in the signal chain of
 Lys(7) forms a peptide bond with the
 C-terminus of the peptide"
 FT Arg located between C-terminus and
 of Lys(7) and forming peptide bond of
 peptide bond with C-terminus of the
 tetrapeptide Arg-Lan-Leu-Leu

XX JPC7670487 A;
 XX
 DE 10 MAY 1996;
 XX
 FE 05 NOV 1994; 94JP-0276912;
 XX
 FE 05 NOV 1994; 94JP-0276912;
 XX
 FE (FUSI) FUSI 1;
 XX
 DE 1005-212954/28;
 XX
 DE Membrane localizing signal peptide, used for cellular penetration
 of drugs into cells, particularly for cancer chemotherapy;
 XX
 PS LUSCOSTRE, Fig 1: 4pp; Japanese
 XX
 DE AAW76704 is a polylysine core peptide of 15 amino acids (in Arabic: lan
 Leu-poly-Lys-Ala-Ala-Leu) and an Arg-Lan-Leu-Leu as a
 signal peptide which when conjugated to a drug molecule, their
 passage through the cell membrane and of the drug into cells
 XX
 XX Sequence 15 AA;

Query Match 45.5%; Score 5; DB 16; length 15;
 Best Local Similarity 100.0%; Fred. No. 1.4e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 7 AKKA 1;
 I I I I
 DE 4 AKKA 8

RESUL 15
 AAW71415
 ID AAW71415 standard; peptide: 15 AA;
 XX
 AC AAW71415;
 XX
 DE 07 DEC 1998 (first entry)
 XX
 DE peptide forming a helix structure;
 XX
 KW Helix structure; alpha-helical coiled coil; enzyme inhibitor;
 KW receptor agonist; antagonist;
 XX
 GS Synthetic;
 XX
 PN JPI0245497 A;
 XX
 PG 14 SEP 1998;
 XX
 PF 05 MAR 1997; 97JP-0047544;
 XX
 PR 03 MAR 1997; 97JP-0047544;
 XX
 PA (SE:R-) SEIBUTSU HONSHI KOSAKU KENKYUSHO KK;
 XX
 DE 1998-051189/47;
 XX
 DE peptide having alpha helical coiled structure - useful as enzyme
 inhibitor etc;

XX Claim 4; Page 2; 1999; Japanese;
 XX
 CC AAW71415-20 represent peptides that form helix structures. They are part
 of a peptide of the formula A-H-C, where parts A (see AAW71415-15) and
 C form helix structures, and H is a linker portion linking A and C with
 covalent bonds. The whole peptide A-H-C (see AAW71421-5) for specific
 examples) has an alpha helical coiled coil structure. The peptide
 A-H-C can be used as an enzyme inhibitor, a receptor agonist and a
 receptor antagonist
 XX
 SQ Sequence 15 AA;

Query Match 45.5%; Score 5; DB 19; length 15;
 Best Local Similarity 100.0%; Fred. No. 1.4e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 6 KKKK 10
 I I I I
 DE 4 KKKK 8

RESUL 15
 AAW8054
 ID AAW8054 standard; peptide: 15 AA;
 XX
 AC AAW8054;
 XX
 DE 06 DEC 1998 (first entry)
 XX
 DE beta-sheet structure forming peptide fragment;
 XX
 XX beta-sheet structure forming peptide fragment;
 XX
 XX beta-sheet structure forming peptide fragment;
 XX
 XX Sequence 15 AA;

XX Claim 10; Page 7; 8pp; English.
 XX Attached to the last AA (Aa-6) is a water-soluble or copolymer of
 XX dimethylacrylamide and N-ethyl-1,6-diaminohexane crosslinked with
 XX bisacrylylamine. This peptide is part of a polymer
 XX addition product (1) which comprises a non-phar peptide backbone of
 XX monomers at least 5,000 (preferably 500,000) to which this
 XX peptide pendant is chemically bonded. (1) are used as highly
 XX efficient adsorbents for bile pigment and bile acid (e.g. cholic
 XX acid), and are particularly useful for the treatment of
 XX hyperbilirubemia by adsorption or elution from blood plasma or
 XX gastro-intestinal tract. (1) can also be used to reduce
 XX hypercholesterolemia. See also AAR6134; 6; AAR6148-99.
 XX (Updated on 25-MAR-2003 to correct PA field.)
 XX (Updated on 25-MAR-2003 to correct P1 field.)
 XX Sequence: B AA;
 SQ

Query Match: 66.4%; Score 4; Dk 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY B KKK A 11
 Eb 111
 1 KKK A 6

RESULT 19
 AAR45126
 10 AAR45126 standard; peptide; B AA;
 XX
 AC AAR45126;
 XX
 DT 25-MAR-2003 (updated)
 DT 21-JUN-1993 (first entry)
 XX
 DE Amphiphilic peptide for N-terminal, lipophilic substituted, amino
 XX
 KW Ion channel; mutagenic; Polar; XPR; Drug; Peptide; Standard; XPR;
 KW amphiphilic; hydrophobic; hydrophobic; hydrophobic; hydrophobic; growth;
 KW inhibition; target; cell; virus; virally infected cell;
 KW antimicrobial; antiviral; antitumor; anti-infective;
 KW spermicide; wound healing; burn; infection;
 XX
 CS Synthetic;
 XX
 FN W 942413g A1;
 XX
 DT 09-08-1993;
 XX
 PF 27 MAY 1993; 93WO-US051942;
 XX
 PR 01 JUN 1992; 92US-0891201;
 XX
 PA (MAGA) MAGAININ PHARM INC;
 XX
 PI Kari U;
 XX
 WP1 1993-405419/50;
 XX
 XX Peptide(s) or proteins with an N-terminal, lipophilic subst.;
 P1 used for inhibiting growth of target cells; virus of
 P1 virally-infected cell
 XX
 PS Disclosure; Page 97-103; 113pp; English;
 XX
 XX A novel compn. for inhibiting growth of a target cell, virus of
 XX virally infected cell comprises a peptide of human T N(W) X (1).
 XX X is a biologically active amphiphilic ion channel-forming peptide
 XX or protein; pref. a magainin peptide; a beta peptide; a XPR
 XX peptide; a cfp peptide; a decapeptide or a sarcophagin
 XX N is the nitrogen of the N-terminal amino group.

XX T is a lipophilic moiety; pref. R CO, where R is a 2-16C
 XX hydrocarbon (alkyl or aromatic or alkylaromatic).
 XX T is pref. an octanoyl group.
 XX W is T or hydroxyl.
 XX Amphiphilic peptides as examples of X are given in AAR45115-134.
 XX The N-terminal substituted peptides and proteins have increased
 XX biological activity as compared with unsubst. peptides or proteins
 XX or peptides subst. at the N terminal with an acetyl gp.
 XX They can be used as antimicrobial agents, antiviral agents,
 XX antitumor agents, antiparasitic agents or spermicides and
 XX can also exhibit other bioactive functions. They can also be
 XX used in promoting or stimulating wound healing, for the treatment
 XX of external burns and to treat and/or prevent skin and burn
 XX infections or eye infections.
 XX (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence: B AA;
 SQ

Query Match: 66.4%; Score 4; Dk 14; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e-05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KKK A 9
 Eb 111
 4 KKK A 7

RESULT 20
 AAR33569
 10 AAR33569 standard; peptide; B AA;
 XX
 AC AAR33569;
 XX
 DT 25-MAR-2003 (updated)
 DT 21-JUN-1993 (first entry)
 XX
 DE Amphiphilic peptide (b).
 XX
 KW Hydrophobic; hydrophilic; neutral; (b); ionophore; channel-forming;
 KW human; virus; antimicrobial; antiviral; antibacterial; antitumor;
 KW spermicide; preservative; sterilant; disinfectant;
 KW wound healing; burn; infection; eye; cysts; spores; trophozoites;
 KW plants; contamination;
 XX
 CS Synthetic;
 XX
 FN Localized/Qualifiers
 P1 Modified site: /note: "May be acetylated"
 P1 Modified site: /note: "May be amidated"
 XX
 PN W09125802-A1
 XX
 PD 01 APR 1993;
 XX
 PF 04-SEP 1992; 92WO-US07622;
 XX
 PR 13-SEP-1991; 91US-0760054;
 PR 20-APR-1992; 92US-0870960;
 XX
 XX (MAGA) MAGAININ PHARM INC;
 XX
 PI Kari UP; Malay WL; Williams JJ;
 XX
 WP1 1993-117245/14;
 XX
 XX New biologically active amphiphilic peptide cpds. having ion
 XX channel-forming properties used for inhibiting growth of target
 XX cells; virus or viral-infected cells
 XX
 PS Claim 27; Page 41; 45pp; English.
 XX

CC useful against bacteria associated with dental implant infections and
 CC the peptides can stimulate the healing of wounds in the oral cavity.
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 8 AA:
 Query Match 36.4% Score 4; DB 15; Length 8;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9

1 1 1

DB 4 KLKK 7

RESULT 24

AAR50559
 ID AAR50559 standard; peptide: 8 AA.

XX AC AAR50559;

XX 25-MAR-2003 (updated);

DT 19-OCT-1994 (first entry)

XX 100 channel forming peptide

XX 100 channel forming peptide; 4 month skin disease malignancy;

XX melanoma; carcinoma; basal cell squamous cell carcinoma; PGLa;

XX CPP peptides; sarcosins; sarcotoxin; melittin; apidaecins; defensins;

XX major basic protein; bacteria permeability increasing protein;

XX porfirin.

XX Synthesis.

XX W09405313-A1.

XX 01-JUN-1994.

XX 23-DEC-1994; 94WO-US11885.

XX 03-SEP-1994; 92US-0984957.

XX (MAGNIN) MAGNIN PHARM INC.

XX Jacob M. Jacob M.

XX WPI: 1994-199465/24.

XX Treating skin cancer with ion channel forming peptide(s) or e.g.

XX magainin, melittin etc., specifically for treating melanoma

XX Disclosure; Page 119; 146pp; English.

XX The peptide is used to treat dermatological malignancies. It

XX may be used to treat especially melanoma but also basal cell and

XX squamous cell carcinomas. It can be used together with an ion which

XX also inhibits/prevents growth of the target cells. Peptides used for

XX such therapy include magainin, PGLa or CPP peptides; sarcosins,

XX sarcotoxins, melittin, apidaecins, defensins, major basic protein of

XX eosinophils; bacteria-permeability increasing protein and porfirin.

XX See also AAR505976-Q55997.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 8 AA:

Query Match 36.4% Score 4; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9

1 1 1

DB 4 KLKK 7

RESULT 25

AAR50444
 ID AAR50444 standard; peptide: 8 AA.

XX AC AAR50444;

XX 25-MAR-2003 (updated);

DT 17-OCT-1994 (first entry)

XX 100 channel forming peptide

XX 100 channel forming peptide; 4 month skin disease malignancy;

XX melanoma; carcinoma; basal cell squamous cell carcinoma; PGLa;

XX CPP peptides; sarcosins; sarcotoxin; melittin; apidaecins; defensins;

XX major basic protein; bacteria permeability increasing protein;

XX porfirin.

XX Synthesis.

XX W09405313-A1.

XX 01-JUN-1994.

XX 23-DEC-1994; 94WO-US11885.

XX 03-SEP-1994; 92US-0984957.

XX (MAGNIN) MAGNIN PHARM INC.

XX Jacob M. Jacob M.

XX WPI: 1994-199465/24.

XX Treating skin cancer with ion channel forming peptide(s) or e.g.

XX magainin, melittin etc., specifically for treating melanoma

XX Disclosure; Page 119; 146pp; English.

XX The peptide is used to treat dermatological malignancies. It

XX may be used to treat especially melanoma but also basal cell and

XX squamous cell carcinomas. It can be used together with an ion which

XX also inhibits/prevents growth of the target cells. Peptides used for

XX such therapy include magainin, PGLa or CPP peptides; sarcosins,

XX sarcotoxins, melittin, apidaecins, defensins, major basic protein of

XX eosinophils; bacteria-permeability increasing protein and porfirin.

XX See also AAR505976-Q55997.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 8 AA:

Query Match 36.4% Score 4; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9

1 1 1

DB 4 KLKK 7

RESULT 24

AAR50559
 ID AAR50559 standard; peptide: 8 AA.

XX AC AAR50559;

XX 25-MAR-2003 (updated);

DT 19-OCT-1994 (first entry)

XX 100 channel forming peptide

XX 100 channel forming peptide; 4 month skin disease malignancy;

XX melanoma; carcinoma; basal cell squamous cell carcinoma; PGLa;

XX CPP peptides; sarcosins; sarcotoxin; melittin; apidaecins; defensins;

XX major basic protein; bacteria permeability increasing protein;

XX porfirin.

XX Synthesis.

XX W09405313-A1.

XX 01-JUN-1994.

XX 23-DEC-1994; 94WO-US11885.

XX 03-SEP-1994; 92US-0984957.

XX (MAGNIN) MAGNIN PHARM INC.

XX Jacob M. Jacob M.

XX WPI: 1994-199465/24.

XX Treating skin cancer with ion channel forming peptide(s) or e.g.

XX magainin, melittin etc., specifically for treating melanoma

XX Disclosure; Page 114; 130pp; English.

XX The sequences given in AAR50452-568 represent amphiphilic, ion forming

XX peptides which may be used to treat gynaecological malignancy.

XX These peptides are based on magainin, PGLa, XPF or CPP, a cecropin, a

XX sarcotoxin, melittin, an apidaecin, a defensin, major basic protein of

XX eosinophils or a bacterial permeability increasing protein. These

XX peptides are esp. used to treat ovarian, esp. stage IC, uterine or

XX cervical cancers.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 8 AA:

Query Match 36.4% Score 4; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9

1 1 1

DB 4 KLKK 7

RESULT 25

AAR50444
 ID AAR50444 standard; peptide: 8 AA.

XX AC AAR50444;

XX 25-MAR-2003 (updated);

DT 17-OCT-1994 (first entry)

XX 100 channel forming peptide

XX 100 channel forming peptide; 4 month skin disease malignancy;

XX melanoma; carcinoma; basal cell squamous cell carcinoma; PGLa;

XX CPP peptides; sarcosins; sarcotoxin; melittin; apidaecins; defensins;

XX major basic protein; bacteria permeability increasing protein;

XX porfirin.

XX Synthesis.

XX W09405313-A1.

XX 01-JUN-1994.

XX 23-DEC-1994; 94WO-US11885.

XX 03-SEP-1994; 92US-0984957.

XX (MAGNIN) MAGNIN PHARM INC.

XX Jacob M. Jacob M.

XX WPI: 1994-199465/24.

XX Treating skin cancer with ion channel forming peptide(s) or e.g.

XX magainin, melittin etc., specifically for treating melanoma

XX Disclosure; Page 114; 130pp; English.

XX The sequences given in AAR50452-568 represent amphiphilic, ion forming

XX peptides which may be used to treat gynaecological malignancy.

XX These peptides are based on magainin, PGLa, XPF or CPP, a cecropin, a

XX sarcotoxin, melittin, an apidaecin, a defensin, major basic protein of

XX eosinophils or a bacterial permeability increasing protein. These

XX peptides are esp. used to treat ovarian, esp. stage IC, uterine or

XX cervical cancers.

XX (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 8 AA:

Query Match 36.4% Score 4; DB 15; Length 8;

Best Local Similarity 100.0%; Pred. No. 9.3e+05;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KLKK 9

1 1 1

DB 4 KLKK 7

Amphiphilic peptide; aprotic organic solvent; alcohol; antitumour;
 antimicrobial; antifungal; antiparasitic; anticancer;
 antiviral; human; animal; plant; ion-channel; forming peptide.

XX Syntactic.
 XX W09419348-AL.
 XX 17 MAR 1994.
 XX 13 AUG 1994: 93WO-080744.
 XX 28 AUG 1994: 92OS-0946505.
 XX (MAGA) MAGA/NIN PHARM INC.
 XX Williams JJ.
 XX WPI: 1994-100845/12.
 XX Purifying amphiphilic protein or peptide by solvent extraction.
 XX Particulate recombinant, ion channel forming peptide(s) such as
 XX magalins, avoids use of chaotropic agents.
 XX Disclosure: Page 124; 135pp; English.
 XX The sequences given in AAR59061 are a group of peptides which
 XX were isolated by the method of the invention. A material containing
 XX amphiphilic peptides such as these, was treated with a mixture of
 XX apolar organic solvent and alcohol to form a stable miscible
 XX solution. This solution was then treated with an aqueous solution to
 XX form an aqueous phase solution containing the peptides and an
 XX organic solvent phase, and the peptides were isolated from the
 XX aqueous phase. The isolated peptides may be used as antibacterial,
 XX antifungal, antifungal, and/or antiviral agents, and/or as
 XX and/or antiviral agents for treatment of tumors, and/or as
 XX these peptides are especially channel forming peptides which enable
 XX biologically active ions to enter cells.
 XX (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence: R AA:
 XX
 XX Query Match 36.4% Score 4; DB 15; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 6 KKK 9
 XX 111
 XX 4 KKK 7
 XX
 XX RESULT 27
 XX AAR59061
 XX ID: AAR59061 standard; peptide: R AA.
 XX AC AAR59061
 XX 25-MAR-2003 (updated)
 XX 21-APR-1995 (first entry)
 XX
 XX DE Cancer treatment, amphiphilic ion channel forming peptide.
 XX KW Amphiphilic ion channel forming peptide; cancer treatment;
 XX KW protease inhibitors.
 XX CS Syntactic.
 XX PN W09419348-AL.
 XX 01 SEP 1994.
 XX 22-FEB-1994: 94WO-080412.
 XX 26-FEB-1994: 94OS-0021607.
 XX (MAGA) MAGA/NIN PHARM INC.
 XX Herlyn M, Jacob LS, Maloy WB.
 XX WPI: 1994-294258/6.
 XX
 XX Treating cancerous growths by administering biologically active
 XX peptide(s) and protease inhibitors.
 XX Claim 2; Page 105; 124pp; English.
 XX AAR59061 to AAR59065 are a group of amphiphilic ion-channel
 XX forming peptides conforming to the same generic sequence.

XX (MAGA) MAGA/NIN PHARM INC.
 XX Herlyn M, Jacob LS, Maloy WB.
 XX WPI: 1994-217804/26.
 XX New conjugates of bioactive amphiphilic peptide(s) and conjugate
 XX moiety are useful for treatment of septic shock
 XX Disclosure: Page 114; 141pp; English.
 XX Septic shock is often due to the body's reaction to foreign
 XX lipopolysaccharide (LPS). The compounds of the invention neutralise
 XX bacterial endotoxins with neutralising essential proteins in the
 XX plasma of patients, e.g. heparins. They also have longer duration of
 XX activity than unconjugated peptides. In general, peptides such as this
 XX are ion-channel forming peptides. The compounds are biologically active
 XX peptides linked to a conjugate moiety, e.g. carbohydrates, proteins,
 XX polyvinylpyrrolidone, polyalkylene glycols and polyvinyl alcohols.
 XX The conjugate moiety may be linked at the C- or N-terminal or
 XX internally of the peptide. AAR5591-531 and AAR56879-957 are examples
 XX of these peptide-conjugate moiety compounds
 XX (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence: R AA:
 XX
 XX Query Match 36.4% Score 4; DB 15; Length 8;
 XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 6 KKK 9
 XX 111
 XX 4 KKK 7
 XX
 XX RESULT 27
 XX AAR59061
 XX ID: AAR59061 standard; peptide: R AA.
 XX AC AAR59061
 XX 25-MAR-2003 (updated)
 XX 21-APR-1995 (first entry)
 XX
 XX DE Cancer treatment, amphiphilic ion channel forming peptide.
 XX KW Amphiphilic ion channel forming peptide; cancer treatment;
 XX KW protease inhibitors.
 XX CS Syntactic.
 XX PN W09419348-AL.
 XX 01 SEP 1994.
 XX 22-FEB-1994: 94WO-080412.
 XX 26-FEB-1994: 94OS-0021607.
 XX (MAGA) MAGA/NIN PHARM INC.
 XX Herlyn M, Jacob LS, Maloy WB.
 XX WPI: 1994-294258/6.
 XX
 XX Treating cancerous growths by administering biologically active
 XX peptide(s) and protease inhibitors.
 XX Claim 2; Page 105; 124pp; English.
 XX AAR59061 to AAR59065 are a group of amphiphilic ion-channel
 XX forming peptides conforming to the same generic sequence.

CC Used in combination with one of more protease inhibitors
CC or other amphiphilic ion channel forming peptides
CC or proteins, they are effective in the treatment of cancer
CC growths. In particular they are effective in the treatment of colon
CC cancer. They may be useful in inhibiting, preventing and/or destroying
CC potential "tumor" malignant cells capable of colonizing other
CC sites.
CC (Updated on 25-MAR-2003 to correct EN field.)
XX Sequence: 8 AA:
SQ
Query Match: 36.4%, Score 41, DB 10, Length 8;
Best Local Similarity: 100.0%, Pred. No. 9, 3e+05;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
QY
ID
AA090255 Standard: peptide: 8 AA.
XX
XX AA090255.
XX
XX 10 JUL 1996 (first entry)
XX
XX Ion channel forming peptide #107 with a hydrophobic N-terminal group.
XX
XX Ion channel forming peptides (epigallocatechin gallate, N-terminal interaction
XX mediator) inhibition; cell death; viral replication; membrane
XX membrane permeability; antimicrobial and bactericidal; and bacterial
XX activity; anti-viral; spectinomycin and tetracycline and paraffin
XX synthesis.
XX
XX Key: location/evaluation
XX Modification site:
XX /note: "N-terminal amino acids are modified
XX described by the peptide sequence
XX octanoyl".
XX
XX W0954509-AL.
XX
XX 20 APR 1996 95W04509-AL.
XX
XX 18 JAN 1996 95W04509-AL.
XX
XX 18 JAN 1994 94US-018444-2.
XX
XX (MAGNA-3) MAGNANIN PHARM INC.
XX
XX Karl JP, Melano M, Williams TJ.
XX
XX W0954509-AL.
XX
XX Ion channel forming amphiphilic peptides with a hydrophobic
XX N-terminal group. Useful for the treatment of bacterial
XX parasitic and antitumor agents.
XX
XX Claim 20; Page 107; 139pp; English.
XX
XX The present peptide is a specific example of a hydrophobic ion channel
XX forming peptide for ion channel forming peptides (hydrophobic)
XX. These receptors are known to have a hydrophobic pocket
XX. Antitumor activity against microorganisms including gram positive
XX and gram negative bacteria, fungi, viruses, protozoa and parasites
XX. N-terminal modification (hydrophobic) is particularly useful to produce
XX an ion channel forming peptide having a hydrophobic N-terminus
XX. Increases the biological activity of the peptides against target cells,
XX viruses and virally-infected cells. Compared to peptides substituted with
XX an acetyl group at the N-terminus, compositions comprising the peptides

CC with lipophilic modifications are claimed for inhibiting growth of a
CC target cell, virus or virally infected cell.
XX
XX Sequence: 8 AA:
SQ
Query Match: 36.4%, Score 41, DB 10, Length 8;
Best Local Similarity: 100.0%, Pred. No. 9, 3e+05;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
QY
ID
AA047993 Standard: peptide: 8 AA.
XX
XX AA047993.
XX
XX 20 APR 1996 (first entry)
XX
XX Bactericidal/permeability increasing peptide XMP-412.
XX
XX Bactericidal/permeability increasing peptide; BPI; fusion protein;
XX bacterial infection; fungal infection; endotoxin; heparin;
XX angiogenesis; angiogenic; recombinant DNA; vector.
XX
XX Home synthesis.
XX Synthetic.
XX
XX W0974509-AL.
XX
XX 20 SEP 1997.
XX
XX 18 MAR 1997 97W04509-AL.
XX
XX 22 MAR 1996 96US-062404.
XX
XX (X-MA-3) X-MA PHARM
XX
XX Section MD;
XX
XX W0974509-AL.
XX
XX Recombinant production of bactericidal/permeability increasing
XX protein by expression as a fusion protein in microbial host cells,
XX then cleaving the BPI peptide from the carrier.
XX
XX Claim for page 142; 146pp; English.
XX
XX A new recombinant DNA vector construct has been developed which encodes
XX a fusion protein and is suitable for introduction into a bacterial host.
XX The vector comprises: (a) DNA encoding at least one cationic
XX bactericidal/permeability increasing peptide (BPI), (b) DNA encoding a
XX carrier protein, and (c) DNA encoding an amino acid (aa) cleavage site
XX located between (a) and (b). The present sequence represents a
XX specifically claimed BPI peptide. The peptides have many uses including
XX the treatment of bacterial and fungal infections. BPI peptides also
XX bind to endotoxins and heparin, neutralising their effects. The
XX peptides have further been shown to inhibit angiogenesis (partly due to
XX heparin binding activity). The fusion proteins have been found to be
XX expressed in large amounts without significant proteolysis, and in some
XX cases are actually secreted from the host cells. This allows the
XX indirect production of anti-microbial BPI peptides in microbial hosts.
XX
XX Sequence: 8 AA:
SQ
Query Match: 36.4%, Score 41, DB 18, Length 8;
Best Local Similarity: 100.0%, Pred. No. 9, 3e+05;
Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
QY

```

ID      111
       1 LKKK 4

RESULT 30
AAW44342
ID      AAW44342 standard; peptide: 8 AA
XX
AC      AAW44342
XX
DT      27-APR-1998 (first entry)
XX
DE      Anti-tumoral peptide #243 based on BPI protein (residues 142-169).
XX
KW      Anti-tumoral peptide; bactericidal-permeability-increasing protein; BPI;
KW      polymorphonuclear leukocyte; fungicide, cysteine
XX
OS      Synthetic
OS      Mammalia
XX
PN      W09704008-AL
XX
PO      06-FEB-1997
XX
PF      27-APR-1998 (first entry)
XX
PP      AAW44342
XX
PR      20-APR-1995 90US-0504041
XX
PA      (XOMA ) XOMA CORP
XX
PI      Fadem MB, Lin E, Little RJ
XX
PP      W0111997-142578/12
XX
PT      Anti-tumoral peptide(S) derived from or based on domain 111 of
PT      bactericidal-permeability-increasing protein - are used in vitro or
PT      in vivo as a fungicides
XX
PS      Claim 11: 111: 20pp: English
XX
CC      This is a spectrally obtained anti fungal peptide which is based on
CC      domain 111 (amino acids 142-169) of bactericidal-permeability-increasing
CC      protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC      leukocytes. It is used in compositions with diluents, carriers or
CC      adjuvants to treat fungal infections in patients. It may also be used in
CC      vitro to kill or inhibit the replication of fungi, such as in
CC      decontaminating fluids and sterilising medical and implant devices.
XX
SQ      Sequence 8 AA:

Query Match 36.4% Score 41 DB 18: Length 8;
Best Local Similarity 100.0% Pred No. 9, 30:05;
Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY      7 LKKK 10
ID      111
       1 LKKK 4

RESULT 30
AAW44342
ID      AAW44342 standard; peptide: 8 AA
XX
AC      AAW44342
XX
DT      27-APR-1998 (first entry)
XX
DE      Arphiphalic peptide
XX
KW      casein, amino acid, antimicrobial; antitumour; wound healing;
KW      CPT; amphiphilic; XPF peptide
XX
OS      Synthetic
XX
PN      US9792541 A
XX
PO      11-APR-1998
XX
PF      17-NOV-1994 340S-043552
XX
PR      05-APR-1993 90US-053740
XX
PA      05-FEB-1993 90US-0475529
XX
PI      14-MAY-1990 90US-0524088
XX
PS      29-APR-1992 92US-0674085
XX
PP      17-NOV-1994 94US-0540082

```

```

ID      111
       1 LKKK 4

RESULT 30
AAW44342
ID      AAW44342 standard; peptide: 8 AA
XX
AC      AAW44342
XX
DT      27-APR-1998 (first entry)
XX
DE      Anti-tumoral peptide #243 based on BPI protein (residues 142-169).
XX
KW      Anti-tumoral peptide; bactericidal-permeability-increasing protein; BPI;
KW      polymorphonuclear leukocyte; fungicide
XX
OS      Synthetic
OS      Mammalia
XX
PN      W09704008-AL
XX
PO      06-FEB-1997
XX
PF      27-APR-1998 (first entry)
XX
PP      AAW44342
XX
PR      20-APR-1995 90US-0504041
XX
PA      (XOMA ) XOMA CORP
XX
PI      Fadem MB, Lin E, Little RJ
XX
PP      W0111997-142578/12
XX
PT      Anti-tumoral peptide(S) derived from or based on domain 111 of
PT      bactericidal-permeability-increasing protein - are used in vitro or
PT      in vivo as a fungicides
XX
PS      Claim 11: 111: 20pp: English
XX
CC      This is a spectrally obtained anti fungal peptide which is based on
CC      domain 111 (amino acids 142-169) of bactericidal-permeability-increasing
CC      protein (BPI), isolated from the granules of mammalian polymorphonuclear
CC      leukocytes. It is used in compositions with diluents, carriers or
CC      adjuvants to treat fungal infections in patients. It may also be used in
CC      vitro to kill or inhibit the replication of fungi, such as in
CC      decontaminating fluids and sterilising medical and implant devices.
XX
SQ      Sequence 8 AA:

Query Match 36.4% Score 41 DB 18: Length 8;
Best Local Similarity 100.0% Pred No. 9, 30:05;
Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY      7 LKKK 10
ID      111
       1 LKKK 4

RESULT 30
AAW44342
ID      AAW44342 standard; peptide: 8 AA
XX
AC      AAW44342
XX
DT      27-APR-1998 (first entry)
XX
DE      Arphiphalic peptide
XX
KW      casein, amino acid, antimicrobial; antitumour; wound healing;
KW      CPT; amphiphilic; XPF peptide
XX
OS      Synthetic
XX
PN      US9792541 A
XX
PO      11-APR-1998
XX
PF      17-NOV-1994 340S-043552
XX
PR      05-APR-1993 90US-053740
XX
PA      05-FEB-1993 90US-0475529
XX
PI      14-MAY-1990 90US-0524088
XX
PS      29-APR-1992 92US-0674085
XX
PP      17-NOV-1994 94US-0540082

```

XX (MAGALIN) MAGALIN PHARM INC.
 PA
 E: Maloy WLL
 XX
 DR WPI: 1999 456190/39.
 XX
 PT Magalins peptide analogues useful as immunomodulators of anti-tumor
 PT agents, etc.
 XX
 PS Disclosure: Column 20; 25pp; English.
 XX
 CC The invention relates to analogues of a mutation of or D1.6 term
 CC analogues, deletion analogues of related peptides. It also relates
 CC to basic polypeptides having at least 16 amino acids, including at least
 CC 8 hydrophobic amino acids and at least a hydrophilic amino acids. The
 CC peptides may be used as anticancer agents, antiviral agents,
 CC antibiotics, antitumor agents, antiparasitic agents, spermicides,
 CC preservatives or sterilants, or agents for promoting wound healing. The
 CC present sequence represents a specific example of a peptide disclosed in
 CC the specification.
 XX
 SQ Sequence: 8 AA:
 Query Match: 36.4%; Score 4; DB 19; Length 8;
 Best Local Similarity: 100.0%; Pred. No. 9.3e+05;
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 KKKK 9
 DB 1 1 1
 4 KKKK 7

RESULT 3:
 IC AAW61744 standard; peptide: 8 AA.
 AC AAW61744;
 XX
 XX 09 NOV 1998 (first entry)
 XX
 DE Peptide mimetic of cytokine receptor gamma chain D1.
 KW Peptide mimetic gamma-chain; cytokine receptor; signal transduction;
 KW autoimmune disease; graft vs. host disease; transplant rejection;
 KW graft rejection; interleukin; immunosuppressants; leukemia; cell
 CS Synthetic.
 XX
 PN WO834141-A1.
 XX
 PZ 13 AUG 1998.
 XX
 XX 06 FEB 1998; 95WO-US02335.
 XX
 XX 07 FEB 1997; 97US-0036941.
 XX
 PA (DR38) UNIV JEFFERSON THOMAS.
 XX
 PT Kornfeld R, Townsend RM;
 XX
 XX WPI: 1998 446544/38.
 XX
 XX New peptide(s) mimicking a loop in the gamma chain of cytokine
 PT receptors inhibit signal transduction through these receptors,
 PT useful as immunosuppressants for treatment or prevention of
 PT leukemia, autoimmune disease, graft rejection
 XX
 PS Claim 2; page 28; 54pp; English.
 XX
 CC The peptide mimetics AAW61734-W6175 and AAW7501-W77014 mimic a loop on
 CC the gamma-chain of cytokine receptors, and interact with a cytokine or
 CC a gamma-chain partner receptor chain of a heterodimeric cytokine

CC receptor. They inhibit signal transduction mediated by cytokine receptor
 CC binding (of cytokines that bind to receptors with a gamma-chain). They
 CC are used to inhibit or suppress cytokine-mediated immune responses.
 CC growth, proliferation, function and activity of cells. Particularly they
 CC are used for treatment or prevention of lymphoma, leukaemia, allergy
 CC (e.g. asthma), autoimmune disease (e.g. rheumatoid arthritis, lupus,
 CC multiple sclerosis or myasthenia gravis), graft vs. host disease and
 CC transplant or graft rejection. They inhibit function of interleukin
 CC (IL) 2, 4, 7, 9, 13 and 15 (the receptors for which include a
 CC common gamma chain), so function as immunosuppressants by reducing
 CC proliferation of T and B cells.
 XX
 SQ Sequence: 8 AA:
 Query Match: 36.4%; Score 4; DB 19; Length 8;
 Best Local Similarity: 100.0%; Pred. No. 9.3e+05;
 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AGSA 4
 DB 3 AGSA 6

RESULT 4:
 AAW56407
 IC AAW56407 standard; peptide: 8 AA.
 AC AAW56407;
 XX
 XX 05 AUG 1998 (first entry)
 XX
 DE Nuclear localisation signal (NLS).
 XX
 KW Signal peptide; nuclear localisation signal; NLS;
 KW immunosuppressive activity; inhibition; nuclear translocation; inhibitor;
 KW nuclear translocation; treatment; immune disorder; autoimmune disease;
 KW hypersensitivity; sepsis; prevention; septic shock; antiviral agent;
 KW tumour growth suppressor.
 XX
 OS Unidentified.
 XX
 PN WO9811907-A.
 XX
 PD 26 MAR 1998.
 XX
 PF 15 SEP 1997; 97WO-US16217.
 XX
 PR 12 SEP 1997; 97US-0928958.
 PR 20 SEP 1996; 96US-0024978.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Blake J, Cleaveland JS, Baffa OK, Nadler SG;
 XX
 XX WPI: 1998-237028/19.
 XX
 PT Nuclear translocation inhibitor polypeptides comprising signal
 PT sequence for delivery through the cytoplasmic membrane and at least
 PT 2 nuclear localisation sequences
 XX
 PS Claim 10; page 44; 69pp; English.
 XX
 CC Peptides AAW56400-13 represent nuclear localisation signals (NLSs). The
 CC sequence is used to construct the nuclear translocation inhibitor
 CC polypeptide of the invention. Nuclear translocation inhibitor
 CC polypeptides comprise a signal sequence peptide capable of delivering
 CC the polypeptide through the cytoplasmic membrane into a cell, and at
 CC least 2 NLSs. The polypeptides can be used to inhibit nuclear
 CC translocation of a cellular protein. In addition, since the nuclear
 CC translocation of certain cellular peptides is required for the host
 CC organism to mount an immune response, the polypeptide inhibitors are
 CC useful as immunosuppression agents. The polypeptides can therefore be
 CC used for the treatment of immune disorders including autoimmune

CC diseases. The polypeptides can also be used for treating physical
 CC symptoms manifested by responses to antigens which can initiate a state
 CC of hypersensitivity, for the treatment of sepsis and in the prevention
 CC of septic shock, antiviral agents, tumor growth suppressors, and for
 CC transcriptionally modulating the expression of cellular genes.

XX Sequence: # AA;

Query Match: 36.4%; Score 4; DB 20; Length 8;

Best Local Similarity: 100.0%; Pred. No. 9.3e+05;

Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKKK 9

DB 2 LKKK 5

RESULT 5

AAAY09615

ID AAAY09615 standard; Peptide: # AA

AC AAAY09615;

DE 07-MAY-1999 (first entry)

DE Antifungal peptide XMP-408.

XX Antifungal; BPI; bactericidal/permeability increasing protein;

KW Candida infection.

XX Synthetic.

XX US5858974-A.

XX 12 JAN 1999.

XX 21-MAR-1996; 96US-0621259.

XX 21-MAR-1996; 96US-0621259.

XX 20-JUL-1995; 95US-0504841.

PA (XOMA) XOMA CORP.

PI Faden MS, Lim E, Little RG;

XX WPI; 1999-119956/10.

PI Antifungal peptides comprising part of the amino acid

PI permeability-increasing protein sequence or related sequence

XX Claim 2: Columns 221-222; 134pp; English.

XX New peptides are provided which are based on Domain III (amino acids

CC 142-169) of human bactericidal/permeability-increasing protein (BPI).

CC The peptides all have a C-terminal amide. More particularly, the claims

CC relate to: (1) a peptide that has an amino acid sequence of human BPI

CC from position 148 to position 161 (KSKVGLQLQFHKK) and variants of the

CC sequence having antifungal activity; and (2) an antifungal peptide

CC having 6-14 amino acids comprising (a) a core sequence selected from

CC LQLQ, LQIF, WLQL, LIQLF and WLQIF and (b) one or more cationic amino

CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric

CC acid) at the N and/or C terminus of the core sequence. The new peptides

CC are used for killing or inhibiting replication of fungi in vitro and

CC for treating fungal infections as given in particular infections of

CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.

CC kruselii, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide

CC can be administered topically, intravenously, orally or as an aerosol,

CC optionally together with a non-peptide antifungal agent.

XX Sequence: # AA;

Query Match

Best Local Similarity: 36.4%; Score 4; DB 20; Length 8;

Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 LKKK 10

DB 1 LKKK 4

RESULT 56

AAAY09619

ID AAAY09619 standard; Peptide: # AA.

AC AAAY09619;

DE 07-MAY-1999 (first entry)

DE Antifungal peptide XMP-412.

XX Antifungal; BPI; bactericidal/permeability increasing protein;

KW Candida infection.

XX Synthetic.

XX US5858974-A.

XX 12 JAN 1999.

XX 21-MAR-1996; 96US-0621259.

XX 21-MAR-1996; 96US-0621259.

XX 20-JUL-1995; 95US-0504841.

PA (XOMA) XOMA CORP.

PI Faden MS, Lim E, Little RG;

XX WPI; 1999-119956/10.

PI Antifungal peptides comprising part of bactericidal or

PI permeability-increasing protein sequence or related sequence

XX Claim 2: Columns 223-224; 134pp; English.

XX New peptides are provided which are based on Domain III (amino acids

CC 142-169) of human bactericidal/permeability-increasing protein (BPI).

CC The peptides all have a C-terminal amide. More particularly, the claims

CC relate to: (i) a peptide that has an amino acid sequence of human BPI

CC from position 148 to position 161 (KSKVGLQLQFHKK) and variants of the

CC sequence having antifungal activity; and (2) an antifungal peptide

CC having 6-14 amino acids comprising (a) a core sequence selected from

CC LQLQ, LQIF, WLQL, LIQLF and WLQIF and (b) one or more cationic amino

CC acids selected from K, R, H, Orn (ornithine) and Dab (diaminobutyric

CC acid) at the N and/or C terminus of the core sequence. The new peptides

CC are used for killing or inhibiting replication of fungi in vitro; and

CC for treating fungal infections in vivo, in particular infections of

CC Candida, Aspergillus or Cryptococcus spp., especially C. albicans, C.

CC kruselii, C. lusitanae, C. parapsilosis or C. tropicalis. The peptide

CC can be administered topically, intravenously, orally or as an aerosol,

CC optionally together with a non-peptide antifungal agent.

XX Sequence: # AA;

Query Match

Best Local Similarity: 36.4%; Score 4; DB 20; Length 8;

Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 57

AAAY09746

ID AAAY09746 standard; Peptide: # AA.

XX OS Human immunodeficiency virus type 1.
 XX W0200124810 A1.
 XX 12 APR 2001.
 XX PF 05 OCT 2000; 2000W0-US27266.
 XX PC 05 OCT 1999; 99US-041286A.
 XX PR 05 OCT 1999; 99US-041286A.
 XX FA (EPIM) EPIMUNE IN.
 XX Settle A., Sidney J., Southwood S., Livingston HC., Chesnut R.,
 Baker EM., Ellis E., Kuhn RT., Grey HM.
 XX W01 2001 454667/47.
 XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV-1)
 peptide groups, useful for vaccinating against HIV-1.
 XX Claim 32; Page 137; 448pp; English.
 XX The present invention describes a composition (I) comprising a prepared
 human immunodeficiency virus-1 (HIV-1) or gp comprising an amino acid
 sequence selected from 51 defined amino acid sequences (ABP25447 to
 ABP25497). (I) has virucide activity and can be used in vaccines. (I)
 may be used for immunising subjects against HIV-1 infections. (I)
 group-based vaccines has several advantages over traditional vaccines,
 particularly when compared to the use of whole antigens in vaccine
 compositions. There is evidence that the immune response to whole
 antigens is directed largely toward variable regions of the antigen,
 allowing for immune escape due to mutations. The groups for inclusion in
 an group-based vaccine may be selected from conserved regions of viral or
 tumour associated antigens, which therefore reduces the likelihood of
 escape mutants. Furthermore, immunosuppressive groups that may be present
 in whole antigens can be avoided with the use of group-based vaccines.
 An additional advantage of an group-based vaccine approach is the ability
 to combine selected groups (CII and HTII), and further, to modify the
 composition of the groups, achieving, for example, enhanced
 immunoreactivity. Accordingly, the immune response can be modulated, as
 appropriate, for the target disease. Similar engineering of the response
 is not possible with traditional approaches. ABP11501 to ABP25412
 represent peptide sequences used in the exemplification of the present
 invention.

XX Sequence: 6 AA:
 Query Match: 0.4%, Score 47, 58 22; Length 8;
 Best Local Similarity: 100.0%, Ident. No. 9, 3e-05;
 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 9 VKKK W
 ID 1
 ID 9 VKKK W

RES001 45
 ABP14544
 ID ABP14544 standard; Peptide: 6 AA.
 XX AC ABP14544;
 XX 15-JUL-2002 (first entry)
 XX HIV A03 super motif pol peptide #18.
 XX HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;
 KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
 KW anti-HIV vaccine; HIV infection; immunisation; virucide.
 XX OS Human immunodeficiency virus type 1.
 XX W0200124810 A1.
 XX 12 APR 2001

XX OS Human immunodeficiency virus type 1.
 XX W0200124810 A1.
 XX 12 APR 2001.
 XX PF 05 OCT 2000; 2000W0-US27266.
 XX PC 05 OCT 1999; 99US-041286A.
 XX PR 05 OCT 1999; 99US-041286A.
 XX FA (EPIM) EPIMUNE INC.
 XX Settle A., Sidney J., Southwood S., Livingston HC., Chesnut R.,
 Baker EM., Ellis E., Kuhn RT., Grey HM.
 XX W01 2001 454667/47.
 XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 peptide groups, useful for vaccinating against HIV-1.
 XX Claim 32; Page 137; 448pp; English.
 XX The present invention describes a composition (I) comprising a prepared
 human immunodeficiency virus-1 (HIV-1) or gp comprising an amino acid
 sequence selected from 51 defined amino acid sequences (ABP25447 to
 ABP25497). (I) has virucide activity and can be used in vaccines. (I)
 may be used for immunising subjects against HIV-1 infections. (I)
 group-based vaccines has several advantages over traditional vaccines,
 particularly when compared to the use of whole antigens in vaccine
 compositions. There is evidence that the immune response to whole
 antigens is directed largely toward variable regions of the antigen,
 allowing for immune escape due to mutations. The groups for inclusion in
 an group-based vaccine may be selected from conserved regions of viral or
 tumour associated antigens, which therefore reduces the likelihood of
 escape mutants. Furthermore, immunosuppressive groups that may be present
 in whole antigens can be avoided with the use of group-based vaccines.
 An additional advantage of an group-based vaccine approach is the ability
 to combine selected groups (CII and HTII), and further, to modify the
 composition of the groups, achieving, for example, enhanced
 immunoreactivity. Accordingly, the immune response can be modulated, as
 appropriate, for the target disease. Similar engineering of the response
 is not possible with traditional approaches. ABP11501 to ABP25412
 represent peptide sequences used in the exemplification of the present
 invention.

XX Sequence: 6 AA:
 Query Match: 0.4%, Score 47, 58 22; Length 8;
 Best Local Similarity: 100.0%, Ident. No. 9, 3e-05;
 Matches: 4; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 7 LKKK LD
 ID 1
 ID 2 LKKK S

RES001 44
 ABP14546
 ID ABP14546 standard; Peptide: 8 AA.
 XX AC ABP14546;
 XX 15-JUL-2002 (first entry)
 XX HIV A03 super motif pol peptide #18.
 XX HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;
 KW vpr; vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
 KW anti-HIV vaccine; HIV infection; immunisation; virucide.
 XX OS Human immunodeficiency virus type 1.
 XX W0200124810 A1.
 XX 12 APR 2001

```

XX 05-OCT-1999; 2000WO-US27766.
XX
XX
XX 05-OCT-1999; 99US 0412863.
XX
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut K;
XX Baker DM, Collins E, Kubo RT, Grey BM;
XX WP: 2001-054887/57.
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1.
XX
XX Claim 32: Page 168; 448pp; English.
XX
XX The present invention describes a composition (1) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (AB25347 to
XX AB25357). (1) has virucide activity and can be used in vaccines. (1)
XX may be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines.
XX An additional advantage of an group-based vaccine approach is the ability
XX to combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP1501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.
XX
XX Sequence 8 AA:
XX
Query Match 36.4%, Score 4, DB 22, Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 LKKK 10
DB 4 LKKK 7
RESULT 46
ABP15845
ID ABP15845 standard; Peptide: 8 AA.
AC ABP15845;
XX
XX 15-JUL-2002 (first entry)
XX
XX HIV A24 super motif pol peptide #25
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;
XX vpr; vpr; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; virucide.
XX
XX Human immunodeficiency virus type 1.
XX
XX WO200124810-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-1999; 2000WO-US27766.
XX
XX
XX (EPIM-) EPIMUNE INC.
XX

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PR 05-OCT-1999; 99US 0412863.
XX
XX (EPIM-) EPIMUNE INC.
XX
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut K;
XX Baker DM, Collins E, Kubo RT, Grey BM;
XX WP: 2001-054887/57.
XX
XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
XX peptide groups, useful for vaccinating against HIV-1.
XX
XX Claim 32: Page 168; 448pp; English.
XX
XX The present invention describes a composition (1) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (AB25347 to
XX AB25357). (1) has virucide activity and can be used in vaccines. (1)
XX may be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumour-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines.
XX An additional advantage of an group-based vaccine approach is the ability
XX to combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP1501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.
XX
XX Sequence 8 AA:
XX
Query Match 36.4%, Score 4, DB 22, Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 VKLK 8
DB 2 VKLK 5
RESULT 47
ABP19387
ID ABP19387 standard; Peptide: 8 AA.
AC ABP19387;
XX
XX 15-JUL-2002 (first entry)
XX
XX HIV B62 super motif pol peptide #193.
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vif;
XX vpr; vpr; tat; cytotoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; virucide.
XX
XX Human immunodeficiency virus type 1.
XX
XX WO200124810-A1.
XX
XX 12-APR-2001.
XX
XX 05-OCT-1999; 2000WO-US27766.
XX
XX 05-OCT-1999; 99US 0412863.
XX
XX (EPIM-) EPIMUNE INC.
XX

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XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI: 2001 454887/47.
XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)
XX peptide groups, useful for vaccinating against HIV 1.
XX Claim 32: Page 266; 448pp; English.
XX The present invention describes a composition (i) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (ABP25347 to
XX ABP25397). (i) has virucide activity and can be used in vaccines. (i)
XX may be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumor-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines.
XX An additional advantage of an group-based vaccine approach is the ability
XX to combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP1501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.
XX Sequence 8 AA:
SQ
Query Match 46.4% Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 VKKK 10
DL 1 11
2 VKKK 5
RESULT 49
ABP19423
XX ABP19423 Standard; Peptide: R AA.
XX ABP19423.
XX 15-JUL-2002 (first entry)
XX HIV H62 super motif pol peptide #429
XX HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; virucide.
XX Human immunodeficiency virus type 1.
XX W0200124810-A1.
XX 12-APR-2001.
XX 05-OCT-2000; 2000W0-US27766.
XX 05-OCT-1999; 990S-0412863.
XX (EPIM ) EPIMUNE INC.
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI: 2001 454887/47.

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XX WP1: 2001 454887/47.
XX Vaccine compositions comprising human immunodeficiency virus 1 (HIV 1)
XX peptide groups, useful for vaccinating against HIV-1.
XX Claim 32: Page 266; 448pp; English.
XX The present invention describes a composition (i) comprising a prepared
XX human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
XX sequence selected from 51 defined amino acid sequences (ABP25347 to
XX ABP25397). (i) has virucide activity and can be used in vaccines. (i)
XX may be used for immunising subjects against HIV-1 infections. The use of
XX group-based vaccines has several advantages over traditional vaccines,
XX particularly when compared to the use of whole antigens in vaccine
XX compositions. There is evidence that the immune response to whole
XX antigens is directed largely toward variable regions of the antigen,
XX allowing for immune escape due to mutations. The groups for inclusion in
XX an group-based vaccine may be selected from conserved regions of viral or
XX tumor-associated antigens, which therefore reduces the likelihood of
XX escape mutants. Furthermore, immunosuppressive groups that may be present
XX in whole antigens can be avoided with the use of group-based vaccines.
XX An additional advantage of an group-based vaccine approach is the ability
XX to combine selected groups (CTL and HTL), and further, to modify the
XX composition of the groups, achieving, for example, enhanced
XX immunogenicity. Accordingly, the immune response can be modulated, as
XX appropriate, for the target disease. Similar engineering of the response
XX is not possible with traditional approaches. ABP1501 to ABP25412
XX represent peptide sequences used in the exemplification of the present
XX invention.
XX Sequence 8 AA:
SQ
Query Match 46.4% Score 4; DB 22; Length 8;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 VKLK 8
DL 1 11
2 VKLK 5
RESULT 49
ABP21678
XX ABP21678 Standard; Peptide: R AA.
XX ABP21678.
XX 15-JUL-2002 (first entry)
XX HIV A63 motif pol peptide #673.
XX HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr;
XX vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope;
XX antigen; vaccine; HIV infection; immunisation; virucide.
XX Human immunodeficiency virus type 1.
XX W0200124810-A1.
XX 12-APR-2001.
XX 05-OCT-2000; 2000W0-US27766.
XX 05-OCT-1999; 990S-0412863.
XX (EPIM ) EPIMUNE INC.
XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX WPI: 2001 454887/47.

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Vaccine compositions comprising at least one immunodeficiency virus 1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.

Claim 42: Page 43: 448pp: English.

The present invention describes a composition (1) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABP25447 to ABP25497). (1) has virulence activity and can be used in vaccines. (1) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumor-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (C12 and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention.

XX Sequence: b AA;

Query Match: 36.4%; Score 4; DB 22; Length 8;

Best Local Similarity: 100.0%; Pred. No. 9.3e+05;

Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VKLK R

LF III

5 VKLK R

Search: Camp, Coda, September 30, 2003, 19:24:59

Job Time: 48.1667 Secs

Vaccine compositions comprising at least one immunodeficiency virus 1 (HIV-1) peptide groups, useful for vaccinating against HIV-1.

Claim 42: Page 43: 448pp: English.

The present invention describes a composition (1) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (ABP25447 to ABP25497). (1) has virulence activity and can be used in vaccines. (1) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumor-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (C12 and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP1501 to ABP25412 represent peptide sequences used in the exemplification of the present invention.

XX Sequence: b AA;

Query Match: 36.4%; Score 4; DB 22; Length 8;

Best Local Similarity: 100.0%; Pred. No. 9.3e+05;

Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 VKLK R

LF III

5 VKLK R

Search: Camp, Coda, September 30, 2003, 19:24:59

Job Time: 48.1667 Secs

229	8	16	AAW61429	PF4-related octapeptide	302	3	27.3	8	19	AAW58658	Platelet factor 4
230	8	16	AAW61430	PF4-related octapeptide	303	3	27.3	8	19	AAW58629	Platelet factor 4
231	8	16	AAW61431	PF4-related octapeptide	304	3	27.3	8	19	AAW58631	Platelet factor 4
232	8	16	AAW61432	PF4-related octapeptide	305	3	27.3	8	19	AAW58634	Platelet factor 4
233	8	16	AAW61433	PF4-related octapeptide	306	3	27.3	8	19	AAW58687	Platelet factor 4
234	8	16	AAW61434	PF4-related octapeptide	307	3	27.3	8	19	AAW58688	Platelet factor 4
235	8	16	AAW61435	PF4-related octapeptide	308	3	27.3	8	19	AAW58689	Platelet factor 4
236	8	16	AAW61436	PF4-related octapeptide	309	3	27.3	8	19	AAW58690	Platelet factor 4
237	8	16	AAW61437	PF4-related octapeptide	310	3	27.3	8	19	AAW58691	Platelet factor 4
238	8	16	AAW61438	PF4-related octapeptide	311	3	27.3	8	19	AAW58692	Platelet factor 4
239	8	17	AAW61439	PF4-related octapeptide	312	3	27.3	8	19	AAW58628	Platelet factor 4
240	8	17	AAW61440	PF4-related octapeptide	313	3	27.3	8	19	AAW48764	Platelet factor 4
241	8	17	AAW61441	PF4-related octapeptide	314	3	27.3	8	19	AAW51167	Platelet factor 4
242	8	17	AAW61442	PF4-related octapeptide	315	3	27.3	8	19	AAW56855	Platelet factor 4
243	8	17	AAW61443	PF4-related octapeptide	316	3	27.3	8	19	AAW57006	Platelet factor 4
244	8	17	AAW61444	PF4-related octapeptide	317	3	27.3	8	19	AAW57007	Platelet factor 4
245	8	18	AAW61445	PF4-related octapeptide	318	3	27.3	8	19	AAW57008	Platelet factor 4
246	8	18	AAW61446	PF4-related octapeptide	319	3	27.3	8	19	AAW41713	Platelet factor 4
247	8	18	AAW61447	PF4-related octapeptide	320	3	27.3	8	19	AAW41720	Platelet factor 4
248	8	18	AAW61448	PF4-related octapeptide	321	3	27.3	8	19	AAW41723	Platelet factor 4
249	8	18	AAW61449	PF4-related octapeptide	322	3	27.3	8	20	AAW45643	Platelet factor 4
250	8	18	AAW61450	PF4-related octapeptide	323	3	27.3	8	20	AAW53547	Platelet factor 4
251	8	18	AAW61451	PF4-related octapeptide	324	3	27.3	8	20	AAW26951	Platelet factor 4
252	8	18	AAW61452	PF4-related octapeptide	325	3	27.3	8	20	AAW48737	Platelet factor 4
253	8	18	AAW61453	PF4-related octapeptide	326	3	27.3	8	20	AAW47210	Platelet factor 4
254	8	18	AAW61454	PF4-related octapeptide	327	3	27.3	8	20	AAW48039	Platelet factor 4
255	8	18	AAW61455	PF4-related octapeptide	328	3	27.3	8	20	AAW29875	Platelet factor 4
256	8	18	AAW61456	PF4-related octapeptide	329	3	27.3	8	20	AAW29877	Platelet factor 4
257	8	18	AAW61457	PF4-related octapeptide	330	3	27.3	8	20	AAW29880	Platelet factor 4
258	8	18	AAW61458	PF4-related octapeptide	331	3	27.3	8	20	AAW33153	Platelet factor 4
259	8	18	AAW61459	PF4-related octapeptide	332	3	27.3	8	20	AAW40234	Platelet factor 4
260	8	18	AAW61460	PF4-related octapeptide	333	3	27.3	8	20	AAW29430	Platelet factor 4
261	8	19	AAW61461	PF4-related octapeptide	334	3	27.3	8	20	AAW26890	Platelet factor 4
262	8	19	AAW61462	PF4-related octapeptide	335	3	27.3	8	20	AAW09449	Platelet factor 4
263	8	19	AAW61463	PF4-related octapeptide	336	3	27.3	8	20	AAW01733	Platelet factor 4
264	8	19	AAW61464	PF4-related octapeptide	337	3	27.3	8	20	AAW05441	Platelet factor 4
265	8	19	AAW61465	PF4-related octapeptide	338	3	27.3	8	20	AAW03681	Platelet factor 4
266	8	19	AAW61466	PF4-related octapeptide	339	3	27.3	8	20	AAW05146	Platelet factor 4
267	8	19	AAW61467	PF4-related octapeptide	340	3	27.3	8	20	AAW93238	Human cytochrome P
268	8	19	AAW61468	PF4-related octapeptide	341	3	27.3	8	20	AAW93239	Human cytochrome P
269	8	19	AAW61469	PF4-related octapeptide	342	3	27.3	8	20	AAW10348	T cell epitope/MHC
270	8	19	AAW61470	PF4-related octapeptide	343	3	27.3	8	20	AAW00691	Tumour antigen bo
271	8	19	AAW61471	PF4-related octapeptide	344	3	27.3	8	20	AAW10637	Peptide antigen SE
272	8	19	AAW61472	PF4-related octapeptide	345	3	27.3	8	20	AAW74081	Fragment of gastro
273	8	19	AAW61473	PF4-related octapeptide	346	3	27.3	8	20	AAW97067	Peptidomimetic cap
274	8	19	AAW61474	PF4-related octapeptide	347	3	27.3	8	20	AAW90216	FR4 J-kappa light
275	8	19	AAW61475	PF4-related octapeptide	348	3	27.3	8	20	AAW90213	FR4 J-kappa light
276	8	19	AAW61476	PF4-related octapeptide	349	3	27.3	8	20	AAW86176	Peptide used in a
277	8	19	AAW61477	PF4-related octapeptide	350	3	27.3	8	20	AAW86181	Peptide used in a
278	8	19	AAW61478	PF4-related octapeptide	351	3	27.3	8	20	AAW85893	Peptide derived fr
279	8	19	AAW61479	PF4-related octapeptide	352	3	27.3	8	21	AAB14296	Peptide linker #2
280	8	19	AAW61480	PF4-related octapeptide	353	3	27.3	8	21	AAB13746	Peptide fragment f
281	8	19	AAW61481	PF4-related octapeptide	354	3	27.3	8	21	AAB33649	MHC class I associ
282	8	19	AAW61482	PF4-related octapeptide	355	3	27.3	8	21	AAB23665	Cytotoxic T lympho
283	8	19	AAW61483	PF4-related octapeptide	356	3	27.3	8	21	AAB08674	Antigenic peptide
284	8	19	AAW61484	PF4-related octapeptide	357	3	27.3	8	21	AAB08148	Peptide modulating
285	8	19	AAW61485	PF4-related octapeptide	358	3	27.3	8	21	AAW71500	Human GAGE-1,2 pep
286	8	19	AAW61486	PF4-related octapeptide	359	3	27.3	8	21	AAW82959	Tumour associated
287	8	19	AAW61487	PF4-related octapeptide	360	3	27.3	8	21	AAW02602	Human leukocyte an
288	8	19	AAW61488	PF4-related octapeptide	361	3	27.3	8	21	AAW52280	GAGE-1/2 antigenic
289	8	19	AAW61489	PF4-related octapeptide	362	3	27.3	8	21	AAW84517	Amino acid sequenc
290	8	19	AAW61490	PF4-related octapeptide	363	3	27.3	8	21	AAW84276	Tumour associated
291	8	19	AAW61491	PF4-related octapeptide	364	3	27.3	8	21	AAW82230	Polyoma large T an
292	8	19	AAW61492	PF4-related octapeptide	365	3	27.3	8	21	AAW82959	GAGE-1,2 tumour as
293	8	19	AAW61493	PF4-related octapeptide	366	3	27.3	8	21	AAW78314	SSX-4 derived pept
294	8	19	AAW61494	PF4-related octapeptide	367	3	27.3	8	21	AAW78314	IDF brain natriure
295	8	19	AAW61495	PF4-related octapeptide	368	3	27.3	8	21	AAW78315	IDE brain natriure
296	8	19	AAW61496	PF4-related octapeptide	369	3	27.3	8	21	AAW58257	Protein kinase B (
297	8	19	AAW61497	PF4-related octapeptide	370	3	27.3	8	21	AAW58258	Protein kinase B (
298	8	19	AAW61498	PF4-related octapeptide	371	3	27.3	8	21	AAW56596	GAGE-1,2 gene MHC
299	8	19	AAW61499	PF4-related octapeptide	372	3	27.3	8	21	AAW57106	Linker and spacer
300	8	19	AAW61500	PF4-related octapeptide	373	3	27.3	8	21	AAW61381	Cadherin-7 cell ad
301	8	19	AAW61501	PF4-related octapeptide	374	3	27.3	8	21	AAW64492	Cadherin-7 cell ad

US Anticarpus heterophyllus.
 XX Key Location/Qualifiers
 PT Misc difference 1
 FT Note "unchanged hydrophobic amino acid
 FT - opt. absent"
 XX W0922574-A1.
 XX
 XX 23-DEC-1992.
 XX
 XX 05-JUN-1992. 92MO-PR00510.
 XX
 XX 15-JUN-1992. 91PR-0005043.
 XX
 XX AT-CAN 1992: 92PR-0001127.
 XX
 XX (INRM) INSERM INST NAT SANTE & MED MED.
 XX
 XX Carreau P., Bevaux C., Bernard J., Ravetto A., Nicolas M.,
 PT Linaud J.
 XX W01: 1993-018076/92.
 XX
 XX Jacalin and its new peptide fragments for treating HIV
 PT interacting with the CD4 receptor and specifically preventing
 PT infection of lymphocytes
 XX
 XX Claim 2: Page 14: 27pp: French.
 XX
 XX This fragment of Jacalin interacts with the CD4 receptor and is
 CC homologous with the sequence of the HIV protein gp120. The peptide
 CC and other peptides with biological activity equivalent to that of
 CC Jacalin are useful in treatment of diseases caused by HIV. They
 CC specifically inhibit infection of lymphocytes by HIV. do not affect
 CC normal lymphocyte function and (unlike Jacalin itself) do not
 CC infect target cells.
 CC (Updated on 25-MAR-2003 to correct PN 11034.)
 XX
 XX Sequence 15 AA:
 XX
 XX Query Match 45.5% Score 4: TP 14: Length 15;
 XX Best Local Similarity 100.0% Pred. No. 9.3e-05;
 XX Matches 5: Conservative 2: Mismatches 3: Indels 0: Caps 0:
 XX
 XX 2 INKK1 5
 XX 11 11
 XX 1 INKK1 15
 XX
 XX RESUME
 XX AAW4652P
 XX ID AAW4652P Standard: peptide: 8 AA
 XX
 XX AAW4652P
 XX 15-JUN-1998 (first entry)
 XX
 XX Marker: protein C-terminal fragment
 XX
 XX Marker: protein: target protein, molecular weight, density: determination.
 XX
 XX Synthesis
 XX
 XX E082694 A2.
 XX
 XX 04-MAR-1993.
 XX
 XX 29-AUG-1997: 97EP-0402023.
 XX
 XX 06-AUG-1996: 96JP-C246859.
 XX
 XX (ORLY) ORIENTAL YEAST CO. LTD.
 XX

PI Kihira Y., Matsuo Y.
 XX W01: 1998-161384/15.
 XX
 XX Determination of molecular weight and/or amount of target protein -
 PT by electrophoresis using marker consisting of proteins that have
 PT different molecular weights and are present in different amounts
 XX
 XX Disclosure: Page 5: 11pp: English.
 XX
 XX This peptide is used in a novel method for determining the molecular
 CC weight and/or amount of a target protein. The method involves
 CC subjecting the target protein to electrophoresis simultaneously
 CC with a marker consisting of proteins that have different molecular
 CC weights and are present in different amounts, staining the target
 CC protein and the marker proteins, and comparing the resulting bands by
 CC eye or with a densitometer. The molecular weight can be determined by
 CC comparing the position of the target protein band with the various
 CC positions of the marker protein bands, and the amount can be determined
 CC by comparing the density of the target protein band with the various
 CC densities of the marker protein bands.
 XX
 XX Sequence 8 AA:
 XX
 XX Query Match 36.4% Score 4: DB 19: Length 8;
 XX Best Local Similarity 100.0% Pred. No. 9.3e-05;
 XX Matches 4: Conservative 0: Mismatches 0: Indels 0: Caps 0:
 XX
 XX 6 TSPR 9
 XX 11 11
 XX 1 TSPR 4
 XX
 XX RESUME 7
 XX AAB26867
 XX ID AAB26867 Standard: peptide: 8 AA.
 XX
 XX AAB26867;
 XX
 XX 01-FEB-2002 (first entry)
 XX
 XX PR 39 derived analogues regulatory peptide 3.
 XX
 XX Angiogenesis: stimulation; PR 49: anoxia; myocardial infarction;
 XX myocardial ischaemia; proteasome.
 XX
 XX Synthesis
 XX
 XX W020005755 A1.
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 XX 05-DEC-2000
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 XX 15-MAR-2000. 2000MO-DS07050.
 XX
 XX 26-MAR-1999: 99OS-C276568.
 XX
 XX (HEH) BEIH ISRAEL HEAD-NESS MEDICAL CENT.
 XX
 XX Simons M., Gao Y.
 XX W01: 2000-028117/60.
 XX
 XX Stimulating angiogenesis in situ, useful e.g. for treating anoxia and
 PT infarction, by administering a PR-39 oligopeptide that regulates
 PT enzymatic activity of proteasomes -
 XX
 XX Claim 14: Page 41: 51pp: English.
 XX
 XX This invention relates to a method for the stimulation of angiogenesis in
 CC sites within a targeted collection of viable cells. The method comprises
 CC introducing into the cytoplasm, at least 1 member of the PR-39
 CC oligopeptide collective, which interacts with cytoplasmic proteasomes.
 CC Part of the proteolytic activity of the proteasomes is selectively

11 09 OCT 1997.
 12
 13 01 APR 1997: 9700-080098.
 14
 15 19 JAN 1995: 9505-056564.
 16 30 MAR 1995: 9505-056565.
 17
 18 (MED) MEDICAL RES COUNCIL
 19
 20 Bartford C, Cohen P, Cohen P.W. (1997) Methods
 21
 22 Wt 11: 1997 500235/46.
 23
 24 Identifying compounds for altered protein-protein interactions by
 25 screening for compounds which modulate interaction between a protein
 26 phosphatase, catalytic subunit and a regulatory substrate
 27
 28 Example 2: Page 8: 209pp: English.
 29
 30 The present sequence was used in the development of a novel method
 31 for identifying a compound which modulates the interaction between
 32 a protein phosphatase 1 catalytic subunit and a regulatory
 33 substrate. The method comprises determining if a compound enhances or
 34 disrupts the interaction between a protein and a regulatory substrate
 35 capable of binding p38. The compound identified can be used to
 36 affect cellular metabolism or function and differentiation of
 37 muscle metabolism, physiology of bone and bone formation
 38 disruptors can be used to enhance bone mass and bone strength
 39 hypotension or congestive heart failure and enhance peripheral
 40 suppression, plate interaction stimuli, p38 can be used to lower
 41 blood pressure.
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101 Vasquez NJ, Vortanova A;
 102 WP: 1997 246340/21.
 103
 104 Identifying a modulator of intracellular signal transduction - by
 105 determining the interaction of a signal generating peptide with the
 106 test substance, allows modulation of the immune system.
 107
 108 Example 4: Page 46, 74pp: English.
 109
 110 This sequence is a peptide, designated delta V3-1, that corresponds
 111 to amino acid residues 32-326 in the V3 region of protein kinase C
 112 (PKC) delta. It was tested as a signal generating peptide in
 113 a claimed method for identifying modulators of intracellular signal
 114 transduction. This method assesses the ability of candidate
 115 modulators to affect the interaction between a signal-generating
 116 protein, such as a PKC isozyme peptide (see AAM15778-79, AAM15781,
 117 AAM15784-85, AAM15782-76), and a cognate binding protein involved in
 118 modulating the signal transduction function. Identified substances
 119 are useful as immunomodulators (claimed). They act to reduce
 120 T-cell activity, reduce the rate of graft rejection, reduce the
 121 severity of an autoimmune disorder, ameliorate allergy and/or
 122 asthma, or diminish a cytokine response (claimed).
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QY      5 RRRR 11
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DB      5 RRRR 8

RESULT 19
AAV78498
1D  AAV78498 standard; peptide: 9 AA
XX
AC
XX
DE 19 MAY 2000 (first entry)
XX
DE
XX
KW Cancer: SSX family; SSX 1, SSX 2, SSX 3, SSX 4, SSX 5, NY-ESO-1;
KW HLA binding; human leukocyte antigen; cytotoxic T lymphocyte; CTL;
KW cytotoxic; melanoma; synovial sarcoma
XX
OS Homo sapiens
XX
EN W02000024-A1
XX
PD 06-JAN-2000
XX
PE 25 JUN-1999: 99W0-0514494
XX
PK 26 JUN 1998: 98US-0105849
XX
PA GLOUW 1 LEMING INST CANCER RES.
XX
PI Tureci O., Sahin U., Pfreundschuh M., Ramnussen B., Stoyanovich S.,
PI Qian Y., Gure A., Old LJ
XX
DB 2000 170993/15.
XX
PT Determining the possible presence of breast, endometrial, colorectal,
PT lung, bladder or head-neck cancer
XX
PS Example 13: Page 23; 40pp; English.
XX
CC A method has been developed for determining the possible presence of a
CC cancer, which is not melanoma or synovial sarcoma. The method comprises
CC assaying a sample taken from the subject to determine the expression of
CC an SSX gene, and determining the expression as a determination of the
CC possible presence of cancer. Expression of SSX1 gene indicates possible
CC presence of breast, endometrial, colorectal, lung, bladder or head-neck
CC cancer. These cancers are also detected by SSX2 and SSX4 gene
CC expression. SSX2 gene expression and level of indicates possible presence
CC of lymphoma, renal cell, colorectal, glioma and prostate cancer. Expression
CC of SSX4 gene also indicates possible presence of bladder or stomach
CC cancer. SSX5 gene expression indicates the same cancers as SSX1, except
CC breast cancer. Determining expression of SSX gene can be used to monitor
CC progress of melanoma or synovial sarcoma, which is not cancer. The
CC SSX-derived peptide complex stimulates proliferation of cytolytic T
CC cells. This is useful for treating cancer, especially melanoma. AAV78464
CC to AAV78468 represent specifically HLA binding peptides for use
CC in the method of the invention. AAV8432 to AAV8465 represent JEP
CC primers used in the isolation of SSX genes in the exemplification of the
CC present invention. AAV78469 to AAV78476, and AAV7886 to AAV7872
CC represent peptides derived from SSX proteins of NY-ESO-1, which are used
CC in the exemplification of the present invention
XX
SQ Sequence 9 AA:
Query Match 36.4% Score 4: DB 21: Length 9:
Best Local Similarity 100.0% Prod. No. 9.3e+05
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY      5 RRRR 11
      11
DB      5 RRRR 6

RESULT 20
AAV57964
1D  AAV57964 standard; peptide: 9 AA
XX
AC
XX
DE 28 MAR-2000 (first entry)
XX
DE
XX
KW Protein kinase A optimal peptide substrate sequence SEQ ID NO:17.
XX
KW Protein kinases; phosphorylation site; signal transduction.
XX
OS Synthetic
XX
PN US6004757 A.
XX
PJ 21 DEC 1994
XX
PF 06-JAN 1995: 95US-0459643
XX
PR 07-JAN-1994: 94US-0178570
XX
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.
XX
PI Cantley LC, Schaffhausen B.
XX
DB 2000-096 403/08.
XX
PT Peptide substrate for a kinase, useful for determining substrate
PI specificity
XX
PS Example 5: Column 28; 69pp; English.
XX
CC The present invention describes a substrate for lck comprising a 9 amino
CC acid peptide (1). Also described is a method of inhibiting kinase
CC activity of lck by contacting it with (1) in vitro. The peptide is
CC useful for determining substrate specificity of a protein kinase.
CC Information on the substrate specificity of protein kinases in signal
CC transduction would provide an insight into signal transduction
CC mechanisms and could allow for the design of therapeutic agents. The
CC present sequence represents a peptide used in the exemplification of
CC the present invention.
XX
SQ Sequence 9 AA:
Query Match 46.4% Score 4: DB 21: Length 9:
Best Local Similarity 100.0% Prod. No. 9.3e+05
Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
QY      5 RRRR 9
      11
DB      5 RRRR 5

RESULT 21
AAU06375
1D  AAU06375 standard; peptide: 9 AA
XX
AC
XX
DE 24 OCT-2001 (first entry)
XX
DE
XX
KW Human: Leukocyte Antigen-DR3b (HLA-DR3b) submotif peptide epitope #17.
XX
KW Prostate cancer-associated antigen; supermotif; human leukocyte antigen;
KW HLA; cytotoxic T lymphocyte; helper T lymphocyte; HLA superfamily; CTL;
KW immunoregulatory; immunosuppression; HTL
XX
OS Homo sapiens
XX
EN W0200145728 A2.

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XX 26 JUN 2003
 XX 26 DEC 2003: 2000W0-0825516.
 XX 21 DEC 1999: 990S-0171412
 XX 07 AUG 2000: 2000S-064364
 XX (GFM) : EPIIMUNE INC.
 XX Flixes J., Sotelo A., Sidney J., Santoro D., Chesner W., Cellus E.,
 XX Kozak E.
 XX W911: 2001-062555/55.
 XX Tumor antigen associated group based vaccine, useful for vaccination and
 XX against prostate cancer
 XX Example 5: Page 235: 254pp: English.
 XX The sequences represent prostate cancer associated antigens and derived
 XX form of supermotif epitopes. The peptide epitopes are included in
 XX prostate cancer vaccine compositions due to their ability to bind to
 XX human leukocyte antigen (HLA) molecules, which recognize the motifs.
 XX Peptides with a high binding affinity are further tested for their
 XX ability to induce a cytotoxic lymphocyte (CTL) or a helper T lymphocyte
 XX (HTL) response. Supermotif bearing peptides may also be tested for their
 XX binding affinity to multiple alleles within the HLA superfamily. The
 XX vaccine compositions can be modified, for example, to enhance
 XX immunogenicity, to avoid the inclusion of undesired epitopes, or to
 XX elicit the immune response to suit the target disease. These group based
 XX vaccines allow the focus of an immune response to multiple selected
 XX antigens from the same pathogen. Variability around the immune response
 XX of patients can therefore be alleviated by the inclusion of groups from
 XX multiple antigens in a vaccine.

XX SQ Sequence 9 AA;
 Query Match 36.4%, Score 4, DB 22; Length 9;
 Best Local Similarity 100.0%; Prod. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 6 RRR 11
 QD 11
 6 RRR 9

RESULT 2:
 AA007472
 ID AA007472 Standard: Peptide: 9 AA
 XX A*
 XX AA007472
 XX 26 SEP 2003 (first entry)
 XX Synthetic peptide L-CUR1 (SWV(PI05)/1)
 XX L-CUR1 (SWV(PI05)/1C) anti-hepatocellular carcinoma vaccine
 XX immunomodulatory antibody; secreted by HIV-1 infected
 XX human immunodeficiency virus (HIV-1) infected
 XX immune disorder; auto-immune disorder; tomato spotted wilt virus
 XX Synthetic
 XX W205149714-A2.
 XX 12 JUL 2003
 XX 29 DEC 2003: 2000W0-1700754.
 XX 30 DEC 1999: 9911-RM03903.
 XX (GFM) : ENEA ENTE NUOVE TECNOLOGIE ENERGIE

PA (GFM) : SOC CONSORTILE METAPONIUM AGROHOS SRL.
 XX Genecarte E., Frascari R., Desiderio A., Tavladoraki P;
 XX W911: 2001-062555/55.
 XX Peptides which are able to confer stability and solubility to an
 XX antibody comprising these peptides, useful for treating pathologies
 XX (e.g. tumor) associated with accumulation of a molecule inside or
 XX outside a tumor, or animal cell
 XX Claim 11: Page 65, 109pp: English.
 XX The invention relates to peptides which are able to confer stability and
 XX solubility to an antibody comprising these peptides. The peptides
 XX are especially H-FR1, H-FR2, H-FR3, H-FR4, L-FR1, L-FR2, L-FR3 or L-FR4
 XX present within a variable region of an antibody which makes the antibody
 XX soluble and stable in cytoplasm. Peptides having the sequences of HFR1 to
 XX H-FR4 are present within the variable region of the heavy chain; of an
 XX antibody covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order
 XX (H-FR1)-(H-CDR1)-(H-FR2)-(H-CDR2)-(H-FR3)-(H-CDR3)-(H-CDR4) and
 XX peptides having the sequences of L-FR1 to L-FR4 are present within
 XX the variable region of the light chain of an antibody, covalently
 XX linked to the L-CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-(L-
 XX L-FR2)-(L-CDR2)-(L-FR3)-(L-CDR3)-(L-CDR4). The antibodies and
 XX polynucleotides (e.g. by gene therapy) are useful for the manufacture
 XX of a medicament for the treatment of pathologies associated with
 XX accumulation of a molecule inside or outside a human, animal, cell
 XX or plant cell. The pathologies are infectious (e.g. viral infections such
 XX as HIV, human immunodeficiency virus, infections), tumour, metabolic and
 XX immune (especially auto-immune) pathologies. The present sequence
 XX represents the peptide L-CUR1 (SWV(PI05)/1C which, when included in an
 XX antibody molecule, gives specificity for tomato spotted wilt virus
 XX nucleoprotein

XX SQ Sequence 9 AA;
 Query Match 36.4%, Score 4, DB 22; Length 9;
 Best Local Similarity 100.0%; Prod. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QV 7 GRP 10
 QD 11
 4 GRP 7

RESULT 2:
 AA007586
 ID AA007586 Standard: Peptide: 9 AA
 XX A*
 XX AA007586
 XX 08 JAN 2003 (first entry)
 XX Anti neovascular preparation associated epitope #41.
 XX Cell mediated immunity; cellular immune response; CTL response;
 XX tumour neovascularization; anti-angiogenesis.
 XX Homo sapiens.
 XX W0220269927-A2.
 XX 12 SEP 2002
 XX 07-MAR-2002: 2002W0-US01204.
 XX 07-MAR-2001: 2001US-27454P.
 XX (GFM) : CTL IMMUNOTHERAPIES CORP.
 XX Simard J.L., Diamond SP.


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XX      1111
XX      5 KK03 9
XX
XX      RES001.29
XX      ABL0127.6
XX      ID:  AB0127.6 standard: Peptide: 9 AA
XX      AC:  ABL0127.6
XX      DE:  10 DEC 2002 (first entry)
XX      SE:  Human 125p5c8 epitope #1941
XX      KW:  Human 125p5c8 cancer; cytostatic; prostate cancer;
XX      KW:  bladder cancer; kidney cancer; ovarian cancer;
XX      CS:  Homo sapiens
XX      PN:  W0202/2785 A2
XX      PD:  19 SEP 2002
XX      PF:  13 MAR 2002: 2002W0 US07855
XX      PE:  14 MAR 2001: 2001S 060649
XX      PA:  (A)EN 1 AGENSYS INC
XX      PI:  Fatus M., Chellita and PM., Burnett RS., Altar DEH., Raitano AB., Ge W.,
XX      PI:  Mortenson PK., Mortenson K., Jakubovits A.
XX      IP:  2002/1650/77
XX      PS:  disclosed: Page 161: 273pp, 6 q. 16.
XX      SC:  The present invention relates to compositions comprising a substance that
XX      SC:  modulates the status of 125p5c8 or a molecule that is modulated by
XX      SC:  125p5c8. The status of a cell that expresses 125p5c8 is modulated by
XX      SC:  composition is useful for treating cancer, particularly prostate
XX      SC:  bladder, kidney, colon, ovary or breast cancer. The 125p5c8 protein
XX      SC:  and/or a nucleotide sequence encoding the protein is useful for
XX      SC:  identifying a mammal, diagnosing cancer, or for identifying a
XX      SC:  epitope shown in the exemplification of the invention.
XX      SE:  September 9 AA
XX
XX      Query Match: 6.34, Score 1, 100.00, 100.00, 100.00, 100.00
XX      Best Local Similarity: 100.00, 100.00, 100.00, 100.00, 100.00
XX      Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0
XX
XX      1111
XX      5 KK03 7
XX      5 KK03 8
XX
XX      RES001.29
XX      ABL0127.6
XX      ID:  AB0127.6 standard: Peptide: 9 AA
XX      AC:  ABL0127.6
XX      DE:  10 DEC 2002 (first entry)
XX      SE:  Human 125p5c8 epitope #1941
XX      KW:  Human 125p5c8 cancer; cytostatic; breast cancer; prostate cancer;
XX      KW:  bladder cancer; kidney cancer; ovary cancer; ovarian cancer;
XX      CS:  Homo sapiens
XX      PN:  W0202/2785 A2
XX      PD:  19 SEP 2002
XX      PF:  13 MAR 2002: 2002W0 US07855
XX      PE:  14 MAR 2001: 2001S 060649
XX      PA:  (A)EN 1 AGENSYS INC
XX      PI:  Fatus M., Chellita and PM., Burnett RS., Altar DEH., Raitano AB., Ge W.,
XX      PI:  Mortenson PK., Mortenson K., Jakubovits A.
XX      IP:  2002/1650/77
XX      PS:  disclosed: Page 161: 273pp, 6 q. 16.
XX      SC:  The present invention relates to compositions comprising a substance that
XX      SC:  modulates the status of 125p5c8 or a molecule that is modulated by
XX      SC:  125p5c8. The status of a cell that expresses 125p5c8 is modulated by
XX      SC:  composition is useful for treating cancer, particularly prostate
XX      SC:  bladder, kidney, colon, ovary or breast cancer. The 125p5c8 protein
XX      SC:  and/or a nucleotide sequence encoding the protein is useful for
XX      SC:  identifying a mammal, diagnosing cancer, or for identifying a
XX      SC:  epitope shown in the exemplification of the invention.
XX      SE:  September 9 AA
XX
XX      Query Match: 6.34, Score 1, 100.00, 100.00, 100.00, 100.00
XX      Best Local Similarity: 100.00, 100.00, 100.00, 100.00, 100.00
XX      Matches: 4, Conservative 0, Mismatches 0, Indels 0, Gaps 0
XX
XX      1111
XX      5 KK03 7
XX      5 KK03 8
XX
XX      RES001.29
XX      ABL0127.6
XX      ID:  AB0127.6 standard: Peptide: 9 AA
XX      AC:  ABL0127.6
XX      DE:  10 DEC 2002 (first entry)
XX      SE:  Human 125p5c8 epitope #1941
XX      KW:  Human 125p5c8 cancer; cytostatic; prostate cancer;
XX      KW:  bladder cancer; kidney cancer; ovary cancer; ovarian cancer;
XX      CS:  Homo sapiens
XX      PN:  W0202/2785 A2
XX      PD:  19 SEP 2002
XX      PF:  13 MAR 2002: 2002W0 US07855
XX      PE:  14 MAR 2001: 2001S 060649
XX      PA:  (A)EN 1 AGENSYS INC
XX      PI:  Fatus M., Chellita and PM., Burnett RS., Altar DEH., Raitano AB., Ge W.,
XX      PI:  Mortenson PK., Mortenson K., Jakubovits A.
XX      IP:  2002/1650/77
XX      PS:  disclosed: Page 161: 273pp, 6 q. 16.
XX      SC:  The present invention relates to compositions comprising a substance that
XX      SC:  modulates the status of 125p5c8 or a molecule that is modulated by
XX      SC:  125p5c8. The status of a cell that expresses 125p5c8 is modulated by
XX      SC:  composition is useful for treating cancer, particularly prostate
XX      SC:  bladder, kidney, colon, ovary or breast cancer. The 125p5c8 protein
XX      SC:  and/or a nucleotide sequence encoding the protein is useful for
XX      SC:  identifying a mammal, diagnosing cancer, or for identifying a
XX      SC:  epitope shown in the exemplification of the invention.
XX      SE:  September 9 AA

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1F 001: 2002-714510/77.
 2F New composition comprising a substance that modulates the status of a
 3F 125p528 gene or a molecule that is modulated by 125p528, useful for
 4F treating or preventing cancer that expresses or over expresses 125p528.
 5F
 6F
 7F Disclosure: Page 174: 274pp; English.
 8F
 9F The present invention relates to compositions comprising a substance that
 10F modulates the status of 125p528 or a molecule that is modulated by
 11F 125p528. The status of a cell that expresses 125p528 is modulated, the
 12F composition is useful for treating cancer, particularly prostate,
 13F bladder, kidney, colon, ovary or breast cancer. The 125p528 protein
 14F and/or a nucleotide sequence encoding the protein is useful for
 15F identifying a mammal against cancer. The present sequence is a 125p528
 16F peptide shown to the exemplification of the invention.
 17F
 18F Sequence: 9 AA:
 19F Query Match: 36.4%; Score 4; DB 23; Length 9;
 20F Best Local Similarity: 100.0%; Fred. No. 9.3e-05;
 21F Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 22F
 23F 4 KKKG 7
 24F 5 KKKG 8
 25F
 26F 29 NOV 2002 (first entry)
 27F
 28F PP2AA-binding peptide from human PAK-1.
 29F
 30F Cytotoxic T lymphocyte associated protein (CTLA4)
 31F protein phosphatase 2; PP2AA; immune response; T cell; cancer therapy;
 32F autoimmune disorder; rheumatoid arthritis; myasthenia gravis;
 33F autoimmune thyroiditis; systemic lupus erythematosus; Graves' disease;
 34F type 1 diabetes mellitus; multiple sclerosis; transplant;
 35F graft versus host disease; inflammatory disorder;
 36F bacterial infection; viral infection; HIV; parasitic infection;
 37F human immunodeficiency virus; hepatitis; malaria; PAK-1.
 38F
 39F Homo sapiens.
 40F
 41F W20020605 A2.
 42F 29 AUG 2002
 43F 15 FEB 2002: 2002W0-6S0459.
 44F 16 FEB 2001: 2001S-2697572.
 45F
 46F GENE: GENETICS INST LLC.
 47F (3400) RECENTS RES INST CORP.
 48F (3400) BRUSHAM 5 WOMENS HEALTH.
 49F
 50F COLLINS M. Madrenas J. Carrion R. Kuchel V.
 51F WPI: 2002-674892/72.
 52F
 53F Modulating an immune response. The treated subject having a
 54F condition that would benefit from down-regulation of an immune
 55F response, e.g. autoimmune disorders, comprises: (a) inhibiting the
 56F interaction between CTLA4 and PP2AA.
 57F
 58F Example 5: Fig 1; 84pp; English

00 The invention relates to modulating an immune response comprising
 01 contacting a cell expressing at least one first molecule having a
 02 CTLA4 (cytotoxic T lymphocyte associated protein 4) lysine rich
 03 motif, and at least one second molecule having a PP2AA (protein
 04 phosphatase 2A regulatory subunit A) CTLA4-interacting domain with an
 05 agent that modulates the interaction between the first molecule and the
 06 second molecule. Also included are: (1) treating a subject having a
 07 condition that would benefit from down-regulation of an immune response,
 08 comprises administering an agent that inhibits the interaction between a
 09 first molecule and a second molecule described above; (2) identifying a
 10 compound that modulates the interaction of CTLA4 and PP2AA, and
 11 (3) identifying a compound which modulates the interaction of a
 12 molecule comprising at least one CTLA4 lysine rich motif and a PP2AA
 13 molecule comprising a PP2AA CTLA4-interacting domain.
 14 The methods are useful for modulating an immune response and
 15 treating a subject having a condition that would benefit from
 16 down-regulation of an immune response, such as autoimmune disorder
 17 (e.g. rheumatoid arthritis, myasthenia gravis, autoimmune thyroiditis,
 18 systemic lupus erythematosus, type 1 diabetes mellitus, Graves' s
 19 disease, or multiple sclerosis), a transplant (e.g. a bone marrow
 20 transplant, a stem cell transplant, a heart transplant, a lung
 21 transplant, a liver transplant, a kidney transplant, a cornea
 22 transplant, or a skin transplant), graft versus host disease, an
 23 allergy, or an inflammatory disorder. Enhancing an immune
 24 response is useful in treating bacterial, viral (e.g. HIV-1 or 2,
 25 human immunodeficiency virus, hepatitis B or C) or parasitic infections.
 26 The present sequence is a PP2AA-binding peptide from human PAK-1.
 27
 28 Sequence: 9 AA:
 29 Query Match: 36.4%; Score 4; DB 23; Length 9;
 30 Best Local Similarity: 100.0%; Fred. No. 9.3e-05;
 31 Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 33 QY 4 KKKG 5
 34 5 KKKG 6
 35 3 KKKG 5
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XX WP1: 2002-06-19/08.
XX New substituted 1,2,4 triazole 3,5-diol and derivatives useful for
XX treating selective kinase of d.c. kinase mediated disorders and cancer
XX tumor growth and angiogenesis.
XX Example 2: Page 95: 147pp: English.
XX The invention relates to substituted 1,2,4 triazole 3,5 diol and
XX derivatives useful for treating selective kinase mediated kinase
XX mediated disorders. The invention is used in the treatment of
XX kinase mediated disorders such as cancer, tumor and AIDS.
XX Vascularisation, angiopathy, angiogenesis, chemotherapy induced
XX alopecia and testosterone as an adjunct to chemotherapy and radiation
XX therapy in combination with chemotherapeutic agent to treat cancer.
XX The present sequence is a lysine peptide substrate used in kinase
XX selective assays. This sequence is used in the exemplification
XX of the invention.
XX Sequence 9 AA;
XX
XX Query Match 46.4%; Score 4; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 01 6 TGR 9
XX 1 1
XX 2 TGR 4
XX
XX 14 NOV-2002 (first entry)
XX Haemophilus influenzae BASB23 protein (T-helper cell epitope 6).
XX BASB23, gene therapy; vaccines; cellis media; immunomod
XX Haemophilus influenzae infection; substrates; nosocomial infection;
XX invasive disease; T-helper cell epitope.
XX
XX Haemophilus influenzae.
XX W2002040501 A2.
XX 29 April 02.
XX 25 FEBRUARY 2002 020200 EP026550.
XX 24 FEBRUARY 2002 020100-000864.
XX (SMK) 3 SM,IRKLINE BEECHAM PHARM INC.
XX (Inventor 3)
XX WP1: 2002-07-09/72.
XX New BASB23 polypeptide and polypeptide analogs useful for the preparation
XX of a medicament used in generating an immune response in an animal, and
XX for diagnosing, preventing and/or treating bacterial diseases with it.
XX influenza infection.
XX Example 13: Page 70: 87pp: English.
XX The invention comprises the amino acid and/or lipid sequences of
XX Haemophilus influenzae BASB23 proteins. The BASB23 DNA and protein
XX sequences of the invention are useful for generating an immune response
XX in an animal. In particular, the BASB23 DNA and protein sequences are
XX useful for diagnosing, preventing and/or treating bacterial diseases with

XX H. influenzae infection (e.g. otitis media, pneumonia, sinusitis,
XX nosocomial infections and invasive diseases). The present amino acid
XX sequence represents a potential T-helper cell epitope from a
XX H. influenzae BASB23 protein.
XX Sequence 9 AA;
XX
XX Query Match 46.4%; Score 4; DB 23; Length 9;
XX Best Local Similarity 100.0%; Pred. No. 9.3e+05;
XX Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 01 5 KGR 8
XX 1 1 1 1
XX 5 KGR 8
XX
XX RESULT 32
XX ABB98430
XX ID ABB98430 standard: peptide; 9 AA.
XX AC ABB98430;
XX XX
XX 07 14-OCT-2002 (first entry)
XX Bovine protein kinase A peptide substrate.
XX
XX Protein kinase A; bovine; macroheterocyclic; protein kinase C inhibitor;
XX glycogen synthase kinase-3 inhibitor; cardiovascular disease; diabetes;
XX inflammation disease; immunological disorder; dermatological disorder;
XX cancer; central nervous system disorder; antidiabetic; antiinflammatory;
XX dermatological; cerebroprotective; cardiac; cytostatic; neuroprotective.
XX
XX Bas sp.
XX Key location/qualifiers
XX FH Modified-site 1
XX FI Modified-site 9 /note: "labelled with biotin"
XX FI Modified-site 9 /note: "C-terminal amide"
XX FN W0200241197 A1.
XX 13-JUN-2002.
XX 06-DEC-2001 200100-0847865.
XX 08-DEC-2001 200100S-254117.
XX (GMR) 3 GMR, MCNEIL PHARM INC.
XX 840 G. 860197. Deaneffs A. Zhang H.
XX WP1: 2002-09-16/54.
XX New macroheterocyclic compounds useful in the treatment of a kinase
XX mediated disorder such as cardiovascular diseases e.g. acute stroke
XX Example 2: Page 108: 143pp: English.
XX The present invention relates to novel macroheterocyclic compounds, which
XX are protein kinase C (preferably C alpha, C beta-II, C gamma) and
XX glycogen synthase kinase-3 (preferably 3beta) inhibitors. The compounds
XX are used for treating or ameliorating a kinase mediated disorder such as
XX cardiovascular diseases, diabetes, inflammation diseases, immunological
XX disorders, dermatological disorders, cancer and central nervous system
XX disorders. Assays to test inhibition of a compound of the invention for
XX kinases were performed using methods that measure the amount of
XX phosphorylation of a biotinylated peptide substrate. The present sequence
XX is one such biotinylated peptide substrate, used in an example from the
XX invention.
XX Sequence 9 AA;
XX

Query Match 46.4% Score 47 DB 23 Length 9
 Best Local Similarity 100.0% Prod No. 9.3e+05
 Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 6 TGRK 9
 DB 3 TGRK 6

RESULT 45
 A067614
 AB07614 standard: Peptide: 9 AA
 AA: Asp76145
 22 MAY 2002 (first entry)
 Protein kinase A substrate peptide
 Protein kinase A: tyrosine kinase; autophosphorylation; phosphatase; tumorigenesis; elevated in retinopathy; the catalytic domain; endometrial cancer; tyrosine kinase; antitumor; activated; and activation; and in hematopoietic; antiproliferative; ophthalmological; and neurodegenerative; enzyme; substrate; Synthesis

Key Location/Qualifiers
 Modified site 1 /note "N terminal modified"
 Modified site 9 /note "C terminal modified"

W020224451-A2
 28-MAR-2002
 19 SEP 2001: 2001KW-DS29175
 20 SEP 2001: 2000US-243964P
 (KIB) ORTHO-McNEIL PHARM INC.
 Kao GR, Nishimura P, Proby G, Puchner A, West A, Jullitte J, Middleton S, Emanuel S
 WPI: 2002-4-19/8/43
 New pyrazine derivative used in treatment of various diseases and psoriasis
 Example 1: Page 17; 20 pages entire
 The present sequence is a modified peptide substrate of protein kinase A. The peptide was used in a kinase selectivity assay to determine the ability of test pyrazine derivatives to inhibit kinase activity. The invention provides pyrazine derivatives that inhibit tyrosine kinase activity. They are useful as anti-tumor agents and to treat solid tumor cancers, diabetes, endometrial, diabetic retinopathy, rheumatoid arthritis, endometriosis and psoriasis (all claimed)

Sequence 9 AA:
 Query Match 46.4% Score 47 DB 23 Length 9
 Best Local Similarity 100.0% Prod No. 9.3e+05
 Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 6 TGRK 9
 DB 3 TGRK 6

RESULT 44

AA014454
 ID AA014454 standard: peptide: 9 AA
 AC AA014454
 16-MAY-2002 (first entry)
 Peptide of the substrate of PKA kinase (Ser/Thr)
 Substrate multiplexed; enzyme; receptor-kinase; cell-signaling pathway; inhibits; stimulates; receptor; ligand; receptor-enzyme; insulin; EGF; receptor II kinase; ligand activated; epidermal growth factor; extracellular signal regulated kinase; substrate; PKA-kinase (Ser/Thr).
 Unidentified
 Key Location/Qualifiers
 Modified site 1 /note "Fluorescein isothiocyanate (FITC)"
 W0200212547-A1
 14-FEB-2002
 08 AUG 2001: 2001KW-DS2475P
 08-AUG-2000: 2000US-224842P
 (ACLA) ACLA BIO SCIENCES INC.
 Xue Q, Gibbons I
 WPI: 2002-241771/29
 Multiplexed enzyme assay comprises performing enzyme reactions in presence of substrates to convert substrate to product, separating them, detecting their separation characteristic and determining amount of product
 Example 1: Page 22; 55pp; English
 The invention relates to a multiplexed enzyme assay comprising performing a number of enzyme reactions in presence of a number of enzyme substrates. The purpose of which is to convert substrates to their corresponding product, separating substrates and products in single separation medium, detecting separation characteristic effective to identify products and substrates, and signal related to amount of products and substrates, and determining amount of substrates converted to products in each of the reactions. The assay of the invention is used in determining the levels of activity of each of a number of different enzymes in a cell, determining changes in the levels of activity of each of a group of enzymes (selected from receptor kinase enzymes and cell-signaling pathway enzymes) in a cell, assaying the effect of one or more agents in inhibiting or stimulating the activity of a selected enzyme, evaluating a test compound capable of affecting enzyme activity, assaying interactions between a receptor enzyme and a ligand known to affect the receptor-enzyme activity, specifically insulin, epidermal growth factor (EGF), extracellular signal regulated kinase and receptor II kinase. The assay of the invention is also useful for assaying the ability or effect of one or more test agents to interfere with ligand-activated enzyme activity. This sequence represents a peptide of a substrate of PKA-kinase (Ser/Thr) (an enzyme of the invention).

Sequence 9 AA:
 Query Match 36.4% Score 47 DB 23 Length 9
 Best Local Similarity 100.0% Prod No. 9.3e+05
 Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY 6 TGRK 9
 DB 3 TGRK 6


```

XX WPI: 1993-134624/16.
XX Request for detecting antibodies to hepatitis C virus - comprises
PI peptide(s) with the same sequence as an epitope of an HCV
PT structural region
XX Claim 1: Page 46; 51pp; Japanese.
XX The sequences given in AAK4417-25 are peptides which can be used in a
CC test reagent for the detection of antibodies against hepatitis C.
CC The peptides represent epitopes of an HCV structural region and they
CC react specifically with antibodies against the HCV structural region.
CC Detection is sensitive and accurate and allows diagnosis of the
CC infection at a very early stage.
CC (Updated on 25 MAR-2003 to correct PN field.)
XX Sequence: 10 AA.
XX
XX Query Match: 36.4%, Score 4; DB 14; Length 10;
XX Host Local Similarity: 100.0%, Pred. No. 8.5e+02;
XX Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX CY 7 GRPP 10
XX DB 111
XX 7 GRPP 10
XX
XX RESULT 47
XX AAK4419
XX 10 AAK4419 standard; peptide: 10 AA.
XX
XX AC AAK4419;
XX
XX 25-MAR-2003 (updated);
XX DT 05-AUG-1993 (first entry)
XX
XX DE Hepatitis C Ab detection peptide #4.
XX
XX KW Test reagent: detection antibody; hepatitis C; virus; HCV; epitope;
XX KW structural region; diagnosis; SS.
XX
XX OS Synthetic.
XX
XX PN W9137486 A1.
XX
XX PG 15 APR-1994.
XX
XX PF 02-SEP-1994; 92WP JPO/276.
XX
XX PG 02-SEP-1994; 92JP 9259524.
XX PG 26-MAR-1992; 92JP 9268695.
XX
XX PA (EIKEN) EIKEN KASAKO KK.
XX PA (TAKA) TAKARA SEIYAKU CO.
XX PA (OSAKA) UNIV OSAKA.
XX
XX PI Ishibashi K., Ito M., Shibutani I., Takamizawa A., Yoshida I.
XX
XX WPI: 1993-134624/16.
XX
XX Request for detecting antibodies to hepatitis C virus - comprises
PI peptide(s) with the same sequence as an epitope of an HCV
PT structural region
XX Disclosure: Page 42; 51pp; Japanese.
XX
XX The sequences given in AAK4417-25 are peptides which can be used in a
CC test reagent for the detection of antibodies against hepatitis C.
CC The peptides represent epitopes of an HCV structural region and they
CC react specifically with antibodies against the HCV structural region.
CC Detection is sensitive and accurate and allows diagnosis of the
CC infection at a very early stage.
CC (Updated on 25 MAR-2003 to correct PN field.)
XX
XX Sequence: 10 AA.
XX
XX Query Match: 36.4%, Score 4; DB 14; Length 10;
XX Host Local Similarity: 100.0%, Pred. No. 8.5e+02;
XX Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX CY 7 GRPP 10
XX DB 111
XX 7 GRPP 10
XX
XX RESULT 49
XX AAK67409
XX 10 AAK67409 standard; peptide: 10 AA.

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XX
XX Sequence: 10 AA;
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XX Query Match: 36.4%, Score 4; DB 14; Length 10;
XX Host Local Similarity: 100.0%, Pred. No. 8.5e+02;
XX Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX CY 7 GRPP 10
XX DB 111
XX 7 GRPP 10
XX
XX RESULT 46
XX AAK44420
XX 10 AAK44420 standard; peptide: 10 AA.
XX
XX AC AAK44420;
XX
XX 25-MAR-2003 (updated);
XX DT 05-AUG-1993 (first entry)
XX
XX DE Hepatitis C Ab detection peptide #4.
XX
XX KW Test reagent: detection antibody; hepatitis C; virus; HCV; epitope;
XX KW structural region; diagnosis; SS.
XX
XX OS Synthetic.
XX
XX PN W9137486 A1.
XX
XX PG 15 APR-1994.
XX
XX PF 02-SEP-1994; 92WP JPO/276.
XX
XX PG 02-SEP-1994; 92JP 9259524.
XX PG 26-MAR-1992; 92JP 9268695.
XX
XX PA (EIKEN) EIKEN KASAKO KK.
XX PA (TAKA) TAKARA SEIYAKU CO.
XX PA (OSAKA) UNIV OSAKA.
XX
XX PI Ishibashi K., Ito M., Shibutani I., Takamizawa A., Yoshida I.
XX
XX WPI: 1993-134624/16.
XX
XX Request for detecting antibodies to hepatitis C virus - comprises
PI peptide(s) with the same sequence as an epitope of an HCV
PT structural region
XX Disclosure: Page 42; 51pp; Japanese.
XX
XX The sequences given in AAK4417-25 are peptides which can be used in a
CC test reagent for the detection of antibodies against hepatitis C.
CC The peptides represent epitopes of an HCV structural region and they
CC react specifically with antibodies against the HCV structural region.
CC Detection is sensitive and accurate and allows diagnosis of the
CC infection at a very early stage.
CC (Updated on 25 MAR-2003 to correct PN field.)
XX
XX Sequence: 10 AA.
XX
XX Query Match: 36.4%, Score 4; DB 14; Length 10;
XX Host Local Similarity: 100.0%, Pred. No. 8.5e+02;
XX Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX CY 7 GRPP 10
XX DB 111
XX 7 GRPP 10
XX
XX RESULT 44
XX AAK67409
XX 10 AAK67409 standard; peptide: 10 AA.

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configure version 1.1.6
Copyright (c) 1993 - 2003 Compuser, Inc.

10M protein, protein search, using SW-MakeIt

Run on: September 09, 2003, 14:30:34, Search time: 21.0 Seconds
(without database)
224,438 Residues with updates/srv

Title: US-09-787-443-9
Protein source: 1: AINKKKGRKRP 1:
Sequence: 22

Scoring table:
Gap-P 40.0, Gap-Ext 6.0

Searched: 566894 seqs, 15116704 residues

Word size: 0

Total number of hits satisfying chosen parameters: 6847

Minimum DB Seq Length: 8

Maximum DB Seq Length: 15

Post-processing: Listing first 500 sequences

Database: 1: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
2: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
3: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
4: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
5: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
6: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
7: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
8: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
9: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
10: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
11: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
12: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
13: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
14: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
15: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
16: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
17: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
18: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
19: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep
20: /cqn2_6/prodat/a/2/ptdata/US02_9-oli.rapb.pep

Pro 1: 8. Use the number of residues in the protein to be searched
score greater than or equal to 1.0. The database is sorted by protein
and is divided by analysts 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 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417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 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107	3	27.3	8	11	US-09-875-22-A-117	Sequence 117, Appl	162	3	27.3	8	15	US-10-006-869-2383	Sequence 2483, Appl
108	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	163	3	27.3	8	15	US-10-006-869-2443	Sequence 2443, Appl
109	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	164	3	27.3	8	15	US-10-006-869-2503	Sequence 2503, Appl
110	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	165	3	27.3	8	15	US-10-006-869-2613	Sequence 2613, Appl
111	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	166	3	27.3	8	15	US-10-006-869-2633	Sequence 2633, Appl
112	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	167	3	27.3	8	15	US-10-006-869-2649	Sequence 2649, Appl
113	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	168	3	27.3	8	15	US-10-006-869-2653	Sequence 2653, Appl
114	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	169	3	27.3	8	15	US-10-006-869-2664	Sequence 2664, Appl
115	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	170	3	27.3	8	15	US-10-006-869-2679	Sequence 2679, Appl
116	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	171	3	27.3	8	15	US-10-006-869-2683	Sequence 2683, Appl
117	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	172	3	27.3	8	15	US-10-006-869-2694	Sequence 2694, Appl
118	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	173	3	27.3	8	15	US-10-006-869-2712	Sequence 2712, Appl
119	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	174	3	27.3	8	15	US-10-006-869-2799	Sequence 2799, Appl
120	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	175	3	27.3	8	15	US-10-006-869-2862	Sequence 2862, Appl
121	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	176	3	27.3	8	15	US-10-006-869-2925	Sequence 2925, Appl
122	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	177	3	27.3	8	15	US-10-006-869-2988	Sequence 2988, Appl
123	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	178	3	27.3	8	15	US-10-006-869-3048	Sequence 3048, Appl
124	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	179	3	27.3	8	15	US-10-006-869-3071	Sequence 3071, Appl
125	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	180	3	27.3	8	15	US-10-006-869-3116	Sequence 3116, Appl
126	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	181	3	27.3	8	15	US-10-006-869-3161	Sequence 3161, Appl
127	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	182	3	27.3	8	15	US-10-006-869-3206	Sequence 3206, Appl
128	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	183	3	27.3	8	15	US-10-006-869-3251	Sequence 3251, Appl
129	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	184	3	27.3	8	15	US-10-006-869-3299	Sequence 3299, Appl
130	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	185	3	27.3	8	15	US-10-006-869-3668	Sequence 3668, Appl
131	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	186	3	27.3	8	15	US-10-006-869-3774	Sequence 3774, Appl
132	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	187	3	27.3	8	15	US-10-006-869-3860	Sequence 3860, Appl
133	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	188	3	27.3	8	15	US-10-006-869-4050	Sequence 4050, Appl
134	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	189	3	27.3	8	15	US-10-277-622-4	Sequence 4, Appl1
135	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	190	3	27.3	8	15	US-10-283-838-16	Sequence 16, Appl1
136	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	191	3	27.3	8	15	US-10-161-097-9	Sequence 9, Appl1
137	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	192	3	27.3	8	15	US-10-211-088-185	Sequence 185, Appl
138	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	193	3	27.3	8	15	US-10-211-088-198	Sequence 198, Appl
139	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	194	3	27.3	8	15	US-10-170-387-3	Sequence 3, Appl1
140	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	195	3	27.3	8	15	US-10-113-424-4	Sequence 4, Appl1
141	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	196	3	27.3	8	15	US-10-224-286-26	Sequence 26, Appl1
142	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	197	3	27.3	8	15	US-10-055-711-7	Sequence 7, Appl1
143	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	198	3	27.3	8	15	US-10-193-768-35	Sequence 35, Appl1
144	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	199	3	27.3	8	15	US-10-098-238-30	Sequence 30, Appl1
145	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	200	3	27.3	8	15	US-10-098-238-31	Sequence 31, Appl1
146	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	201	3	27.3	8	15	US-06-344-824-80	Sequence 80, Appl1
147	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	202	3	27.3	8	15	US-06-344-824-138	Sequence 138, Appl
148	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	203	3	27.3	8	15	US-06-344-824-142	Sequence 142, Appl
149	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	204	3	27.3	8	15	US-06-344-824-146	Sequence 146, Appl
150	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	205	3	27.3	8	15	US-06-344-824-161	Sequence 161, Appl
151	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	206	3	27.3	8	15	US-06-344-824-165	Sequence 165, Appl
152	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	207	3	27.3	8	15	US-08-821-739A-57	Sequence 57, Appl1
153	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	208	3	27.3	8	15	US-08-821-739A-69	Sequence 69, Appl1
154	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	209	3	27.3	8	15	US-09-760-599-5	Sequence 5, Appl1
155	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	210	3	27.3	8	15	US-09-760-599-6	Sequence 6, Appl1
156	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	211	3	27.3	8	15	US-09-760-599-7	Sequence 7, Appl1
157	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	212	3	27.3	8	15	US-09-760-599-8	Sequence 8, Appl1
158	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	213	3	27.3	8	15	US-09-760-599-21	Sequence 21, Appl1
159	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	214	3	27.3	8	15	US-09-760-599-22	Sequence 22, Appl1
160	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	215	3	27.3	8	15	US-09-760-599-23	Sequence 23, Appl1
161	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	216	3	27.3	8	15	US-09-760-599-24	Sequence 24, Appl1
162	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	217	3	27.3	8	15	US-09-765-086-114	Sequence 114, Appl
163	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	218	3	27.3	8	15	US-09-658-349-15	Sequence 15, Appl1
164	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	219	3	27.3	8	15	US-09-828-644-117	Sequence 117, Appl
165	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	220	3	27.3	8	15	US-09-796-294-48	Sequence 48, Appl1
166	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	221	3	27.3	8	15	US-09-796-294-50	Sequence 50, Appl1
167	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	222	3	27.3	8	15	US-09-835-695-9	Sequence 9, Appl1
168	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	223	3	27.3	8	15	US-09-834-765-544	Sequence 544, Appl
169	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	224	3	27.3	8	15	US-09-811-284-258	Sequence 258, Appl
170	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	225	3	27.3	8	15	US-09-810-700-3	Sequence 3, Appl1
171	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	226	3	27.3	8	15	US-09-750-373-28	Sequence 28, Appl1
172	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	227	3	27.3	8	15	US-09-938-315-4	Sequence 4, Appl1
173	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	228	3	27.3	8	15	US-09-832-723-91	Sequence 91, Appl1
174	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	229	3	27.3	8	15	US-09-780-053-58	Sequence 58, Appl1
175	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	230	3	27.3	8	15	US-09-780-053-648	Sequence 648, Appl
176	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	231	3	27.3	8	15	US-09-782-745-5	Sequence 5, Appl1
177	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	232	3	27.3	8	15	US-09-782-745-6	Sequence 6, Appl1
178	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	233	3	27.3	8	15	US-09-782-745-8	Sequence 8, Appl1
179	3	27.3	8	11	US-09-875-22-A-117	Sequence 120, Appl	234	3	27.3	8	15		

245	9	10	US-09-782-745-22	Sequence 22, Appl	308	9	12	US-10-062-109A-553	Sequence 553, App
246	9	10	US-09-872-632-25	Sequence 28, Appl	309	9	12	US-10-062-109A-562	Sequence 562, App
247	9	10	US-09-828-432-29	Sequence 10, Appl	310	9	12	US-10-062-109A-564	Sequence 564, App
248	9	10	US-09-961-902-3	Sequence 4, Appl	311	9	12	US-10-077-106-17	Sequence 12, Appl
249	9	10	US-09-961-902-4	Sequence 6, Appl	312	9	12	US-10-077-106-17	Sequence 17, Appl
249	9	10	US-09-961-902-6	Sequence 12, Appl	313	9	12	US-10-312-495-12	Sequence 702, App
249	9	10	US-09-961-902-12	Sequence 14, Appl	315	9	12	US-10-224-999A-702	Sequence 702, App
249	9	10	US-09-961-902-13	Sequence 17, Appl	316	9	12	US-09-833-039-76	Sequence 76, Appl
249	9	10	US-09-961-902-14	Sequence 18, Appl	317	9	12	US-09-833-039-77	Sequence 77, Appl
249	9	10	US-09-961-902-15	Sequence 19, Appl	318	9	12	US-09-833-039-99	Sequence 99, Appl
249	9	10	US-09-961-902-16	Sequence 20, Appl	319	9	12	US-10-020-269-109	Sequence 109, App
249	9	10	US-09-961-902-17	Sequence 21, Appl	320	9	12	US-10-231-417-379	Sequence 379, App
249	9	10	US-09-961-902-18	Sequence 22, Appl	321	9	12	US-10-239-313A-522	Sequence 522, App
249	9	10	US-09-961-902-19	Sequence 23, Appl	322	9	14	US-10-012-756-26	Sequence 26, Appl
249	9	10	US-09-961-902-20	Sequence 24, Appl	323	9	15	US-10-211-207-12	Sequence 12, Appl
249	9	10	US-09-961-902-21	Sequence 25, Appl	324	9	15	US-10-211-207-17	Sequence 17, Appl
249	9	10	US-09-961-902-22	Sequence 26, Appl	325	9	15	US-10-102-283-131	Sequence 131, App
249	9	10	US-09-961-902-23	Sequence 27, Appl	326	9	15	US-10-001-546-42	Sequence 42, Appl
249	9	10	US-09-961-902-24	Sequence 28, Appl	327	9	15	US-10-062-710-198	Sequence 198, App
249	9	10	US-09-961-902-25	Sequence 29, Appl	328	9	15	US-10-274-017-5	Sequence 5, Appl
249	9	10	US-09-961-902-26	Sequence 30, Appl	329	9	15	US-10-116-8468-29	Sequence 29, Appl
249	9	10	US-09-961-902-27	Sequence 31, Appl	330	9	15	US-10-080-013-28	Sequence 28, Appl
249	9	10	US-09-961-902-28	Sequence 32, Appl	331	9	15	US-10-273-541-69	Sequence 69, Appl
249	9	10	US-09-961-902-29	Sequence 33, Appl	332	9	15	US-10-135-795-131	Sequence 131, App
249	9	10	US-09-961-902-30	Sequence 34, Appl	333	9	15	US-10-040-862-9701	Sequence 9701, App
249	9	10	US-09-961-902-31	Sequence 35, Appl	334	9	15	US-10-040-862-9758	Sequence 9758, App
249	9	10	US-09-961-902-32	Sequence 36, Appl	335	9	15	US-10-040-862-9832	Sequence 9832, App
249	9	10	US-09-961-902-33	Sequence 37, Appl	336	9	15	US-10-040-862-9890	Sequence 9890, App
249	9	10	US-09-961-902-34	Sequence 38, Appl	337	9	15	US-10-040-862-9904	Sequence 9904, App
249	9	10	US-09-961-902-35	Sequence 39, Appl	338	9	15	US-10-040-862-10089	Sequence 10089, App
249	9	10	US-09-961-902-36	Sequence 40, Appl	339	9	15	US-10-040-862-10116	Sequence 10116, App
249	9	10	US-09-961-902-37	Sequence 41, Appl	340	9	15	US-10-040-862-10130	Sequence 10130, App
249	9	10	US-09-961-902-38	Sequence 42, Appl	341	9	15	US-10-040-862-10136	Sequence 10136, App
249	9	10	US-09-961-902-39	Sequence 43, Appl	342	9	15	US-10-040-862-10214	Sequence 10214, App
249	9	10	US-09-961-902-40	Sequence 44, Appl	343	9	15	US-10-040-862-10299	Sequence 10299, App
249	9	10	US-09-961-902-41	Sequence 45, Appl	344	9	15	US-10-040-862-10421	Sequence 10421, App
249	9	10	US-09-961-902-42	Sequence 46, Appl	345	9	15	US-10-040-862-10424	Sequence 10424, App
249	9	10	US-09-961-902-43	Sequence 47, Appl	346	9	15	US-10-040-862-10426	Sequence 10426, App
249	9	10	US-09-961-902-44	Sequence 48, Appl	347	9	15	US-10-006-869-210	Sequence 210, App
249	9	10	US-09-961-902-45	Sequence 49, Appl	348	9	15	US-10-006-869-280	Sequence 280, App
249	9	10	US-09-961-902-46	Sequence 50, Appl	349	9	15	US-10-006-869-308	Sequence 308, App
249	9	10	US-09-961-902-47	Sequence 51, Appl	350	9	15	US-10-006-869-403	Sequence 403, App
249	9	10	US-09-961-902-48	Sequence 52, Appl	351	9	15	US-10-006-869-431	Sequence 431, App
249	9	10	US-09-961-902-49	Sequence 53, Appl	352	9	15	US-10-006-869-473	Sequence 473, App
249	9	10	US-09-961-902-50	Sequence 54, Appl	353	9	15	US-10-006-869-503	Sequence 503, App
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US-08-859-499-3

Sequence 3, Application US/08859699A

Publication No. US20010607017A1

GENERAL INFORMATION:

APPLICANT: VELJKOVIC, Veljko

APPLICANT: METLAS, Radmila

TITLE OF INVENTION: PEPTIDES WHICH REACT WITH ANTIBODY REPRESENTING THE

TITLE OF INVENTION: PROGNOSTIC MARKER FOR HIV DISEASE PROGRESSION

FILE REFERENCE: VELJKOVIC et al., 08/859, 699

CURRENT APPLICATION NUMBER: US/08/859, 699A

CURRENT FILING DATE: 1997-05-21

EARLIER APPLICATION NUMBER: GB 9610673.7

EARLIER FILING DATE: 1996-05-22

EARLIER APPLICATION NUMBER: GB 9623340.8

EARLIER FILING DATE: 1996-11-08

NUMBER OF SEQ ID NOS: 26

SOURCE: Patented, Vet. 2.0

SEQ ID NO. 3

LENGTH: 14

TYPE: PRT

RESULTS:

US-08-859-499-3

Sequence 3, Application US/08859699A

Publication No. US20010607017A1

GENERAL INFORMATION:

APPLICANT: VELJKOVIC, Veljko

APPLICANT: METLAS, Radmila

TITLE OF INVENTION: PEPTIDES WHICH REACT WITH ANTIBODY REPRESENTING THE

TITLE OF INVENTION: PROGNOSTIC MARKER FOR HIV DISEASE PROGRESSION

FILE REFERENCE: VELJKOVIC et al., 08/859, 699

CURRENT APPLICATION NUMBER: US/08/859, 699A

CURRENT FILING DATE: 1997-05-21

EARLIER APPLICATION NUMBER: GB 9610673.7

EARLIER FILING DATE: 1996-05-22

EARLIER APPLICATION NUMBER: GB 9623340.8

EARLIER FILING DATE: 1996-11-08

NUMBER OF SEQ ID NOS: 26

SOURCE: Patented, Vet. 2.0

SEQ ID NO. 3

LENGTH: 14

TYPE: PRT

ALIGNMENTS

US-09-859-699-7

: Sequence 3, Application US/04859699A
 : Publication No. US2001360701A1
 : GENERAL INFORMATION:
 : APPLICANT: VELLKOVIC, Veljko
 : APPLICANT: METILAS, Radmila
 : TITLE OF INVENTION: PEPTIDES WHICH REACT WITH ANTIBODY REPRESENTING THE
 : FILE REFERENCE: VELLKOVIC et al., 08/859,699
 : CURRENT FILING DATE: 1997-05-21
 : EARLIER APPLICATION NUMBER: GB 9610673.7
 : EARLIER FILING DATE: 1996-05-22
 : EARLIER APPLICATION NUMBER: GB 9623340.8
 : NUMBER OF SEQ ID NOS: 26
 : SOFTWARE: Patent In Ver. 2.0
 : SEQ ID NO 3
 : LENGTH: 14
 : TYPE: PRT

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1 ORGANISM: Artificial Sequence
2 FEATURE:
3 OTHER INFORMATION: Description of Artificial Sequence: Protein Kinase A Substrate
4 US 09-787-443-9-oli
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6 Query Match: 45,584 Score 61 DB 11: Length 9;
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1  FEATURE:
2  OTHER INFORMATION: Optimized substrate peptide
3  US 10 294 086 141
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5  Query Match: 96.4%, Score 4, DB 12, Length 9,
6  Best Local Similarity: 100.0%, Prod. No. 5, 1e+05,
7  Matches 4, Conservative 0, Mismatches 0, Gaps 0
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10 111
11 4 GRR 6
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13 RESULT 6
14 US 10 294 086 141
15 1 Sequence 24, Application US/2002/000000
16 2 Publication No. US2002/000000A1
17 3 GENERAL INFORMATION:
18 4 APPLICANT: BERNARDINI, ROBERT
19 5 APPLICANT: FRANKLIN, ROSELLA
20 6 APPLICANT: DESIDERIO, ANGELA
21 7 APPLICANT: FAVAIORAKI, PARASKEVI
22 8 TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANALOGUES
23 9 TITLE OF INVENTION: WHICH INCLUDE THEM
24 10 FILE REFERENCE: 411 4
25 11 CURRENT APPLICATION NUMBER: US/10/09, 053
26 12 PRIOR APPLICATION NUMBER: 87/112/20054
27 13 PRIOR FILING DATE: 2002-10-29
28 14 PRIOR FILING DATE: 2000-12-29
29 15 PRIOR APPLICATION NUMBER: 11 899/460000
30 16 PRIOR FILING DATE: 1999-12-06
31 17 NUMBER OF SEQ ID NOS: 118
32 18 SOFTWARE: Patent In Ver. 2.1
33 19 SEQ ID NO: 24
34 20 LENGTH: 9
35 21 TYPE: PRI
36 22 ORGANISM: Artificial Sequence
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38 24 OTHER INFORMATION: Description of Artificial Sequence: See SEQ ID NO: 24
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49 RESULT 7
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51 1 Sequence 10, Application US/01/011000
52 2 Publication No. US2002/006541A1
53 3 GENERAL INFORMATION:
54 4 APPLICANT: Bellus, Mary
55 5 APPLICANT: MACHENAS, JOAQUIN
56 6 APPLICANT: COUTOPO, BEATRY
57 7 APPLICANT: KACHOOL, VILAY
58 8 TITLE OF INVENTION: METHODS FOR STABILIZING PEPTIDES
59 9 TITLE OF INVENTION: RESPONSE BY MODULATING THE INTERACTION BETWEEN PEPTIDES
60 10 TITLE OF INVENTION: EP2A
61 11 FILE REFERENCE: ANN 027
62 12 CURRENT APPLICATION NUMBER: US/10/011000
63 13 PRIOR APPLICATION NUMBER: 2002-02-26
64 14 PRIOR FILING DATE: 2002-02-26
65 15 PRIOR FILING DATE: 2001-02-16
66 16 NUMBER OF SEQ ID NOS: 25
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69 19 LENGTH: 9
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71 21 ORGANISM: Homo sapiens

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1  ORGANISM: Homo sapiens
2  US 10 077 106 14
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12 RESULT 8
13 US 09 433 094 23
14 1 Sequence 24, Application US/ 09/000000
15 2 Publication No. US2002/000000A1
16 3 GENERAL INFORMATION:
17 4 APPLICANT: LUGANI, STEVE
18 5 APPLICANT: SABLE, DUSTY
19 6 APPLICANT: GRIFFIN-SCHULZ, MICHAEL
20 7 TITLE OF INVENTION: Lipo-Associated Peptide and Uses Thereof
21 8 FILE REFERENCE: LIP 5622.1
22 9 CURRENT APPLICATION NUMBER: US/09/043,039
23 10 CURRENT FILING DATE: 2001-04-12
24 11 PRIOR APPLICATION NUMBER: US 09/409,455
25 12 PRIOR FILING DATE: 1999-09-30
26 13 PRIOR APPLICATION NUMBER: US 09/409,455
27 14 PRIOR FILING DATE: 1999-09-30
28 15 PRIOR APPLICATION NUMBER: US 09/444,046
29 16 PRIOR FILING DATE: 1998-06-26
30 17 PRIOR APPLICATION NUMBER: US 09/405,899
31 18 PRIOR APPLICATION NUMBER: US 09/451,130
32 19 PRIOR FILING DATE: 1997-05-05
33 20 NUMBER OF SEQ ID NOS: 129
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39
40 Query Match: 97.4%, Score 4, DB 12, Length 9,
41 Best Local Similarity: 100.0%, Prod. No. 5, 1e+05,
42 Matches 4, Conservative 0, Mismatches 0, Gaps 0
43
44 Q9 3 INK 11
45 111
46 3 INK 6
47
48 RESULT 9
49 US 09 433 094 23
50 1 Sequence 48, Application US/09/000000
51 2 Publication No. US2002/000000A1
52 3 GENERAL INFORMATION:
53 4 APPLICANT: LUGANI, STEVE
54 5 APPLICANT: SABLE, DUSTY
55 6 APPLICANT: GRIFFIN-SCHULZ, MICHAEL
56 7 TITLE OF INVENTION: Lipo-Associated Peptide and Uses Thereof
57 8 FILE REFERENCE: LIP 5622.1
58 9 CURRENT APPLICATION NUMBER: US/09/043,039
59 10 CURRENT FILING DATE: 2001-04-12
60 11 PRIOR APPLICATION NUMBER: US 09/409,455
61 12 PRIOR FILING DATE: 1999-09-30
62 13 PRIOR APPLICATION NUMBER: US 09/444,046
63 14 PRIOR FILING DATE: 1999-09-30
64 15 PRIOR APPLICATION NUMBER: US 09/405,899
65 16 PRIOR APPLICATION NUMBER: US 09/451,130
66 17 PRIOR FILING DATE: 1997-05-05
67 18 NUMBER OF SEQ ID NOS: 129
68 19 SEQ ID NO: 48
69 20 LENGTH: 9
70 21 TYPE: PRI
71 22 ORGANISM: Homo sapiens

```


FILE REFERENCE: Human patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000 05 17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: Prototient version 1.0
 SEQ ID NO: 481
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURES:
 OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 83 92 and may interact with
 OTHER INFORMATION: Sequence 481 in this patent
 US 09 572 404B 481

Query Match 36.48; Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6, 1e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TGRK 9
 L I I
 DB 6 TGRK 9

RESULT 15
 US 09 572 404B 483
 Sequence 483; Application: US/09/572,404B
 Publication No. US20030078374A1

GENERAL INFORMATION:
 APPLICANT: Prototient Ltd
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000 05 17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: Prototient version 1.0
 SEQ ID NO: 483
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURES:
 OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 83 92 and may interact with
 OTHER INFORMATION: Sequence 484 in this patent
 US 09 572 404B 483

Query Match 36.48; Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6, 1e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TGRK 9
 L I I
 DB 6 TGRK 10

RESULT 16
 US 09 572 404B 499
 Sequence 499; Application: US/09/572,404B
 Publication No. US20030078374A1

GENERAL INFORMATION:
 APPLICANT: Prototient Ltd
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000 05 17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: Prototient version 1.0
 SEQ ID NO: 499
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURES:
 OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 82 91 and may interact with
 OTHER INFORMATION: Sequence 499 in this patent
 US 09 572 404B 499

Query Match 36.48; Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6, 1e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TGRK 9
 L I I
 DB 6 TGRK 5

Query Match 36.48; Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6, 1e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TGRK 9
 L I I
 DB 7 TGRK 10

RESULT 17
 US 09 572 404B 405
 Sequence 405; Application: US/09/572,404B
 Publication No. US20030078374A1

GENERAL INFORMATION:
 APPLICANT: Prototient Ltd
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000 05 17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: Prototient version 1.0
 SEQ ID NO: 405
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURES:
 OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 83 92 and may interact with
 OTHER INFORMATION: Sequence 406 in this patent
 US 09 572 404B 405

Query Match 36.48; Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6, 1e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TGRK 9
 L I I
 DB 6 TGRK 9

RESULT 18
 US 09 572 404B 411
 Sequence 411; Application: US/09/572,404B
 Publication No. US20030078374A1

GENERAL INFORMATION:
 APPLICANT: Prototient Ltd
 TITLE OF INVENTION: Complementary peptide ligands from the human genome
 FILE REFERENCE: Human patent
 CURRENT APPLICATION NUMBER: US/09/572,404B
 CURRENT FILING DATE: 2000 05 17
 NUMBER OF SEQ ID NOS: 4203
 SOFTWARE: Prototient version 1.0
 SEQ ID NO: 411
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Homo Sapiens
 FEATURES:
 OTHER INFORMATION: sequence located in NPR3 OR ANPRC at 87 96 and may interact with
 OTHER INFORMATION: Sequence 412 in this patent
 US 09 572 404B 411

Query Match 36.48; Score 4; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6, 1e-02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TGRK 9
 L I I
 DB 6 TGRK 5

RESULT 19
 US 09 572 404B 588
 Sequence 588; Application: US/09/572,404B

```
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
FILE OF INVENTION: Complementary peptide libraries from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProPatent version 1.0
SEQ ID NO 588
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: Sequence located in US/09/572,404B and may interact with Sequence 2156.
US 09 572 404B 588

Query Match
Best Local Similarity 100.0%; App. Location: US/09/572,404B
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 5 KRER 8
LE 1 KRER 4

RESULT 20
US 09 572-404B-2156
Sequence 2156, Application US/09/572,404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
FILE OF INVENTION: Complementary peptide libraries from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProPatent version 1.0
SEQ ID NO 2156
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
OTHER INFORMATION: Sequence located in US/09/572,404B and may interact with Sequence 2156.
US 09 572-404B-2156

Query Match
Best Local Similarity 100.0%; App. Location: US/09/572,404B
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 7 GRER 10
LE 1 GRER 4

RESULT 21
US 09 572 404B 2904
Sequence 2904, Application US/09/572,404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
FILE OF INVENTION: Complementary peptide libraries from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProPatent version 1.0
SEQ ID NO 2904
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens
```

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FEATURE:
OTHER INFORMATION: Sequence located in MK167 at 2835-2844 and may interact with
US-09-572 404B-2904

Query Match
Best Local Similarity 100.0%; App. Location: US/09/572,404B
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 6 KRER 11
LE 6 KRER 9

RESULT 22
US 09 572-270A-655
Sequence 655, Application US/09/572,270A
Publication No. US2003005611A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
FILE OF INVENTION: Inter-complementary peptide listing
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/572,270A
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 1144
SOFTWARE: ProPatent version 1.0
SEQ ID NO 655
LENGTH: 10
TYPE: PRT
ORGANISM: Arabidopsis Thaliana
OTHER INFORMATION: Sequence located in GASAL at 47-56 and may interact with
US-09-572 270A-655

Query Match
Best Local Similarity 100.0%; App. Location: US/09/572,270A
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 KRER 11
LE 6 KRER 9

RESULT 23
US 09 802-109-7
Sequence 7, Application US/09/802109+
Patent No. US2002005611A1
GENERAL INFORMATION:
APPLICANT: Steico, Steico
FILE OF INVENTION: CARRIER FOR IN VIVO DELIVERY OF A THERAPEUTIC
FILE REFERENCE: 601 1 983
CURRENT APPLICATION NUMBER: US/09/802,109
CURRENT FILING DATE: 2002-04-08
PRIORITY APPLICATION NUMBER: 09/044,411
PRIORITY FILING DATE: 1998-03-19
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentL: Ver. 2.0
SEQ ID NO 7
LENGTH: 11
TYPE: PRT
ORGANISM: Human immunodeficiency virus type 1
FEATURE:
OTHER INFORMATION: Same as Sequence ID 2, but with a substitution of
OTHER INFORMATION: Gln to Pro.
NAME/KEY: BINDING
LOCATION: (10)
OTHER INFORMATION: Cys(biotin)
OTHER INFORMATION: Peptide has an N-terminal acetyl group.
OTHER INFORMATION: Peptide has a C-terminal amide group.
US 09-802-109-7

Query Match
Best Local Similarity 100.0%; App. Location: US/09/802,109
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0
```



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RESULT 29
US 10 115-665-29
: Sequence 29, Application US/1011565
: Publication No. US2003074694A1
: GENERAL INFORMATION:
: APPLICANT: Beckmeyer, Brian A
: APPLICANT: Kellward, Thomas A
: TITLE OF INVENTION: Calcium Modulated Kinase
: FILING DATE: 2002-09-10
: PRIOR APPLICATION NUMBER: US/1011565
: CURRENT FILING DATE: 2002-09-10
: PRIOR APPLICATION NUMBER: US/1011565
: PRIOR FILING DATE: 1998-08-12
: PRIOR APPLICATION NUMBER: US/1011565
: PRIOR FILING DATE: 1998-08-12
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 29
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US 10 115-665-29

Query Match: 36.4%, Score 41, DB 12, Length 12;
Best Local Similarity: 100.0%, Pred. No. 76-02;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 INKK 7
DB 1 INKK 7

RESULT 30
US 10 172-4258-51
: Sequence 30, Application US/101724258
: Publication No. US20030147906A1
: GENERAL INFORMATION:
: APPLICANT: Kacmpter, Raymond
: APPLICANT: Akai, Gilla
: TITLE OF INVENTION: PROAD SPECTRUM ANTAGONISTS AND VACCINES
: TITLE OF INVENTION: PREPARED AGAINST PYROGENIC EXOTOXINS
: FILE REFERENCE: A31967-PCT USA A 066041.0164
: CURRENT APPLICATION NUMBER: US/101724258
: CURRENT FILING DATE: 2002-06-13
: PRIOR APPLICATION NUMBER: US/101724258
: PRIOR FILING DATE: 1998-09-10
: PRIOR APPLICATION NUMBER: PCT/IL77/00448
: PRIOR FILING DATE: 1997-12-30
: PRIOR APPLICATION NUMBER: ISRAEL 119948
: PRIOR FILING DATE: 1999-12-30
: NUMBER OF SEQ ID NOS: 57
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 51
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Streptococcus aureus
US 10 172-4258-51

Query Match: 36.4%, Score 41, DB 12, Length 12;
Best Local Similarity: 100.0%, Pred. No. 76-02;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 INKK 7
DB 1 INKK 7

RESULT 31
US 10 172-4258-51
: Sequence 31, Application US/101724258
: Publication No. US20030147906A1
: GENERAL INFORMATION:
: APPLICANT: Kacmpter, Raymond
: APPLICANT: Akai, Gilla
: TITLE OF INVENTION: PROAD SPECTRUM ANTAGONISTS AND VACCINES
: TITLE OF INVENTION: PREPARED AGAINST PYROGENIC EXOTOXINS
: FILE REFERENCE: A31967-PCT USA A 066041.0164
: CURRENT APPLICATION NUMBER: US/101724258
: CURRENT FILING DATE: 2002-06-13
: PRIOR APPLICATION NUMBER: US/101724258
: PRIOR FILING DATE: 1998-09-10
: PRIOR APPLICATION NUMBER: PCT/IL77/00448
: PRIOR FILING DATE: 1997-12-30
: PRIOR APPLICATION NUMBER: ISRAEL 119948
: PRIOR FILING DATE: 1999-12-30
: NUMBER OF SEQ ID NOS: 57
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO: 51
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Streptococcus aureus
US 10 172-4258-51

Query Match: 36.4%, Score 41, DB 12, Length 12;
Best Local Similarity: 100.0%, Pred. No. 76-02;
Matches: 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 INKK 7
DB 1 INKK 7

RESULT 32
US 10 339-645-41
: Sequence 41, Application US/10039645
: Publication No. US20020147170A1
: GENERAL INFORMATION:
: APPLICANT: Kellward, Thomas
: APPLICANT: Beckmeyer, Brian
: TITLE OF INVENTION: Constitutively Active, Hypersensitive,
: TITLE OF INVENTION: and NO: US20020147170A1 Functional Receptors as No. US200201

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FILE REFERENCE: 00398/510602
 CURRENT APPLICATION NUMBER: US/1997/011645
 CURRENT FILING DATE: 2001-10-26
 PRIOR APPLICATION NUMBER: US 63/243,550
 PRIOR FILING DATE: 2000-10-26
 NUMBER OF SEQ ID NOS: 87
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 41
 LENGTH: 12
 TYPE: PRT
 ORGANISM: Homo sapiens
 US 10 114 809 2

Query Match 66.4% Score 41 DB 14 Length 12
 Best Local Similarity 100.0% Prod. No. 787-443
 Matches 41 Conservative 0 Mismatches 0 Gaps 0

QY 1 AINX 4
 DB 2 AINX 5

RESULT 33
 US 10 114 809 2
 Sequence 33 Application US/1997/011645
 Patent No. US2002077574A
 GENERAL INFORMATION:
 APPLICANT: Mascherk, Hans, E.
 TITLE OF INVENTION: EXOTOXIN
 FILE REFERENCE: MHP-011XX
 CURRENT APPLICATION NUMBER: US/1997/011645
 CURRENT FILING DATE: 2002-03-29
 PRIOR APPLICATION NUMBER: US 63/243,550
 PRIOR FILING DATE: 2000-10-26
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 12
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Bacterially Expressed Protein
 US 10 114 809 2

Query Match 66.4% Score 41 DB 14 Length 12
 Best Local Similarity 100.0% Prod. No. 787-443
 Matches 41 Conservative 0 Mismatches 0 Gaps 0

QY 2 AINX 5
 DB 3 AINX 4

RESULT 44
 US 10 114 809 2
 Sequence 44 Application US/1997/011645
 Patent No. US2002077574A
 GENERAL INFORMATION:
 APPLICANT: Mascherk, Hans, E.
 TITLE OF INVENTION: EXOTOXIN
 FILE REFERENCE: MHP-011XX
 CURRENT APPLICATION NUMBER: US/1997/011645
 CURRENT FILING DATE: 2002-03-29
 PRIOR APPLICATION NUMBER: US 63/243,550
 PRIOR FILING DATE: 2000-10-26
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 2
 LENGTH: 12
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Bacterially Expressed Protein
 US 10 114 809 2

US 10 114 809 2

Query Match 66.4% Score 41 DB 14 Length 12
 Best Local Similarity 100.0% Prod. No. 787-443
 Matches 41 Conservative 0 Mismatches 0 Gaps 0

QY 2 AINX 5
 DB 3 AINX 4

RESULT 45
 US 10 114 809 2
 Sequence 45 Application US/1997/011645
 Patent No. US2002077574A
 GENERAL INFORMATION:
 APPLICANT: Mascherk, Hans, E.
 TITLE OF INVENTION: EXOTOXIN
 FILE REFERENCE: MHP-011XX
 CURRENT APPLICATION NUMBER: US/1997/011645
 CURRENT FILING DATE: 2002-03-29
 PRIOR APPLICATION NUMBER: US 63/243,550
 PRIOR FILING DATE: 2000-10-26
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO 41
 LENGTH: 12
 TYPE: PRT
 ORGANISM: Homo sapiens
 US 10 114 809 2

Query Match 66.4% Score 41 DB 15 Length 12
 Best Local Similarity 100.0% Prod. No. 787-443
 Matches 41 Conservative 0 Mismatches 0 Gaps 0

QY 1 AINX 4
 DB 2 AINX 5

RESULT 46
 US 09 150 947R 5
 Sequence 46 Application US/09/150,947R
 Patent No. US200202211A1
 GENERAL INFORMATION:
 APPLICANT: Kacper, Raymond
 APPLICANT: Alad, Gila
 TITLE OF INVENTION: BROAD SPECTRUM PYRAGENIC EXOTOXINS
 FILE REFERENCE: A1997 PCT/US/97/00438
 CURRENT APPLICATION NUMBER: US/09/150,947R
 CURRENT FILING DATE: 1998-09-15
 PRIOR APPLICATION NUMBER: PCT/IL97/00438
 PRIOR FILING DATE: 1997-12-30
 PRIOR APPLICATION NUMBER: ISRAEL 119938
 PRIOR FILING DATE: 1996-12-30
 NUMBER OF SEQ ID NOS: 2
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 5
 LENGTH: 13
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 FEATURE:
 NAME/KEY: LIP10
 LOCATION: (1) (1)
 OTHER INFORMATION: N-larryl cysteine residue
 US-09-150-947R 5

Query Match 66.4% Score 41 DB 9 Length 13
 Best Local Similarity 100.0% Prod. No. 787-443
 Matches 41 Conservative 0 Mismatches 0 Gaps 0

QY 2 INKK 5
1-11
DB 2 INKK 5

RESULT 47
US-10-120-604-59
Sequence 59, Application: US/10120604
Publication No. US2003096347A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYPEPTIDES ENCODING TWO NOVEL HUMAN G PROTEIN COUPLED R
FILE REFERENCE: A31957-PCT/US/A 01/01154
CURRENT APPLICATION NUMBER: US/10-120-604
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: US 60/284,145
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/284,161
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/288,468
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US 60/300,619
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE
NAME/KEY: LIPID
LOCATION: (1)...(1)
OTHER INFORMATION: N lauryl cysteine residues
US-10-120-604-59

Query Match 36.4%, Score 4; BB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 2 INKK 5
1-11
DB 2 INKK 5

RESULT 48
US-10-120-604-78
Sequence 25, Application: US/10120604
Publication No. US20030152946A1
GENERAL INFORMATION:
APPLICANT: SUMITOMO, Shigeomi
TITLE OF INVENTION: BH4-fused polypeptides
FILE REFERENCE: 1422-G5370
CURRENT APPLICATION NUMBER: US/10-120-604
CURRENT FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: JP 11-471449
PRIOR FILING DATE: 1999-12-27
PRIOR APPLICATION NUMBER: PCT/JP99/09293
PRIOR FILING DATE: 2000-12-26
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn version 4.1
SEQ ID NO 25
LENGTH: 13
TYPE: PRT
ORGANISM: Human T lymphocyte cell line
US-10-120-604-78

Query Match 36.4%, Score 4; BB 12; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 8 INKK 11

DB 4 INKK 7
1-11

RESULT 49
US-10-120-604-59
Sequence 59, Application: US/10120604
Publication No. US2003096347A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYPEPTIDES ENCODING TWO NOVEL HUMAN G PROTEIN COUPLED R
FILE REFERENCE: A31957-PCT/US/A 01/01154
CURRENT APPLICATION NUMBER: US 60/284,145
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: US 60/284,161
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/288,468
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US 60/300,619
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 226
SOFTWARE: PatentIn version 3.0
SEQ ID NO 59
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-120-604-59

Query Match 36.4%, Score 4; BB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 6 INKK 9
1-11
DB 6 INKK 9

RESULT 40
US-10-120-604-78
Sequence 78, Application: US/10120604
Publication No. US2003096347A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: POLYPEPTIDES ENCODING TWO NOVEL HUMAN G PROTEIN COUPLED R
FILE REFERENCE: A31957-PCT/US/A 01/01154
CURRENT APPLICATION NUMBER: US/10-120-604
CURRENT FILING DATE: 2002-04-11
PRIOR APPLICATION NUMBER: US 60/284,145
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/284,161
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: US 60/288,468
PRIOR FILING DATE: 2001-05-03
PRIOR APPLICATION NUMBER: US 60/300,619
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 226
SOFTWARE: PatentIn version 3.0
SEQ ID NO 78
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-120-604-78

Query Match 36.4%, Score 4; BB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 7.4e-02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 6 INKK 9
1-11

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DB: 6 INKK 5

RESULT 41
US-10-172-425B-22
? Sequence 22, Application: US/0172425B
? Publication No. US2003014790A1
? GENERAL INFORMATION:
? APPLICANT: Parag, Yoon
? APPLICANT: Barnes, Thomas M
? TITLE OF INVENTION: A NOVEL PEPTIDE RELATED TO BETA-LA CTAMINOLIN PEPTIDE
? FILE OF INVENTION: AND GENE THEREOF
? FILE REFERENCE: 07434-52521
? CURRENT APPLICATION NUMBER: US/0172425B
? CURRENT FILING DATE: 2001-02-14
? PRIOR APPLICATION NUMBER: US 09/487,442
? PRIOR FILING DATE: 1999-09-07
? PRIOR APPLICATION NUMBER: US 09/145,076
? PRIOR FILING DATE: 1998-09-01
? NUMBER OF SEQ ID NOS: 24
? SOFTWARE: Patent In Vet. 4.0
? SEQ ID NO 22
? LENGTH: 14
? TYPE: PPT
? ORGANISM: Streptococcus pyogenes
US-10-172-425B-22

Query Match
Best Local Similarity: 100.0% Score: 4 DB 12 Length: 14
Matches: 4 Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0

CY 2 INKK 5
  1 1 1
DB 3 INKK 6

RESULT 42
US-10-172-425B-26
? Sequence 26, Application: US/1172425B
? Publication No. US2003014790A1
? GENERAL INFORMATION:
? APPLICANT: Kaempfer, Raymond
? APPLICANT: Atad, Gila
? TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
? FILE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
? FILE REFERENCE: A31967-PCT-USA-A 066041.0164
? CURRENT APPLICATION NUMBER: US/0172425B
? CURRENT FILING DATE: 2002-06-14
? PRIOR APPLICATION NUMBER: US/09150,947
? PRIOR FILING DATE: 1998-09-10
? PRIOR APPLICATION NUMBER: PCT/1197/00438
? PRIOR FILING DATE: 1997-12-30
? PRIOR APPLICATION NUMBER: ISRAEL 119948
? PRIOR FILING DATE: 1996-12-30
? NUMBER OF SEQ ID NOS: 57
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 26
? LENGTH: 14
? TYPE: PPT
? ORGANISM: Streptococcus pyogenes
US-10-172-425B-26

Query Match
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Matches: 4 Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0

CY 2 INKK 5
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DB 3 INKK 6

RESULT 43
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? Sequence 27, Application: US/0172425B
? Publication No. US2003014790A1
? GENERAL INFORMATION:
? APPLICANT: Kaempfer, Raymond
? APPLICANT: Atad, Gila
? TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
? FILE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
? FILE REFERENCE: A31967-PCT-USA-A 066041.0164
? CURRENT APPLICATION NUMBER: US/0172425B
? CURRENT FILING DATE: 2002-06-14
? PRIOR APPLICATION NUMBER: US/150,947
? PRIOR FILING DATE: 1998-09-10
? PRIOR APPLICATION NUMBER: PCT/1197/00438
? PRIOR FILING DATE: 1997-12-30
? PRIOR APPLICATION NUMBER: ISRAEL 119948
? PRIOR FILING DATE: 1996-12-30
? NUMBER OF SEQ ID NOS: 57
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 27
? LENGTH: 14
? TYPE: PPT
? ORGANISM: Streptococcus pyogenes
US-10-172-425B-27

Query Match
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Matches: 4 Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0

CY 2 INKK 5
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DB 3 INKK 6

RESULT 45
US-10-172-425B-35
? Sequence 35, Application: US/0172425B
? Publication No. US2003014790A1
? GENERAL INFORMATION:
? APPLICANT: Kaempfer, Raymond
? APPLICANT: Atad, Gila
? TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
? FILE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
? FILE REFERENCE: A31967-PCT-USA-A 066041.0164
? CURRENT APPLICATION NUMBER: US/0172425B
? CURRENT FILING DATE: 2002-06-14
? PRIOR APPLICATION NUMBER: US/150,947
? PRIOR FILING DATE: 1998-09-10
? PRIOR APPLICATION NUMBER: PCT/1197/00438
? PRIOR FILING DATE: 1997-12-30
? PRIOR APPLICATION NUMBER: ISRAEL 119948
? PRIOR FILING DATE: 1996-12-30
? NUMBER OF SEQ ID NOS: 57
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 35
? LENGTH: 14
? TYPE: PPT
? ORGANISM: Staphylococcus aureus
US-10-172-425B-35

Query Match
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Matches: 4 Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0

CY 2 INKK 5
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DB 3 INKK 6

RESULT 46
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? Sequence 36, Application: US/0172425B
? Publication No. US2003014790A1
? GENERAL INFORMATION:

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1 CURRENT FILING DATE: 2002-09-12
2 PRIOR APPLICATION NUMBER: 09/150,047
3 PRIOR FILING DATE: 1998-09-16
4 PRIOR APPLICATION NUMBER: 09/117,270/00409
5 PRIOR FILING DATE: 1997-12-30
6 PRIOR APPLICATION NUMBER: ISRAEL 1,999,000
7 PRIOR FILING DATE: 1996-12-30
8 NUMBER OF SEQ ID NOS: 67
9 SOFTWARE: FASTSEQ for Windows Version 1.4
10 SEQ ID NO: 49
11 LENGTH: 14
12 TYPE: CDS
13 ORGANISM: Staphylococcus aureus
14 US 10,172,425B 48

Query Match
Best Local Similarity: 100.00
Percent Match: 100.00
Matches: 47 Conservative 0 Mismatches 0 Indels 0 Gaps

QY 2 INKK 5
DB 1 INKK 5
   4 INKK 5

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1 Sequence ID: Application: US/1,172,425B
2 Publication No: US20030147906A1
3 GENERAL INFORMATION:
4 APPLICANT: Kometec, Rayco Ltd
5 APPLICANT: Avram, Gila
6 TITLE OF INVENTION: BROAD SPECTRUM ANTIMICROBIAL VACCINES
7 TITLE OF INVENTION: DIRECTED AGAINST PNEUMONIA IN RATS
8 DATE REFERRED: 03/06/2003
9 CURRENT APPLICATION NUMBER: US/09/117,270
10 PRIOR APPLICATION NUMBER: 09/150,047
11 PRIOR FILING DATE: 1998-09-16
12 PRIOR APPLICATION NUMBER: 09/117,270
13 PRIOR FILING DATE: 1997-12-30
14 PRIOR APPLICATION NUMBER: ISRAEL 1,999,000
15 PRIOR FILING DATE: 1996-12-30
16 NUMBER OF SEQ ID NOS: 67
17 SOFTWARE: FASTSEQ for Windows Version 1.4
18 SEQ ID NO: 49
19 LENGTH: 14
20 TYPE: CDS
21 ORGANISM: Staphylococcus aureus
22 US 10,172,425B 50

Query Match
Best Local Similarity: 100.00
Percent Match: 100.00
Matches: 47 Conservative 0 Mismatches 0 Indels 0 Gaps

QY 2 INKK 5
DB 1 INKK 5
   4 INKK 5

Search Completed: September 30, 2003 11:07:18
Job File: 2003-09-30
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260	3	27.3	8	4	US-09-839-542B-158	Sequence 158, App	333	3	27.3	9	2	US-08-593-274B-5	Sequence 5, Appl1
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264	3	27.3	8	4	US-09-839-542B-162	Sequence 162, App	337	3	27.3	9	2	US-08-146-028-194	Sequence 194, App
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306	3	27.3	9	1	US-08-271-180A-14	Sequence 14, App	379	3	27.3	9	2	US-08-443-443B-116	Sequence 116, App
307	3	27.3	9	1	US-08-271-180A-15	Sequence 15, App	380	3	27.3	9	2	US-08-443-443B-116	Sequence 116, App
308	3	27.3	9	1	US-08-271-180A-16	Sequence 16, App	381	3	27.3	9	2	US-08-443-443B-116	Sequence 116, App
309	3	27.3	9	1	US-08-271-180A-17	Sequence 17, App	382	3	27.3	9	2	US-08-443-443B-116	Sequence 116, App
310	3	27.3	9	1	US-08-271-180A-18	Sequence 18, App	383	3	27.3	9	2	US-08-443-443B-116	Sequence 116, App
311	3	27.3	9	1	US-08-271-180A-19	Sequence 19, App	384	3	27.3	9	2	US-08-443-443B-116	Sequence 116, App
312	3	27.3	9	1	US-08-271-180A-20	Sequence 20, App	385	3	27.3	9	2	US-08-443-443B-116	Sequence 116, App
313	3	27.3	9	1	US-08-271-180A-21	Sequence 21, App	386	3	27.3	9	2	US-08-443-443B-116	Sequence 116, App
314	3	27.3	9	1	US-08-271-180A-22	Sequence 22, App	387	3	27.3	9	2	US-08-443-443B-116	Sequence 116, App
315	3	27.3	9	1	US-08-271-180A-23	Sequence 23, App	388	3	27.3	9	2	US-08-443-443B-116	Sequence 116, App
316	3	27.3	9	1	US-08-271-180A-24	Sequence 24, App	389	3	27.3	9	2	US-08-443-443B-116	Sequence 116, App
317	3	27.3	9	1	US-08-271-180A-25	Sequence 25, App	390	3	27.3	9	2	US-08-443-443B-116	Sequence 116, App
318	3	27.3	9	1	US-08-271-180A-26	Sequence 26, App	391	3	27.3	9	2	US-08-443-443B-116	Sequence 116, App
319	3	27.3	9	1	US-08-271-180A-27	Sequence 27, App	392	3	27.3	9	2	US-08-443-443B-116	Sequence 116, App

493	3	27.3	3	27.3	466	3	27.3	9	4	US 09-319-417-6	Sequence 6, Appli
494	3	27.3	4	27.3	467	4	27.3	9	4	US-09-319-417-7	Sequence 7, Appli
495	3	27.3	3	27.3	468	3	27.3	9	4	US-09-025-596-109	Sequence 109, App
496	3	27.3	3	27.3	469	3	27.3	9	4	US-09-227-357-66C	Sequence 160, App
497	3	27.3	3	27.3	470	3	27.3	9	4	US-08-637-654-132	Sequence 132, App
498	3	27.3	3	27.3	471	3	27.3	9	4	US-09-187-859-210	Sequence 210, App
499	3	27.3	3	27.3	472	3	27.3	9	4	US-09-187-859-280	Sequence 280, App
500	3	27.3	3	27.3	473	3	27.3	9	4	US-09-187-859-308	Sequence 308, App
501	3	27.3	3	27.3	474	3	27.3	9	4	US-09-187-859-403	Sequence 403, App
502	3	27.3	3	27.3	475	3	27.3	9	4	US-09-187-859-431	Sequence 431, App
503	3	27.3	3	27.3	476	3	27.3	9	4	US-09-187-859-473	Sequence 473, App
504	3	27.3	3	27.3	477	3	27.3	9	4	US-09-187-859-503	Sequence 503, App
505	3	27.3	3	27.3	478	3	27.3	9	4	US-09-187-859-1381	Sequence 1381, App
506	3	27.3	3	27.3	479	3	27.3	9	4	US-09-187-859-1411	Sequence 1411, App
507	3	27.3	3	27.3	480	3	27.3	9	4	US-09-187-859-1456	Sequence 1456, App
508	3	27.3	3	27.3	481	3	27.3	9	4	US-09-187-859-1486	Sequence 1486, App
509	3	27.3	3	27.3	482	3	27.3	9	4	US-09-187-859-1531	Sequence 1531, App
510	3	27.3	3	27.3	483	3	27.3	9	4	US-09-187-859-1576	Sequence 1576, App
511	3	27.3	3	27.3	484	3	27.3	9	4	US-09-187-859-1805	Sequence 1805, App
512	3	27.3	3	27.3	485	3	27.3	9	4	US-09-187-859-1820	Sequence 1820, App
513	3	27.3	3	27.3	486	3	27.3	9	4	US-09-187-859-1835	Sequence 1835, App
514	3	27.3	3	27.3	487	3	27.3	9	4	US-09-187-859-1850	Sequence 1850, App
515	3	27.3	3	27.3	488	3	27.3	9	4	US-09-187-859-1865	Sequence 1865, App
516	3	27.3	3	27.3	489	3	27.3	9	4	US-09-187-859-1883	Sequence 1883, App
517	3	27.3	3	27.3	490	3	27.3	9	4	US-09-187-859-1951	Sequence 1951, App
518	3	27.3	3	27.3	491	3	27.3	9	4	US-09-187-859-1978	Sequence 1978, App
519	3	27.3	3	27.3	492	3	27.3	9	4	US-09-187-859-2002	Sequence 2002, App
520	3	27.3	3	27.3	493	3	27.3	9	4	US-09-187-859-2028	Sequence 2028, App
521	3	27.3	3	27.3	494	3	27.3	9	4	US-09-187-859-2052	Sequence 2052, App
522	3	27.3	3	27.3	495	3	27.3	9	4	US-09-187-859-2081	Sequence 2081, App
523	3	27.3	3	27.3	496	3	27.3	9	4	US-09-187-859-2326	Sequence 2326, App
524	3	27.3	3	27.3	497	3	27.3	9	4	US-09-187-859-2386	Sequence 2386, App
525	3	27.3	3	27.3	498	3	27.3	9	4	US-09-187-859-2446	Sequence 2446, App
526	3	27.3	3	27.3	499	3	27.3	9	4	US-09-187-859-2506	Sequence 2506, App
527	3	27.3	3	27.3	500	3	27.3	9	5	PCT-US95/00147-40	Sequence 40, Appli

ALIGNMENTS

RESULT 1
 US-09-406-809-1
 : Sequence 1, Application US/064,6809
 : Patent No. 5580789
 : GENERAL INFORMATION:
 : APPLICANT: KIHRA, Yasuhiro I
 : TITLE OF INVENTION: IMMUNOGENIC POLYMER BINDING ARTIFICIAL
 : TITLE OF INVENTION: PROTEIN
 : NUMBER OF SEQUENCES: 11
 : CORRESPONDENT ADDRESS:
 : ADDRESSEE: Brody and Neitzak
 : STREET: 419 Seventh St., NW, Suite 300
 : CITY: Washington
 : STATE: DC
 : COUNTRY: USA
 : ZIP: 20004
 : COMPUTER READABLE FORM:
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC DOS/MS DOS
 : SOFTWARE: Patologic Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/064,6809
 : FILING DATE:
 : CLASSIFICATION: 547
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/064,680,477
 : FILING DATE: 24 MARCH 1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Tarzica, John E.
 : REGISTRATION NUMBER: 35,138
 : REFERENCE/ID# KEY NUMBER: K11174 1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-747-9529
 TELEX: 248634

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRUCTURE: single

FEATURES: linear

MOLECULE TYPE: peptide

US 08 409 800-1

Query Match 36.4% Score 4: DB 1: Length 9:

Best Local Similarity 100.0%: Pseq. No. 2500017

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 CORR 9

1 CORR 4

RESULT 4

US 09-007 288E 147

Sequence 14% Application US/09007288E

Patent No. 6495457

GENERAL INFORMATION:

APPLICANT: ELSA, Claus

APPLICANT: ELSA, Jens

APPLICANT: ELSA, Peter

APPLICANT: ELSA, Shant

APPLICANT: ELSA, Marianna

APPLICANT: ELSA, Allan

APPLICANT: ELSA, Kim

APPLICANT: ELSA, John

APPLICANT: ELSA, Lina

APPLICANT: ELSA, Torben

APPLICANT: ELSA, Jesper

APPLICANT: ELSA, Steen

TITLE OF INVENTION: NO. 6495457-1 Lipolytic Enzymes

FILE REFERENCE: 4455,434 US

CURRENT APPLICATION NUMBER: US/09-007,288E

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patent version 4.1

SEQ ID NO: 14

LENGTH: 9

TYPE: IR

STRUCTURE: Amino acid sequence

FEATURES: linear

TELECOMMUNICATION INFORMATION: Peptide (2002) 887-1500

US-09-007 288E 147

Query Match

Best Local Similarity 36.4% Score 4: DB 1: Length 9:

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 7 GRAP 10

1 GRAP 8

RESULT 4

US 08 129-970 17

Sequence 17% Application US/08129970

Patent No. 5502167

GENERAL INFORMATION:

APPLICANT: Lewis C. Cantley

APPLICANT: Zhou Song Yang

TITLE OF INVENTION: Substrate Specificity of Protein Kinases

NUMBER OF SEQUENCES: 77

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 45 STATE STREET, Suite 510

CITY: BOSTON

STATE: MASSACHUSETTS

COUNTRY: USA

ZIP: 02109-1876

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: ASCII text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/129,970

FILING DATE: JANUARY 7, 1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Gioia A. Jr.

REGISTRATION NUMBER: 41,503

REFERENCE/DOCKET NUMBER: B01-004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

STRUCTURE: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: Informal

US 08 178-573-17

Query Match 36.4% Score 4: DB 1: Length 9:

Best Local Similarity 100.0%: Pseq. No. 2,500,057

Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 4 CORR 9

1 CORR 4

RESULT 4

US 08 594 447 38

Sequence 38% Application US/08594447

Patent No. 5776716

GENERAL INFORMATION:

APPLICANT: Rod, David

APPLICANT: Napolitano, Eugene W.

APPLICANT: Vozobova, Anna P.

TITLE OF INVENTION: MECHANISM FOR IDENTIFYING AGENTS WHICH

TITLE OF INVENTION: BLOCK THE INTERACTION OF FYN WITH PKC-THETA, AND USES

NUMBER OF SEQUENCES: 75

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & MORRISON

STREET: 2000 Pennsylvania Avenue, NW - Ste. 5500

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20036 1828

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/594,447

FILING DATE: 31-JAN 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.

REGISTRATION NUMBER: 29,959

REFERENCE/DOCKET NUMBER: 22550-20025.24

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 887-1500

Query Match 36.4%, Score 4: DB 1: Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 4 KKG 7
 111
 5 KKG 8

DB

RESULT 5
 US-08-541-964 47
 Sequence 37, Application US/08/541-964
 Patent No. 5763425
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Dorit
 APPLICANT: Ron, Dorit
 APPLICANT: Kavar, Lawrence M
 APPLICANT: Napolitano, Eugene W
 TITLE OF INVENTION: A RAPID SCREENING METHOD FOR SELECTING
 TITLE OF INVENTION: OF SIGNAL TRANSDUCTION
 NUMBER OF SEQUENCES: 74
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & PIERSTER
 STREET: 2000 PENNSYLVANIA AVENUE, NW STE. 5500
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20006 1888
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #17 9/18 11/03
 CURRENT APPLICATION DATA:
 FILING DATE: 10-02-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Mulishlag, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 22550-2002-25
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-1508
 TELEFAX: 90 4030 MRSNFORWSH
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 NAME/KEY: Peptide
 LOCATION: 1..9
 OTHER INFORMATION: /label delta-V43

Query Match 36.4%, Score 4: DB 1: Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 4 KKG 7
 111
 5 KKG 8

DB

RESULT 5
 US-08-541-964 47
 Sequence 37, Application US/08/541-964
 Patent No. 5763425
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Dorit
 APPLICANT: Ron, Dorit
 APPLICANT: Kavar, Lawrence M
 APPLICANT: Napolitano, Eugene W
 TITLE OF INVENTION: A RAPID SCREENING METHOD FOR SELECTING
 TITLE OF INVENTION: OF SIGNAL TRANSDUCTION
 NUMBER OF SEQUENCES: 74
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & PIERSTER
 STREET: 2000 PENNSYLVANIA AVENUE, NW STE. 5500
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20006 1888
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #17 9/18 11/03
 CURRENT APPLICATION DATA:
 FILING DATE: 10-02-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Mulishlag, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 22550-2002-25
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-1508
 TELEFAX: 90 4030 MRSNFORWSH
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 NAME/KEY: Peptide
 LOCATION: 1..9
 OTHER INFORMATION: /label delta-V43

Query Match 36.4%, Score 4: DB 1: Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 4 KKG 7
 111
 5 KKG 8

DB

RESULT 5
 US-08-541-964 47
 Sequence 37, Application US/08/541-964
 Patent No. 5763425
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Dorit
 APPLICANT: Ron, Dorit
 APPLICANT: Kavar, Lawrence M
 APPLICANT: Napolitano, Eugene W
 TITLE OF INVENTION: A RAPID SCREENING METHOD FOR SELECTING
 TITLE OF INVENTION: OF SIGNAL TRANSDUCTION
 NUMBER OF SEQUENCES: 74
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & PIERSTER
 STREET: 2000 PENNSYLVANIA AVENUE, NW STE. 5500
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20006 1888
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #17 9/18 11/03
 CURRENT APPLICATION DATA:
 FILING DATE: 10-02-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Mulishlag, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 22550-2002-25
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-1508
 TELEFAX: 90 4030 MRSNFORWSH
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 NAME/KEY: Peptide
 LOCATION: 1..9
 OTHER INFORMATION: /label delta-V43

Query Match 36.4%, Score 4: DB 2: Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 4 KKG 7
 111
 5 KKG 8

DB

RESULT 7
 US-08-541-964 47
 Sequence 17, Application US/08/541-964
 Patent No. 5763425
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Dorit
 APPLICANT: Ron, Dorit
 APPLICANT: Kavar, Lawrence M
 APPLICANT: Napolitano, Eugene W
 TITLE OF INVENTION: A RAPID SCREENING METHOD FOR SELECTING
 TITLE OF INVENTION: OF SIGNAL TRANSDUCTION
 NUMBER OF SEQUENCES: 74
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & PIERSTER
 STREET: 2000 PENNSYLVANIA AVENUE, NW STE. 5500
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20006 1888
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #17 9/18 11/03
 CURRENT APPLICATION DATA:
 FILING DATE: 10-02-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Mulishlag, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 22550-2002-25
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-1508
 TELEFAX: 90 4030 MRSNFORWSH
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 NAME/KEY: Peptide
 LOCATION: 1..9
 OTHER INFORMATION: /label delta-V43

Query Match 36.4%, Score 4: DB 2: Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

QY 4 KKG 7
 111
 5 KKG 8

DB

RESULT 7
 US-08-541-964 47
 Sequence 17, Application US/08/541-964
 Patent No. 5763425
 GENERAL INFORMATION:
 APPLICANT: Mochly-Rosen, Dorit
 APPLICANT: Ron, Dorit
 APPLICANT: Kavar, Lawrence M
 APPLICANT: Napolitano, Eugene W
 TITLE OF INVENTION: A RAPID SCREENING METHOD FOR SELECTING
 TITLE OF INVENTION: OF SIGNAL TRANSDUCTION
 NUMBER OF SEQUENCES: 74
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & PIERSTER
 STREET: 2000 PENNSYLVANIA AVENUE, NW STE. 5500
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20006 1888
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #17 9/18 11/03
 CURRENT APPLICATION DATA:
 FILING DATE: 10-02-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Mulishlag, Kate H.
 REGISTRATION NUMBER: 29,959
 REFERENCE/DOCKET NUMBER: 22550-2002-25
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 887-1500
 TELEFAX: (202) 887-1508
 TELEFAX: 90 4030 MRSNFORWSH
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 NAME/KEY: Peptide
 LOCATION: 1..9
 OTHER INFORMATION: /label delta-V43

11: 5:GRR 6

RESULT 11
US 09-208-960-55

1: Sequence 55, Application US/09-960-55
1: Patent No. 6251355

1: ORGANISM: Human

1: TITLE OF INVENTION: ANTI-POLIO-GEN SYNTHETIC PEPTIDE

1: FILE REFERENCE: 4888/1742

1: CURRENT APPLICATION NUMBER: US/09-208-960-55

1: EARLIER FILING DATE: 1998-12-18

1: EARLIER APPLICATION NUMBER: 602,000,416

1: EARLIER FILING DATE: 1998-04-29

1: EARLIER APPLICATION NUMBER: 602,000,416

1: EARLIER FILING DATE: 1997-12-16

1: NUMBER OF SEQ ID NOS: 57

1: SOFTWARE: Patent In Ver. 2.0

1: SEQ ID NO: 55

1: LENGTH: 11

1: TYPE: PPT

1: ORGANISM: Human

US 09-208-960-55

Query Match: 96.4%, Score: 41, DB: 5, Length: 11,
Best Local Similarity: 100.0%, Pos. No. 2, 46+02,
Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps:

Q7: 8 RRR 11

11: 111

14: 4 RRR 7

RESULT 12

US 09-208-960-57

1: Sequence 57, Application US/09-960-57
1: Patent No. 6251356

1: ORGANISM: Human

1: TITLE OF INVENTION: ANTI-POLIO-GEN SYNTHETIC PEPTIDE

1: FILE REFERENCE: 4888/1742

1: CURRENT APPLICATION NUMBER: US/09-208-960-57

1: EARLIER FILING DATE: 1998-12-18

1: EARLIER APPLICATION NUMBER: 602,000,416

1: EARLIER FILING DATE: 1997-12-16

1: EARLIER APPLICATION NUMBER: 602,000,416

1: NUMBER OF SEQ ID NOS: 57

1: SOFTWARE: Patent In Ver. 2.0

1: SEQ ID NO: 57

1: LENGTH: 11

1: TYPE: PPT

1: ORGANISM: Human

US 09-208-960-57

Query Match: 96.4%, Score: 41, DB: 5, Length: 11,
Best Local Similarity: 100.0%, Pos. No. 2, 46+02,
Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps:

Q7: 8 RRR 11

11: 111

14: 4 RRR 7

RESULT 13

US 09-208-960-57

1: Sequence 57, Application US/09-443-116

1: Patent No. 6251374

1: ORGANISM: Human

1: TITLE OF INVENTION: CARACTER P-48 IN A V

1: FILE REFERENCE: 411, 1883

1: FILE REFERENCE: 411, 1883

1: FILE REFERENCE: 411, 1883

1: FILE REFERENCE: 411, 1883

1: FILE REFERENCE: 411, 1883

1: FILE REFERENCE: 411, 1883

1: FILE REFERENCE: 411, 1883

1: CURRENT APPLICATION NUMBER: US/09-443-411A

1: CURRENT FILING DATE: 1998-04-19

1: NUMBER OF SEQ ID NOS: 10

1: SOFTWARE: Patent In Ver. 2.0

1: SEQ ID NO: 7

1: LENGTH: 11

1: TYPE: PPT

1: ORGANISM: Human

1: TITLE OF INVENTION: CARACTER P-48 IN A V

1: FILE REFERENCE: 411, 1883

1: FILE REFERENCE: 411, 1883

1: FILE REFERENCE: 411, 1883

1: FILE REFERENCE: 411, 1883

1: FILE REFERENCE: 411, 1883

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1: FILE REFERENCE: 411, 1883

1: FILE REFERENCE: 411, 1883

1: FILE REFERENCE: 411, 1883

1: FILE REFERENCE: 411, 1883

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1: FILE REFERENCE: 411, 1883

1 CURRENT APPLICATION DATA:
 2 APPLICATION NUMBER: US/07/247,617
 3 FILING DATE: 20-SEP-1986
 4 PRIORITY APPLICATION DATA:
 5 APPLICATION NUMBER: 102,180
 6 FILING DATE: 29-SEP-1987
 7 SEQ ID NO: 12
 8 LENGTH: 11
 9 6224254 12

Query Match 36.4% Score 4 DB 2 Length 12
 Best Local Similarity 100.0% Pred. No. 2.5e-02
 Matches 4: Conservative 0: Mismatches 0: Indels

QY 6 TGR 9
 DB 4 TGR 7

RESULT 16
 US-08-756-989B-7
 Sequence 7, Application US/08/96984
 Patent No. 585476
 GENERAL INFORMATION:

1 APPLICANT: MacLennan, A. John
 2 TITLE OF INVENTION: Molecular Cloning and Expression of
 3 G-Protein Coupled Receptors
 4 NUMBER OF SEQUENCES: 14
 5 CORRESPONDENCE ADDRESS:
 6 ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
 7 STREET: 2421 N.W. 41st Street, Suite A-1
 8 CITY: Gainesville
 9 STATE: FL
 10 COUNTRY: US
 11 ZIP: 32606

12 COMPUTER READABLE FORM:
 13 COMPUTER: IBM PC compatible
 14 OPERATING SYSTEM: PC DOS/MS-DOS
 15 SOFTWARE: Patent In Release #1.0, Version #1.25
 16 CURRENT APPLICATION DATA:
 17 APPLICATION NUMBER: US/08/796,936
 18 FILING DATE: 15-FEB-1994
 19 CLASSIFICATION: 546

20 ATTORNEY/AGENT INFORMATION:
 21 NAME: Lloyd, Jeff
 22 REGISTRATION NUMBER: 45,589
 23 REFERENCE/DOCKET NUMBER: MAC 100C1
 24 TELECOMMUNICATION INFORMATION:
 25 TELEPHONE: 352-375-8100
 26 TELEFAX: 352-372-5800
 27 INFORMATION FOR SEQ ID NO: 7:
 28 SEQUENCE CHARACTERISTICS:
 29 LENGTH: 12 amino acids
 30 TYPE: amino acid
 31 TOPOLOGY: linear
 32 MOLECULE TYPE: peptide
 33 US-08-796-989B-7

Query Match 36.4% Score 4 DB 2 Length 12
 Best Local Similarity 100.0% Pred. No. 2.5e-02
 Matches 4: Conservative 0: Mismatches 0: Indels

QY 6 TGR 9
 DB 7 TGR 10

RESULT 17
 US-08-760-936-7
 Sequence 7, Application US/08/760943
 Patent No. 585643
 GENERAL INFORMATION:

1 APPLICANT: MacLennan, A. John
 2 TITLE OF INVENTION: Molecular Cloning and Expression of
 3 G-Protein Coupled Receptors
 4 NUMBER OF SEQUENCES: 14
 5 CORRESPONDENCE ADDRESS:
 6 ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
 7 STREET: 2421 N.W. 41st Street, Suite A-1
 8 CITY: Gainesville
 9 STATE: FL
 10 COUNTRY: US
 11 ZIP: 32606

12 COMPUTER READABLE FORM:
 13 COMPUTER: IBM PC compatible
 14 OPERATING SYSTEM: PC DOS/MS-DOS
 15 SOFTWARE: Patent In Release #1.0, Version #1.25
 16 CURRENT APPLICATION DATA:
 17 APPLICATION NUMBER: US/08/796,936
 18 FILING DATE: December 6, 1996
 19 CLASSIFICATION: 546

20 ATTORNEY/AGENT INFORMATION:
 21 NAME: Pace, Brian R.
 22 REGISTRATION NUMBER: 48,261
 23 REFERENCE/DOCKET NUMBER: MAC 100C1
 24 TELECOMMUNICATION INFORMATION:
 25 TELEPHONE: 352-375-8100
 26 TELEFAX: 352-372-5800
 27 INFORMATION FOR SEQ ID NO: 7:
 28 SEQUENCE CHARACTERISTICS:
 29 LENGTH: 12 amino acids
 30 TYPE: amino acid
 31 TOPOLOGY: linear
 32 MOLECULE TYPE: peptide
 33 US-08-796-936-7

Query Match 46.4% Score 4 DB 2 Length 12
 Best Local Similarity 100.0% Pred. No. 2.5e-02
 Matches 4: Conservative 0: Mismatches 0: Indels

QY 6 TGR 9
 DB 7 TGR 10

RESULT 18
 US-08-752-852A-221
 Sequence 221, Application US/08/752852A
 Patent No. 5944306
 GENERAL INFORMATION:

1 APPLICANT: Grant, Conway
 2 APPLICANT: Gu, Chao-Liang
 3 APPLICANT: Gwyn, Jie
 4 APPLICANT: Stelberger, Deborah
 5 APPLICANT: Leibel, Robert
 6 APPLICANT: Barish, Sylvia
 7 TITLE OF INVENTION: FINE TUNED PROTEOLINS
 8 NUMBER OF SEQUENCES: 242
 9 CORRESPONDENCE ADDRESS:
 10 ADDRESSEE: PENNIE & FORDMANS LLP
 11 STREET: 1155 Avenue of the Americas
 12 CITY: New York
 13 STATE: NY
 14 COUNTRY: USA
 15 ZIP: 10036-2711

16 COMPUTER READABLE FORM:
 17 MEDIUM TYPE: Diskette
 18 COMPUTER: IBM compatible
 19 OPERATING SYSTEM: DOS
 20 SOFTWARE: FASTSEQ Version 2.0
 21 CURRENT APPLICATION DATA:
 22 APPLICATION NUMBER: US/08/752,852A
 23 FILING DATE: 21-NOV-1996
 24 CLASSIFICATION: 435

PRIOR APPLICATION DATA:

1 FILING DATE:
 2 ATTORNEY/AGENT INFORMATION:
 3 NAME: CORUZZI, CATARA A.
 4 REGISTRATION NUMBER: 30,742
 5 REFERENCE/OFFSET NUMBER: 0002, 14, 999
 6 TELECOMMUNICATION INFORMATION:
 7 TELEPHONE: 212-790-9090
 8 TELEFAX: 212-869-4742
 9 TELEX: 86241
 10 INFORMATION FOR SEQ ID NO: 1
 11 SEQUENCE CHARACTERISTICS:
 12 LENGTH: 12 amino acids
 13 TYPE: amino acid
 14 STRANDEDNESS: unknown
 15 TOPLOGY: unknown
 16 MOLECULE TYPE: peptide
 17 US 08 752 052A 221

Query Match: 96.4% Score 41 DB 4: Length 12;
 Best Local Similarity: 100.0% Pred. No. 2.5e+02;
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EPPR 1

LD 4 EPPR 7

RESULT 19

1 US-09-725-024-7
 2 Sequence No. Application US/9225624

3 Filing Date: 05/24/94
 4 General Information:
 5 Applicant: MacGowan, A. John
 6 Title of Invention: Method and apparatus for
 7 Title of Invention: G-Protein coupled receptor
 8 Number of Sequences: 16
 9 Correspondence Address:
 10 Addressee: Saltwater, Lloyd S Saltwater
 11 Street: 441 N.W. 41st Street, Suite 511
 12 City: Gainesville
 13 State: FL
 14 Country: US

15 ZIP: 32608
 16 Computer Readable Form:
 17 Medium Type: Floppy disk
 18 Computer: IBM PC compatible
 19 Operating System: PC DOS/MS-DOS
 20 Software: WordPerfect 5.1
 21 Current Application Data:
 22 Application Number: US/9225624
 23 Filing Date: 05/24/94
 24 Classification: 435
 25 Prior Application Data:

26 Application Number: 08/752052A
 27 Filing Date: 05-Dec-1996
 28 Prior Application Data:
 29 Application Number: 08/752052A
 30 Filing Date: 15-Feb-1994
 31 Attorney/Agent Information:
 32 Name: Peter Dorian R.
 33 Registration Number: 98,291
 34 Reference/Offset Number: 9A, 10, 11
 35 Telecommunication Information:
 36 Telephone: 452-375-8126
 37 Telefax: 452-372-5808

38 INFORMATION FOR SEQ ID NO: 7
 39 SEQUENCE CHARACTERISTICS:
 40 LENGTH: 12 amino acids
 41 TYPE: amino acid
 42 Topology: linear
 43 MOLECULE TYPE: peptide

US-09-725-024-7

Query Match: 96.4% Score 41 DB 4: Length 12;
 Best Local Similarity: 100.0% Pred. No. 2.5e+02;
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPPR 1

LD 7 EPPR 10

RESULT 20

1 US-08-061-889-10
 2 Sequence No. Application US/98061889

3 Filing Date: 05/04/98
 4 General Information:
 5 Applicant: Lerman, Michael J., Latif,
 6 Title of Invention: VON HIPPEL-LINER, MARSTON
 7 Title of Invention: DISEASE GENE AND CORRESPONDING CUNA AND
 8 Title of Invention: METHODS FOR DETECTING CARRIERS OF THE VIL
 9 Title of Invention: DISEASE GENE
 10 Number of Sequences: 20
 11 Correspondence Address:
 12 Addressee: Morgan S. Finnegan
 13 Street: 145 PARK AVENUE
 14 City: NEW YORK
 15 State: NEW YORK
 16 Country: USA
 17 ZIP: 10014
 18 Computer Readable Form:
 19 Medium Type: Floppy disk
 20 Computer: IBM PC compatible
 21 Operating System: PC DOS/MS-DOS
 22 Software: WordPerfect 5.1
 23 Current Application Data:
 24 Application Number: US/98/061,889
 25 Filing Date: 14 MAY 1997
 26 Classification: 435
 27 Attorney/Agent Information:
 28 Name: RICHARD W. BOER
 29 Registration Number: 96,459
 30 Reference/Offset Number: 3626, 4, 78
 31 Telecommunication Information:
 32 Telephone: (212) 756,4800
 33 Telefax: (212) 756,6849
 34 Telex: 42179Z
 35 Information for Seq ID No: 101
 36 Sequence Characteristics:
 37 Length: 14 amino acid residues
 38 Type: amino acid
 39 Strandedness: unknown
 40 Topology: unknown
 41 Molecule Type: unknown

US 08 061 889 10

Query Match: 96.4% Score 41 DB 1: Length 13;
 Best Local Similarity: 100.0% Pred. No. 2.7e+02;
 Matches 4: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 EPPR 9

LD 2 EPPR 5

RESULT 21

1 US-08-482-611-0
 2 Sequence No. Application US/98482611

3 Filing Date: 05/04/98
 4 General Information:
 5 Applicant: Lerman, Michael J., Latif,
 6 Title of Invention: VON HIPPEL-LINER, MARSTON
 7 Title of Invention: DISEASE GENE AND CORRESPONDING CUNA AND

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1 TITLE OF INVENTION: METHODS FOR DETECTING CARRIERS OF THE VHL
2 TITLE OF INVENTION: DISEASE GENE
3 NUMBER OF SEQUENCES: 20
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: MORGAN & FINNEGAN
6 STREET: 345 PARK AVENUE
7 CITY: NEW YORK
8 STATE: NEW YORK
9 ZIP: 10154
10 COUNTRY: USA
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: FLOPPY DISK
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: WORDPERFECT 5.1
15 CURRENT APPLICATION DATA:
16 APPLICATION NUMBER: US/08/442,611
17 FILING DATE: 05-JUNE 1995
18 CLASSIFICATION: 435
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 08/041,489
21 FILING DATE: 14 MAY 1993
22 CLASSIFICATION: 435
23 ATTORNEY/AGENT INFORMATION:
24 NAME: RICHARD W. BORK
25 REGISTRATION NUMBER: 36,457
26 REFERENCE/DOCKET NUMBER: 2026-407803
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: (212) 758-4800
29 TELEFAX: (212) 751-6849
30 TELEX: 422792
31 INFORMATION FOR SEQ ID NO: 10:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 13 amino acid residues
34 TYPE: amino acid
35 SPANADDRESS: unknown
36 TAG: unknown
37 US 08-442-611-10
38
39 Query Match 36.48% Score 41 DB 11 Length 13
40 Best Local Similarity 100.0% Pred. No. 2 787-443
41 Matches 4: Conservative 0: Mismatches 0: Indels 0:
42
43 QY 4 TORR 9
44 111
45 2 TORR 5
46
47 RESULT 22
48 US 08-751-767A-64
49 Sequence 64, Application US/08/751767A
50 Patent No. 594104
51 GENERAL INFORMATION:
52 APPLICANT: ANDERSON, ROBERT G.
53 APPLICANT: GRANT, HUGH
54 APPLICANT: MACDONALD, IAN D.
55 TITLE OF INVENTION: INTERLEUKIN-12 SUBUNIT PROTEIN
56 NUMBER OF SEQUENCES: 80
57 CORRESPONDENCE ADDRESS:
58 ADDRESSEE: NIXON & VANDERKIEF, P.C.
59 STREET: 1103 NORTH GLEBE ROAD
60 CITY: ARLINGTON
61 STATE: VA
62 COUNTRY: USA
63 ZIP: 22201
64 COMPUTER READABLE FORM:
65 MEDIUM TYPE: Floppy disk
66 COMPUTER: IBM PC compatible
67 OPERATING SYSTEM: PC-DOS/MS-DOS
68 SOFTWARE: PatentIn Release #1.0, Version #1.0.0
69 CURRENT APPLICATION DATA:
70 APPLICATION NUMBER: US/08/751,767A
71 FILING DATE: 08-NOV-1995

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1 CLASSIFICATION: 536
2 ATTORNEY/AGENT INFORMATION:
3 NAME: SADOFF, R.J.
4 REGISTRATION NUMBER: 36,563
5 REFERENCE/DOCKET NUMBER: 117-221
6 TELECOMMUNICATION INFORMATION:
7 TELEPHONE: 7038164091
8 TELEFAX: 7038164100
9 INFORMATION FOR SEQ ID NO: 64:
10 SEQUENCE CHARACTERISTICS:
11 LENGTH: 13 amino acids
12 TYPE: amino acid
13 TOPOLOGY: linear
14 MOLECULE TYPE: protein
15 US-08-751-767A-64
16
17 Query Match 36.48% Score 41 DB 2 Length 13
18 Best Local Similarity 100.0% Pred. No. 2 787-02
19 Matches 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
20
21 QY 6 TORR 9
22 111
23 6 TORR 9
24
25 RESULT 23
26 US-08-623-4280-36
27 Sequence 36, Application US/08/6234280
28 Patent No. 6312890
29 GENERAL INFORMATION:
30 APPLICANT: W. MARSTON LINEHAN, MICHAEL
31 LERNAN, FARIDA LATIF AND BERTON
32 ZHAK
33 TITLE OF INVENTION: PARTIAL INTRON SEQUENCE
34 OF VHL DISEASE GENE AND ITS USE IN DIAGNOSIS
35 OF DISEASE CARRIERS
36 NUMBER OF SEQUENCES: 63
37 CORRESPONDENCE ADDRESS:
38 ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
39 STREET: 345 PARK AVENUE
40 CITY: NEW YORK
41 STATE: NEW YORK
42 COUNTRY: USA
43 ZIP: 10154
44 COMPUTER READABLE FORM:
45 MEDIUM TYPE: FLOPPY DISK
46 OPERATING SYSTEM: IBM PC COMPATIBLE
47 SOFTWARE: MICROSOFT WORD 97
48 CURRENT APPLICATION DATA:
49 APPLICATION NUMBER: US/08/623,428
50 FILING DATE: 05-Sep-2000
51 PRIOR APPLICATION DATA:
52 APPLICATION NUMBER: 08/623,428
53 FILING DATE: MARCH 28, 1996
54 APPLICATION NUMBER: 08/061,889
55 FILING DATE: May 14, 1993
56 ATTORNEY/AGENT INFORMATION:
57 NAME: KATHY M. BROWN
58 REGISTRATION NUMBER: 34,556
59 REFERENCE/DOCKET NUMBER: 2026-407803
60 TELECOMMUNICATION INFORMATION:
61 TELEPHONE: (212) 758-4800
62 TELEFAX: (212) 751-6849
63 TELEX: 422792
64 INFORMATION FOR SEQ ID NO: 36:
65 SEQUENCE CHARACTERISTICS:
66 LENGTH: 13 amino acids
67 TYPE: amino acid
68 TOPOLOGY: linear
69 SEQUENCE DESCRIPTION: SEQ ID NO: 36:
70 US-08-623-4280-36

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Country Ref ID: 26.48, Score: 4, Pos: 4, Length: 10
Best Local Similarity: 100.0%, Pos: 1, Length: 10
Matches: 4, Conservative: 0, Read: 0, Gaps: 0

23 100% 9
24 100% 5

RESULT 24
Sequence 10: Application 10/US-4-1994
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN
SERVICES
TITLE OF INVENTION: VIRAL HEPATITIS (VIRAL)
TITLE OF INVENTION: DISEASE GENE AND VACCINE
TITLE OF INVENTION: METHODS FOR DETECTING CARRIERS OF THE VIR
TITLE OF INVENTION: DISEASE GENE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: MORGAN & FINKEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10017
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: MICROPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 10/US-4-1994
FILING DATE: 12-MAY-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/061,449
FILING DATE: 14-MAY-1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: RICHARD W. BORK
SEQUENCE/ALIGNMENT NUMBER: 4,459
SEQUENCE/ALIGNMENT NUMBER: 4,459
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4440
TELEFAX: (212) 751-6614
INTERNET: 421712
ADDRESSER: RICHARD W. BORK, JR.
SPECIFIC CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 4,459
TYPE: amino acid
MEDIUM TYPE: floppy disk
CORRESPONDENCE ADDRESS:
ADDRESSER: UNKNOWN
STREET: UNKNOWN
CITY: UNKNOWN
STATE: UNKNOWN
COUNTRY: UNKNOWN
ZIP: UNKNOWN
US-4-1994-10
Country Ref ID: 26.48, Score: 4, Pos: 4, Length: 10
Best Local Similarity: 100.0%, Pos: 1, Length: 10
Matches: 4, Conservative: 0, Read: 0, Gaps: 0

23 100% 9
24 100% 5

RESULT 25
Sequence 10: Application US/09-4-1994
GENERAL INFORMATION:
APPLICANT: CHRISTOPHER P.
APPLICANT: PIERCE, FENNER & SMITH

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APPLICANT: SRI, JESSE
TITLE OF INVENTION: METHOD OF REPERFUSION INJURY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSER: BEVEY, WILLIAMS, TIMMONS & COLLINS
STREET: 2425 GRAND BLVD., SUITE 400
CITY: KANSAS CITY
STATE: MO
COUNTRY: USA
ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.50
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,975
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/802,406
FILING DATE: 18-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COLLINS, JOHN M.
SEQUENCE/ALIGNMENT NUMBER: 26,262
SEQUENCE/ALIGNMENT NUMBER: 25580-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 816/474-9050
TELEFAX: 816/474-9057
INTERNET: 41
SEQUENCE CHARACTERISTICS:
LENGTH: 24 amino acids
TYPE: amino acid
MEDIUM TYPE: floppy disk
CORRESPONDENCE ADDRESS:
ADDRESSER: UNKNOWN
STREET: UNKNOWN
CITY: UNKNOWN
STATE: UNKNOWN
COUNTRY: UNKNOWN
ZIP: UNKNOWN
US-09-024-975-4
Country Match: 26.48, Score: 4, Pos: 3, Length: 14
Best Local Similarity: 100.0%, Pos: 1, Length: 14
Matches: 4, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

23 100% 11
24 100% 5

RESULT 26
Sequence 10: Application 09/US-4-1994
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: POLYMER AS A SPECIFIC LEAD FOR PCR
NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.50 (EP-0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,006
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/1100,000-11
FILING DATE: 12-JUN-1994
INFORMATION FOR SEQUENCING:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
SEQUENCE/ALIGNMENT NUMBER: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: UNKNOWN
STREET: UNKNOWN
CITY: UNKNOWN
STATE: UNKNOWN
COUNTRY: UNKNOWN
ZIP: UNKNOWN
US-09-081-006-11

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Query Match: 46.4%, Score 4: 1b 4: Length 14:
Best Local Similarity: 100.0%, Prod. No. 2.8e+02
Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 6 GRRP 9
ID 111
10 10 GRRP 13

RESULT 27
US 09-787-443-9-17
Sequence 17: Application US/09-06077
Patent No. 6,543,949
GENERAL INFORMATION:
APPLICANT: Per Antonsson, Per Bjork, Mikael Eriksson,
APPLICANT: Johan Hansson, Torje Karlsson, Lars
APPLICANT: Abrahamson and Goran Forsberg
TITLE OF INVENTION: MODIFIED/HUMANIZED SUPPLEMENTARY
TITLE OF INVENTION: AND THEIR USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Traveler, Hewlett, Kimberly S. Kasper
STREET: 1177 West Loop South, Suite 1000
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/014475
FILING DATE: March 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Kellum, Paul E.
REGISTRATION NUMBER: 25,499
REFERENCE/AGENT INFORMATION:
TELEPHONE: 713-850-3165
TELEFAX: 713-850-3165
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPLOGY: unknown
MOLECULE TYPE: peptide
PCT: US95-06077

Query Match: 46.4%, Score 4: 1b 4: Length 14:
Best Local Similarity: 100.0%, Prod. No. 2.8e+02
Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 2 INKK 5
ID 111
10 10 INKK 13

RESULT 28
PCT US95-06077-7
Sequence 7: Application: PC/TUS9506077
GENERAL INFORMATION:
APPLICANT: Immunobiology Research, Inc.
TITLE OF INVENTION: Vaccine for the treatment of malaria
TITLE OF INVENTION: Transfection of genes for the production of
TITLE OF INVENTION: and other characterizing data that viruses
TITLE OF INVENTION: Incorporated into a vector
NUMBER OF SEQUENCES: 38

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CORRESPONDENCE ADDRESS:
ADDRESSEE: Jensen and Rosen,
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 15477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/US95/06077
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/247,991
FILING DATE: 23-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bok, Mary E.
REGISTRATION NUMBER: 41,215
REFERENCE/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9209
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPLOGY: unknown
MOLECULE TYPE: peptide
PCT: US95-06077-7

Query Match: 46.4%, Score 4: 1b 5: Length 14:
Best Local Similarity: 100.0%, Prod. No. 2.8e+02
Matches: 4: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

QY 8 GRRP 11
ID 111
10 7 GRRP 10

RESULT 29
US 09-787-443-9-14
Sequence 14: Application US/09-06077-14
Patent No. 6,543,949
GENERAL INFORMATION:
APPLICANT: ELLER, JEFFREY S.; EGGELMAN, BRUCE M.; ROSEN,
BRADLEY M.; WHITE, JYLIN S.
TITLE OF INVENTION: RNA ENCODING HUMAN ADIPSIN WITH COMPLEMENT
ACTIVITY
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/277,943
FILING DATE: 20-NOV-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 34,203
FILING DATE: 02-APR-1997
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
US 09-787-443-9-14
Sequence 14: Application US/09-06077-14
Patent No. 6,543,949
GENERAL INFORMATION:
APPLICANT: Immunobiology Research, Inc.
TITLE OF INVENTION: Vaccine for the treatment of malaria
TITLE OF INVENTION: Transfection of genes for the production of
TITLE OF INVENTION: and other characterizing data that viruses
TITLE OF INVENTION: Incorporated into a vector
NUMBER OF SEQUENCES: 38

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1 Patent No. 5486547
2 GENERAL INFORMATION:
3 APPLICANT: LAFITA, SYDNEY K
4 APPLICANT: KALIVAPERUMAL, Arunach.
5 TITLE OF INVENTION: LOCALIZATION OF MAJOR PROTEIN AND ENZYME PLETHORAS IN NON-PROTEINOLYTIC
6 TITLE OF INVENTION: LOCALIZATION OF MAJOR PROTEIN AND ENZYME PLETHORAS IN NON-PROTEINOLYTIC
7 FILE REFERENCE: 290 LAB. (3662 6/7)
8 CURRENT APPLICATION NUMBER: US/97/011101
9 CURRENT FILING DATE: 2000 04 28
10 PRIOR APPLICATION NUMBER: 08 60/111111
11 PRIOR FILING DATE: 1999 04 28
12 NUMBER OF SEQ ID NOS: 41
13 SOFTWARE: PATENTED VERSION 3.1
14 SEQ ID NO: 10
15 LENGTH: 15
16 TYPE: PRO
17 ORGANISM: Artificial Sequence
18 FEATURES
19 OTHER INFORMATION: History (1)
20 US 97 06 490E-10
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1 APPLICANT: Ausich, Rodney L.
 2 APPLICANT: Brinkhaus, Friedrich E.
 3 APPLICANT: Mukharji, Indrani
 4 APPLICANT: Proffitt, John H.
 5 APPLICANT: Yarger, James G.
 6 APPLICANT: Yen, Hwei-Chue B.
 7 TITLE OF INVENTION: Beta Crystallin Mutant Library in
 8 TITLE OF INVENTION: Genetically Engineered Hosts
 9 NUMBER OF SEQUENCES: 79
 10 CORRESPONDENCE ADDRESS:
 11 ADDRESSEE: Amoco Corp., Patents and Technology Dept
 12 STREET: 200 E Randolph St
 13 CITY: Chicago
 14 STATE: IL
 15 COUNTRY: USA
 16 ZIP: 60606-0703
 17 COMPUTER READABLE FORM:
 18 MEDIUM TYPE: Floppy disk
 19 COMPUTER: IBM PC compatible
 20 OPERATING SYSTEM: PC-DOS/MS-DOS
 21 SOFTWARE: Patent In Release #1.24
 22 CURRENT APPLICATION DATA:
 23 APPLICATION NUMBER: US/09/785,566
 24 FILING DATE: 27-OCT-1997
 25 CLASSIFICATION: 445
 26 PRIOR APPLICATION DATA:
 27 APPLICATION NUMBER: US 07/785,566
 28 FILING DATE: 30-OCT-1997
 29 ATTORNEY/AGENT INFORMATION:
 30 NAME: Gallowsy, No. 5530194941 B
 31 TELECOMMUNICATION INFORMATION:
 32 TELEPHONE: 3128567180
 33 TELEFAX: 3128564972
 34 INFORMATION FOR SEQ ID NO: 54
 35 SEQUENCE CHARACTERISTICS:
 36 LENGTH: 8 amino acids
 37 TYPE: amino acid
 38 TOPOLOGY: linear
 39 MOLECULE TYPE: peptide
 40 US-09-095,726 54

Query Match 27.8% Score 31 DB 1 Length 8;
 Best Local Similarity 100.0% Prod. No. 2.5e-05;
 Matches 4: Conservative 0: Mismatches 0: Indels 0:

1 US-09-095,726 54
 2 Sequence 54: Application US/09095726
 3 Patent No. 5530189
 4 GENERAL INFORMATION:
 5 APPLICANT: Ausich, Rodney L.
 6 APPLICANT: Brinkhaus, Friedrich E.
 7 APPLICANT: Mukharji, Indrani
 8 APPLICANT: Proffitt, John H.
 9 APPLICANT: Yarger, James G.
 10 APPLICANT: Yen, Hwei-Chue B.
 11 TITLE OF INVENTION: Lysopene Biosynthesis in
 12 TITLE OF INVENTION: Genetically Engineered Hosts
 13 NUMBER OF SEQUENCES: 79
 14 CORRESPONDENCE ADDRESS:
 15 ADDRESSEE: Amoco Corp., Patents and Technology Dept
 16 STREET: 200 E Randolph St
 17 CITY: Chicago
 18 STATE: IL
 19 COUNTRY: USA
 20 ZIP: 60606-0703
 21 COMPUTER READABLE FORM:
 22 MEDIUM TYPE: Floppy disk

1 COMPUTER: IBM PC compatible
 2 OPERATING SYSTEM: PC-DOS/MS-DOS
 3 SOFTWARE: Patent In Release #1.24
 4 CURRENT APPLICATION DATA:
 5 APPLICATION NUMBER: US/09/786,043
 6 FILING DATE: 22-JUN-1998
 7 CLASSIFICATION: 435
 8 PRIOR APPLICATION DATA:
 9 APPLICATION NUMBER: US 07/785,566
 10 FILING DATE: 30-OCT-1997
 11 ATTORNEY/AGENT INFORMATION:
 12 NAME: Gallowsy, No. 5530194941 B
 13 TELECOMMUNICATION INFORMATION:
 14 TELEPHONE: 3128567180
 15 TELEFAX: 3128564972
 16 INFORMATION FOR SEQ ID NO: 51:
 17 SEQUENCE CHARACTERISTICS:
 18 LENGTH: 8 amino acids
 19 TYPE: amino acid
 20 TOPOLOGY: linear
 21 MOLECULE TYPE: peptide
 22 US-09-096-043 51
 23 Query Match 27.8% Score 31 DB 1 Length 8;
 24 Best Local Similarity 100.0% Prod. No. 2.5e-05;
 25 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:
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1 INFORMATION FOR SEQ ID NO: 1:
2 SEQUENCE CHARACTERISTICS:
3 LENGTH: 8 amino acids
4 TYPE: amino acid
5 TOPOLOGY: unknown
6 MOLECULE TYPE: peptide
7 FEATURES:
8 NAME/KEY: Modified site
9 LOCATION: 1
10 OTHER INFORMATION: /note "The 1st residue at position 1 is
11 OTHER INFORMATION: be phosphorylated."
12 US-09-787-443-9

13 Query Match: 27.4% Score 3: DB 1: Length 8:
14 Best Local Similarity: 100.0%: Pred. No. 2.5e+05:
15 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

16 QY 7 KKT 7
17 1
18 1 KKT 8

19 RESULT 37
20 US-09-787-443-9
21 Sequence 17: Application US/09-787-443-9
22 Patent No. 594135
23 GENERAL INFORMATION:
24 APPLICANT: BOWEN, WILLIAM J.
25 TITLE OF INVENTION: PEPTIDE INHIBITORS OF METABOLISM AND
26 TITLE OF INVENTION: METABOLISM
27 NUMBER OF SEQUENCES: 3
28 CURRENT INVENTION ADDRESS:
29 ADDRESSEE: BOWEN, WILLIAM J.
30 STREET: 1755 S. Jefferson Davis Highway, Suite 100
31 CITY: Arlington
32 STATE: Virginia
33 COUNTRY: U.S.A.
34 ZIP: 22202
35 COMPUTER READABLE FORM:
36 MEDIUM TYPE: Floppy disk
37 OPERATING SYSTEM: IBM PC compatible
38 SOFTWARE: Patent In Release #1.0, Version #1.25
39 CURRENT APPLICATION DATA:
40 APPLICATION NUMBER: US/09-787-443-9
41 FILING DATE: 27 JUN 1994
42 CLASSIFICATION: 530
43 PRIOR APPLICATION DATA:
44 APPLICATION NUMBER: 09-787-443-9
45 FILING DATE: 30 JUN 1994
46 PRIOR APPLICATION DATA:
47 APPLICATION NUMBER: 09-787-443-9
48 FILING DATE: 18 APR 1994
49 ATTORNEY/AGENT INFORMATION:
50 NAME: GILSON, NO. 5594106000 P.
51 REGISTRATION NUMBER: 24,618
52 REFERENCE/DOCKET NUMBER: 703 413-3009
53 TELEPHONE: (703) 413-2222
54 TELEFAX: (703) 413-2222
55 OTHER INFORMATION: /note "The 1st residue at position 1 is
56 OTHER INFORMATION: be phosphorylated."
57 US-09-787-443-9

1 INFORMATION FOR SEQ ID NO: 1:
2 SEQUENCE CHARACTERISTICS:
3 LENGTH: 8 amino acids
4 TYPE: amino acid
5 TOPOLOGY: unknown
6 MOLECULE TYPE: peptide
7 FEATURES:
8 NAME/KEY: Modified site
9 LOCATION: 1
10 OTHER INFORMATION: /note "The 1st residue at position 1 is
11 OTHER INFORMATION: be phosphorylated."
12 US-09-787-443-9

13 Query Match: 27.4% Score 3: DB 1: Length 8:
14 Best Local Similarity: 100.0%: Pred. No. 2.5e+05:
15 Matches 3: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

16 QY 7 KKT 7
17 1
18 1 KKT 8

19 RESULT 37
20 US-09-787-443-9
21 Sequence 17: Application US/09-787-443-9
22 Patent No. 594135
23 GENERAL INFORMATION:
24 APPLICANT: BOWEN, WILLIAM J.
25 TITLE OF INVENTION: PEPTIDE INHIBITORS OF METABOLISM AND
26 TITLE OF INVENTION: METABOLISM
27 NUMBER OF SEQUENCES: 3
28 CURRENT INVENTION ADDRESS:
29 ADDRESSEE: BOWEN, WILLIAM J.
30 STREET: 1755 S. Jefferson Davis Highway, Suite 100
31 CITY: Arlington
32 STATE: Virginia
33 COUNTRY: U.S.A.
34 ZIP: 22202
35 COMPUTER READABLE FORM:
36 MEDIUM TYPE: Floppy disk
37 OPERATING SYSTEM: IBM PC compatible
38 SOFTWARE: Patent In Release #1.0, Version #1.25
39 CURRENT APPLICATION DATA:
40 APPLICATION NUMBER: US/09-787-443-9
41 FILING DATE: 27 JUN 1994
42 CLASSIFICATION: 530
43 PRIOR APPLICATION DATA:
44 APPLICATION NUMBER: 09-787-443-9
45 FILING DATE: 30 JUN 1994
46 PRIOR APPLICATION DATA:
47 APPLICATION NUMBER: 09-787-443-9
48 FILING DATE: 18 APR 1994
49 ATTORNEY/AGENT INFORMATION:
50 NAME: GILSON, NO. 5594106000 P.
51 REGISTRATION NUMBER: 24,618
52 REFERENCE/DOCKET NUMBER: 703 413-3009
53 TELEPHONE: (703) 413-2222
54 TELEFAX: (703) 413-2222
55 OTHER INFORMATION: /note "The 1st residue at position 1 is
56 OTHER INFORMATION: be phosphorylated."
57 US-09-787-443-9

[illegible]

1 COUNTRY: USA
2 ZIP: 60606
3 COMPUTER READABLE FORM:
4 MEDIUM TYPE: Floppy Disk
5 COMPUTER: IBM PC compatible
6 OPERATING SYSTEM: PC DOS/MS DOS
7 SOFTWARE: Patent In Release #1.0, Version #1.30
8 CURRENT APPLICATION DATA:
9 APPLICATION NUMBER: US/08/096,623A
10 FILING DATE: 22-JUL-1993
11 CLASSIFICATION: 415
12 PRIOR APPLICATION DATA:
13 APPLICATION NUMBER: US 07/605,061
14 FILING DATE: 09-SEP-1991
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 07/662,927
17 FILING DATE: 26-FEB-1991
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 07/562,674
20 FILING DATE: 03-AUG-1990
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: US 07/525,551
23 FILING DATE: 15-MAY-1990
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: US 07/487,613
26 FILING DATE: 02-MAR-1990
27 ATTORNEY/AGENT INFORMATION:
28 NAME: Jamison, Edward P.
29 REGISTRATION NUMBER: 29,481
30 REFERENCE/CKET NUMBER: AMO-306.1
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (312) 655-1500
33 TELEFAX: (312) 655-1501
34 INFORMATION FOR SEQ ID NO: 59:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 8 amino acids
37 TYPE: amino acid
38 STRANDEDNESS: Linear
39 TOPOLOGY: Linear
40 MOLECULE TYPE: peptide
41 US 08-096,623A-59
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Sequence 4, Application US/3537049

GENERAL INFORMATION:

APPLICANT: Was den Eynde, Robert; Lebrun, Robert

APPLICANT: Was den Eynde, Robert

TITLE OF INVENTION: Isolated, Truncated Nucleic Acid

TITLE OF INVENTION: Nucleic Acid, Code for Use for Report in Address

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Folio & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5 1/4 inch, 5 1/4 inch

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/3537049

FILING DATE: 10 JANUARY 1991

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/250,192

FILING DATE: 27 MAY 1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/06,000

FILING DATE: 22 JULY 1993

AGENCY/AGENT INFORMATION:

NAME: Hanson, No. 54482400 D

REGISTRATION NUMBER: 40,440

SEQUENCE/INVENT NUMBER: 100,000

TELEPHONE: (212) 688-9200

FAX: (212) 688-9881

TELEPHONE FOR SEQ ID NO: 4

SEQUENCE CHARACTERISTICS:

LENGTH: 6,000 amino acids

TYPE: amino acid

FUNCTION: Enzyme

US-08 26,634 4

GENERAL INFORMATION:

Sequence 59, Application: US/3537049

APPLICANT: Aisch, Rodney D.

APPLICANT: Brinkhaus, Friedrich

APPLICANT: Mukherji, Indran

APPLICANT: Proffitt, John H.

APPLICANT: Varner, James G.

APPLICANT: Yen, Huei-Chen H.

TITLE OF INVENTION: Biosynthesis of compound and

TITLE OF INVENTION: Glycosylated compound and

NUMBER OF SEQUENCES: 104

CORRESPONDENCE ADDRESS:

ADDRESSEE: Welsh & Katz, Ltd.

STREET: 120 S. Riverside Plaza

CITY: Chicago

STATE: IL

```

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/09/041,885
3 FILING DATE:
4 CLASSIFICATION: 536
5 PRIOR APPLICATION DATA:
6 APPLICATION NUMBER: 07/067,192
7 FILING DATE: 15-JUL-96
8 CLASSIFICATION: 536
9 ALLIANCE/AGENT INFORMATION:
10 NAME: SATTILAGGER, David R.
11 REGISTRATION NUMBER: 41,794
12 REFERENCE/SKETCH NUMBER: 9A
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE: (954) 475-8146
15 FAX: (904) 472-5860
16 INFORMATION FOR SEQ ID NO: 1
17 SEQUENCE CHARACTERISTICS:
18 LENGTH: 8 amino acids
19 TYPE: amino acid
20 SOURCE: single
21 QUALITY: linear
22 MOLECULE TYPE: peptide
23 US 09/291,418 9
24
25 Query Match: 27.0% Score: 43 DB 1 Length: 8
26 Best Local Similarity: 100.0% Ident: 8
27 Matches: 3 Conservative: 0 Mismatches: 0 Gaps: 0
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FILING DATE: 16-JUN-1994
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Mitchell, Leonard C.
 REGISTRATION NUMBER: 29,609
 REFERENCE/PACKET NUMBER: 604,285
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4005
 TELEFAX: (703) 816-4100
 TELEX: 200757 NIXN UR
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MODULE TYPE: peptide
 US 08 244 855 3

Query Match: 27.38% Score 41 DB 13 Length 8
 Best Local Similarity: 100.0% Prod. No. 2,560,057
 Matches: 3 Conservative 0 Mismatches 0 Indels 0 Gaps 0

27 8 RRP 10
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 3 RRP 5

RESULT 44
 US 08 244 855 4
 Sequence 4, Application US/0824485
 Patent No. 5762906
 GENERAL INFORMATION:
 APPLICANT: Creighton, Andrew M.
 TITLE OF INVENTION: FURTHER IMPROVEMENTS RELATING TO
 TITLE OF INVENTION: RADIO-LABELLING OF PROTEINS
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERBYE
 STREET: 818 FLOOR, 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/24485
 FILING DATE: 16-JUN-1994
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Mitchell, Leonard C.
 REGISTRATION NUMBER: 29,609
 REFERENCE/PACKET NUMBER: 604,285
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4005
 TELEFAX: (703) 816-4100
 TELEX: 200757 NIXN UR
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MODULE TYPE: peptide
 US 08 244 855 4

Query Match: 27.38% Score 41 DB 13 Length 8
 Best Local Similarity: 100.0% Prod. No. 2,560,057
 Matches: 3 Conservative 0 Mismatches 0 Indels 0 Gaps 0

27 8 RRP 10
 111
 3 RRP 5

RESULT 45
 US 08 244 855 5
 Sequence 15, Application US/0824485
 Patent No. 5762906
 GENERAL INFORMATION:
 APPLICANT: Creighton, Andrew M.
 TITLE OF INVENTION: FURTHER IMPROVEMENTS RELATING TO
 TITLE OF INVENTION: RADIO-LABELLING OF PROTEINS
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERBYE
 STREET: 818 FLOOR, 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VIRGINIA
 COUNTRY: U.S.A.
 ZIP: 22201-4714

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/244,855
 FILING DATE: 16-JUN-1994
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
 NAME: Mitchell, Leonard C.
 REGISTRATION NUMBER: 29,609
 REFERENCE/PACKET NUMBER: 604,285
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 816-4005
 TELEFAX: (703) 816-4100
 TELEX: 200757 NIXN UR
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MODULE TYPE: peptide
 US 08 244 855 5

Query Match: 27.38% Score 41 DB 13 Length 8
 Best Local Similarity: 100.0% Prod. No. 2,560,057
 Matches: 3 Conservative 0 Mismatches 0 Indels 0 Gaps 0

27 8 RRP 10
 111
 3 RRP 5

RESULT 46
 US 08 191 388 3
 Sequence 3, Application US/08191388
 Patent No. 5753164
 GENERAL INFORMATION:
 APPLICANT: Genentech, Inc.
 TITLE OF INVENTION: Immunogenic Cancer Proteins and Peptides
 TITLE OF INVENTION: and Method of Use
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Barker
 STREET: 321 No. 5763164th, Clark Street, Suite 800
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60611

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1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: Patent In Release #1.0, Version #1.25
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/08/191,438A
8  FILING DATE: 12-JAN-1994
9  CLASSIFICATION: 436
10 ATTORNEY/AGENT INFORMATION:
11 NAME: No. 5763164thrup, Thomas E.
12 REGISTRATION NUMBER: 33,268
13 REFERENCE/DOCKET NUMBER: 0000002
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 312-744-0090
16 TELEFAX: 312-755-4489
17 INFORMATION FOR SEQ ID NO: 3:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 8 amino acids
20 TYPE: amino acid
21 STRANDEDNESS: single
22 TOPOLOGY: linear
23 MOLECULE TYPE: peptide
24 FEATURE:
25 NAME/KEY: Xaa
26 LOCATION: 2-3
27 IDENTIFICATION METHOD: Phosphorylated Serine
28 US-08 191-438A 3
29
30 Query Match 27.38; Score 3; DB 1; Length 8;
31 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
32 Matches 3; Conservative 0; Mismatches 0; Indels 0; Caps 0;
33
34 QY 7 GRR 9
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36 GB 4 GRR 6
37
38 RESULT 48
39 US-08 191-438A-20
40 Sequence 20; Application US/08/191438A
41 Patent No. 5763164
42 GENERAL INFORMATION:
43 APPLICANT: Catesoft, Emanuel
44 TITLE OF INVENTION: Immunogenic Cancer Proteins and Peptides
45 TITLE OF INVENTION: and Method of Use
46 NUMBER OF SEQUENCES: 38
47 CORRESPONDENCE ADDRESS:
48 ADDRESSEE: Arnold, White & Burke
49 STREET: 321 No. 5763164th Clark Street, Suite 800
50 CITY: Chicago
51 STATE: IL
52 COUNTRY: USA
53 ZIP: 60610
54 COMPUTER READABLE FORM:
55 MEDIUM TYPE: Floppy disk
56 COMPUTER: IBM PC compatible
57 OPERATING SYSTEM: PC-DOS/MS-DOS
58 SOFTWARE: Patent In Release #1.0, Version #1.25
59 CURRENT APPLICATION DATA:
60 APPLICATION NUMBER: US/08/191,438A
61 FILING DATE: 12-JAN-1994
62 CLASSIFICATION: 436
63 ATTORNEY/AGENT INFORMATION:
64 NAME: No. 5763164thrup, Thomas E.
65 REGISTRATION NUMBER: 33,268
66 REFERENCE/DOCKET NUMBER: 0000002
67 TELECOMMUNICATION INFORMATION:
68 TELEPHONE: 312-744-0090
69 TELEFAX: 312-755-4489
70 INFORMATION FOR SEQ ID NO: 20:
71 SEQUENCE CHARACTERISTICS:
72 LENGTH: 9 amino acids
73 TYPE: amino acid
74 STRANDEDNESS: single
75 TOPOLOGY: linear
76 MOLECULE TYPE: peptide
77 FEATURE:
78 NAME/KEY: Xaa
79 LOCATION: 2-3
80 IDENTIFICATION METHOD: Phosphorylated Serine
81 US-08 191-438A-20
82
83 Query Match 27.38; Score 3; DB 1; Length 8;
84 Best Local Similarity 100.0%; Pred. No. 2.5e+05;
85 Matches 3; Conservative 0; Mismatches 0; Indels 0; Caps 0;
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87 QY 7 GRR 9
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89 GB 4 GRR 6

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Query Match: 27.1% Score 3; DB 1; Length 8;
Best Local Similarity: 100.0% Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

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QY 7 GRX 9
DB 4 GRX 6

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Search completed: September 30, 2003, 10:28:41
Job time: 14,9:67 secs

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RESULT 50
US-09-787-443-9.oli.ra1
Sequence 22, Application: US/08/191.338A
Patent No. 5763164
GENERAL INFORMATION:
APPLICANT: Calenoff, Emanuel
TITLE OF INVENTION: Immunogenic Factor Products and Peptides
TITLE OF INVENTION: and Method of Use
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Burke
STREET: 421 No. 5763164th Clark Street, Suite 800
CITY: Chicago
STATE: IL
COUNTRY: USA

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ZIP: 60610
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/191.338A
FILING DATE: 12 JAN 1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: No. 5763164th Clark Street, Suite 800, Thomas E.
REGISTRATION NUMBER: 03,265
REFERENCE/KEY NUMBER: 03,265
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-744-0090
TELEFAX: 312-744-4489
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Xaa
LOCATION: 1
IDENTIFICATION METHOD: Phosphorylated Serine
FEATURE:
NAME/KEY: Xaa
LOCATION: 8
IDENTIFICATION METHOD: Phosphorylated Serine
US-09-787-443-9.oli.ra1

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Query Match: 27.1% Score 3; DB 1; Length 8;
Best Local Similarity: 100.0% Pred. No. 2.5e+05;
Matches 4; Conservative 0; Mismatches 0; Gaps 0;

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QY 7 GRX 9
DB 4 GRX 6

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241	2	18.2	10	7	Q95HE6	Q95HE6 papio anub	314	2	18.2	10	12	Q9QJ47	Q9QJ47 hepatitis q
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263	2	18.2	10	8	Q8SH14	Q8SH14 caecilia fer	335	2	18.2	11	2	Q47451	Q47451 escherichia
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282	2	18.2	10	8	Q97KE7	Q97KE7 kunzea bakt	355	2	18.2	11	4	Q9UQJ1	Q9UQJ1 homo sapien
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287	2	18.2	10	8	Q97KE0	Q97KE0 acholestom	359	2	18.2	11	5	P82698	P82698 leucophaea
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293	2	18.2	10	10	Q87788	Q87788 zea mays tm	365	2	18.2	11	7	Q29831	Q29831 homo sapien
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303	2	18.2	10	12	Q94V66	Q94V66 polyomaviru	375	2	18.2	11	8	Q94VH7	Q94VH7 varanus gil
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306	2	18.2	10	12	Q94V49	Q94V49 hepatitis q	378	2	18.2	11	9	Q37925	Q37925 bacterioph
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308	2	18.2	10	12	Q94V87	Q94V87 polyomaviru	381	2	18.2	11	10	Q8RUE7	Q8RUE7 zea mays (m


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* Eukaryota: Metazoa; Chordata; Cladocera; Vertebrata; Euteleostomi;
* Mammalia; Eutheria; Cetartiodactyla; Artibeus; and members of the phylum
* Chiroptera.
BX NM_124167.2:240:
KN 11
RP SEQUENCE FROM N.A.
RA Harte M.P., Clouston S., Kruseon L., Olmstead R.G.
*Slow Evolution of Genes Encoding Hyaline Placental Proteins for
*Specialized Systematics and Conservation.
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
DS EMBL: AF140625; AAF98675.1;
DB EMBL: AF140625; AAF98675.1;
EX EMBL: AF140625; AAF98675.1;
FI NON-TER 9
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Quality Match 27.0% Score 9 DB 9 Length 10:
Best Local Similarity 100.0% Pred. No. Gaps 0:
Matches 9 Conservative 0 Mismatches 0 Indels 0 Gaps 0:

CY 9 RPK 11
DB 5 RPK 7

RESULT 11
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AC QRMZ9
DT 01-07-2002 (EMBLrel: 22, Created)
ET 01-07-2002 (EMBLrel: 22, Last sequence update)
EE 01-07-2002 (EMBLrel: 22, Last annotation update)
EF Fseq (Fragment)
GN Fseq
OS Eukaryota; Metazoa; Chordata; Cladocera; Euteleostomi;
* Eukaryota; Vertebrata; Streptophyta; Embryophyta; Tracheophyta;
* Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
* Asteridaceae; Camellia; Solanaceae; Convolvulaceae; Dieracostyles
* NM_124167.2:240:
KN 11
RP SEQUENCE FROM N.A.
RA Harte M.P., Clouston S., Kruseon L., Olmstead R.G.
*Slow Evolution of Genes Encoding Hyaline Placental Proteins for
*Specialized Systematics and Conservation.
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
DS EMBL: AF140625; AAF98675.1;
DB EMBL: AF140625; AAF98675.1;
EX EMBL: AF140625; AAF98675.1;
FI NON-TER 9
SI SEQUENCE 9 AA: 1049 MW: 106643.44086131AA CRC64:
Quality Match 27.0% Score 9 DB 9 Length 10:
Best Local Similarity 100.0% Pred. No. Gaps 0:
Matches 9 Conservative 0 Mismatches 0 Indels 0 Gaps 0:

CY 9 RPK 11
DB 5 RPK 7

RESULT 12
QRMZ9
ID QRMZ9 PRELIMINARY FRT 10 AA
AC QRMZ9
DT 01-07-2002 (EMBLrel: 22, Created)
ET 01-07-2002 (EMBLrel: 22, Last sequence update)
EE 01-07-2002 (EMBLrel: 22, Last annotation update)
EF Fseq (Fragment)
GN Fseq
OS Eukaryota; Metazoa; Chordata; Cladocera; Euteleostomi;
* Eukaryota; Vertebrata; Streptophyta; Embryophyta; Tracheophyta;
* Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
* Asteridaceae; Camellia; Solanaceae; Convolvulaceae; Dieracostyles
* NM_124167.2:240:
KN 11
RP SEQUENCE FROM N.A.
RA Harte M.P., Clouston S., Kruseon L., Olmstead R.G.
*Slow Evolution of Genes Encoding Hyaline Placental Proteins for
*Specialized Systematics and Conservation.
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
DS EMBL: AF140625; AAF98675.1;
DB EMBL: AF140625; AAF98675.1;
EX EMBL: AF140625; AAF98675.1;
FI NON-TER 9
SI SEQUENCE 9 AA: 1049 MW: 106643.44086131AA CRC64:
Quality Match 27.0% Score 9 DB 9 Length 10:
Best Local Similarity 100.0% Pred. No. Gaps 0:
Matches 9 Conservative 0 Mismatches 0 Indels 0 Gaps 0:

CY 9 RPK 11
DB 5 RPK 7

RESULT 13
QRMZ9
ID QRMZ9 PRELIMINARY FRT 10 AA
AC QRMZ9
DT 01-07-2002 (EMBLrel: 22, Created)
ET 01-07-2002 (EMBLrel: 22, Last sequence update)
EE 01-07-2002 (EMBLrel: 22, Last annotation update)
EF Fseq (Fragment)
GN Fseq
OS Eukaryota; Metazoa; Chordata; Cladocera; Euteleostomi;
* Eukaryota; Vertebrata; Streptophyta; Embryophyta; Tracheophyta;
* Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
* Asteridaceae; Camellia; Solanaceae; Convolvulaceae; Dieracostyles
* NM_124167.2:240:
KN 11
RP SEQUENCE FROM N.A.
RA Harte M.P., Clouston S., Kruseon L., Olmstead R.G.
*Slow Evolution of Genes Encoding Hyaline Placental Proteins for
*Specialized Systematics and Conservation.
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
DS EMBL: AF140625; AAF98675.1;
DB EMBL: AF140625; AAF98675.1;
EX EMBL: AF140625; AAF98675.1;
FI NON-TER 9
SI SEQUENCE 9 AA: 1049 MW: 106643.44086131AA CRC64:
Quality Match 27.0% Score 9 DB 9 Length 10:
Best Local Similarity 100.0% Pred. No. Gaps 0:
Matches 9 Conservative 0 Mismatches 0 Indels 0 Gaps 0:

CY 9 RPK 11
DB 5 RPK 7

RESULT 14
QRMZ9
ID QRMZ9 PRELIMINARY FRT 10 AA
AC QRMZ9
DT 01-07-2002 (EMBLrel: 22, Created)
ET 01-07-2002 (EMBLrel: 22, Last sequence update)
EE 01-07-2002 (EMBLrel: 22, Last annotation update)
EF Fseq (Fragment)
GN Fseq
OS Eukaryota; Metazoa; Chordata; Cladocera; Euteleostomi;
* Eukaryota; Vertebrata; Streptophyta; Embryophyta; Tracheophyta;
* Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
* Asteridaceae; Camellia; Solanaceae; Convolvulaceae; Dieracostyles
* NM_124167.2:240:
KN 11
RP SEQUENCE FROM N.A.
RA Harte M.P., Clouston S., Kruseon L., Olmstead R.G.
*Slow Evolution of Genes Encoding Hyaline Placental Proteins for
*Specialized Systematics and Conservation.
RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
DS EMBL: AF140625; AAF98675.1;
DB EMBL: AF140625; AAF98675.1;
EX EMBL: AF140625; AAF98675.1;
FI NON-TER 9
SI SEQUENCE 9 AA: 1049 MW: 106643.44086131AA CRC64:
Quality Match 27.0% Score 9 DB 9 Length 10:
Best Local Similarity 100.0% Pred. No. Gaps 0:
Matches 9 Conservative 0 Mismatches 0 Indels 0 Gaps 0:

CY 9 RPK 11
DB 5 RPK 7

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QS  Lactobacillus casei.
CA  Bacteroides Firmicutes; Lactobacillales; Lactobacillaceae.
CA  Lactobacillus
CA  NCBI_TaxID:15623
EN  1
SE  SEQUENCE
EE  MELLISE 9431947; PubMed 8605243
EA  Barton M.P., Neuhaus P. J.
SC  3 Bacteroides; 176,161,690,1,943
SQ  SEQUENCE 15 AA; 153; MW: 42246AAALGAPPA 19.94
    Query Match 27.4%; Score 3; DB 2; Length 15;
    Best Local Similarity 100.0%; Pred. No. 8.5e-03;
    Matches 3; Conservative 0; Mismatches 0; Indels 0;
QY  4 KK: 1
LE  1
RESULF 44
QY9549  PRELIMINARY; PRT; 15 AA.
AC  Q9549
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DI  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE  01-DEC-2001 (TrEMBLrel. 15, Last annotation update)
DE  EXO-alpha-1,4-glucosidase (EC 3.2.1.20) (Fragment).
OS  Bacteroides thetaiotaomicron.
OC  Bacteroides; Firmicutes; Bacilliales; Geobacillus.
OX  NCBI_TaxID:1422
RN  [1]
RP  SEQUENCE.
RX  MELLISE 92249510; PubMed 1555585;
RA  Suzuki Y., Yonezawa K., Baffori M., Iokii Y.;
RT  "Assignment of Bacteroides thetaiotaomicron K1071 alpha-
RT  1-glucosidase I to an exo-alpha-1,4-glucosidase, and its striking
RT  similarity to bacteroides 1,6-glucosidases in N-terminal sequence
RT  and in structural parameters calculated from the amino acid
RT  composition."
RI  Eur. J. Biochem. 205:243-256(1992).
SQ  SEQUENCE 15 AA; 193; MW: 62046AAALGAPPA 19.94
    Query Match 27.4%; Score 3; DB 2; Length 15;
    Best Local Similarity 100.0%; Pred. No. 8.5e-03;
    Matches 3; Conservative 0; Mismatches 0; Indels 0;
QY  4 KK: 6
LE  2 KK: 4
RESULF 45
QY9549  PRELIMINARY; PRT; 15 AA.
AC  Q9549
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DI  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE  01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE  Procollagen C-proteinase 3 (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID:9606
RN  [1]
RP  SEQUENCE FROM N.A.
RT  Tissue-ovary:
RI  Hirshfeld J., Tomita M., Uneyama K., Urakami K.;
RI  "New splicing pattern of the gene for procollagen C-proteinase."
RI  Cell Struct. Funct. 23:125-125(1998).
DE  EMBL: AB012698, BAA76106.1;
KW  Collagen.
RT  NON-TER
SQ  SEQUENCE 15 AA; 1603; MW: 455FD9975E2724EC CRC64;
    Query Match 27.4%; Score 3; DB 4; Length 15;
    Best Local Similarity 100.0%; Pred. No. 8.5e-03;
    Matches 3; Conservative 0; Mismatches 0; Indels 0;

```

```

QS  Lactobacillus casei.
CA  Bacteroides Firmicutes; Lactobacillales; Lactobacillaceae.
CA  Lactobacillus
CA  NCBI_TaxID:15623
EN  1
SE  SEQUENCE
EE  MELLISE 9431947; PubMed 8605243
EA  Barton M.P., Neuhaus P. J.
SC  3 Bacteroides; 176,161,690,1,943
SQ  SEQUENCE 15 AA; 153; MW: 42246AAALGAPPA 19.94
    Query Match 27.4%; Score 3; DB 2; Length 15;
    Best Local Similarity 100.0%; Pred. No. 8.5e-03;
    Matches 3; Conservative 0; Mismatches 0; Indels 0;
QY  4 KK: 1
LE  1
RESULF 44
QY9549  PRELIMINARY; PRT; 15 AA.
AC  Q9549
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DI  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE  01-DEC-2001 (TrEMBLrel. 15, Last annotation update)
DE  EXO-alpha-1,4-glucosidase (EC 3.2.1.20) (Fragment).
OS  Bacteroides thetaiotaomicron.
OC  Bacteroides; Firmicutes; Bacilliales; Geobacillus.
OX  NCBI_TaxID:1422
RN  [1]
RP  SEQUENCE.
RX  MELLISE 92249510; PubMed 1555585;
RA  Suzuki Y., Yonezawa K., Baffori M., Iokii Y.;
RT  "Assignment of Bacteroides thetaiotaomicron K1071 alpha-
RT  1-glucosidase I to an exo-alpha-1,4-glucosidase, and its striking
RT  similarity to bacteroides 1,6-glucosidases in N-terminal sequence
RT  and in structural parameters calculated from the amino acid
RT  composition."
RI  Eur. J. Biochem. 205:243-256(1992).
SQ  SEQUENCE 15 AA; 193; MW: 62046AAALGAPPA 19.94
    Query Match 27.4%; Score 3; DB 2; Length 15;
    Best Local Similarity 100.0%; Pred. No. 8.5e-03;
    Matches 3; Conservative 0; Mismatches 0; Indels 0;
QY  4 KK: 6
LE  2 KK: 4
RESULF 45
QY9549  PRELIMINARY; PRT; 15 AA.
AC  Q9549
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DI  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE  01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE  Procollagen C-proteinase 3 (Fragment).
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID:9606
RN  [1]
RP  SEQUENCE FROM N.A.
RT  Tissue-ovary:
RI  Hirshfeld J., Tomita M., Uneyama K., Urakami K.;
RI  "New splicing pattern of the gene for procollagen C-proteinase."
RI  Cell Struct. Funct. 23:125-125(1998).
DE  EMBL: AB012698, BAA76106.1;
KW  Collagen.
RT  NON-TER
SQ  SEQUENCE 15 AA; 1603; MW: 455FD9975E2724EC CRC64;
    Query Match 27.4%; Score 3; DB 4; Length 15;
    Best Local Similarity 100.0%; Pred. No. 8.5e-03;
    Matches 3; Conservative 0; Mismatches 0; Indels 0;

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Q7 8 KRP 10
DB 15 KRP 15

PES-12 47
Q75444 PRELIMINARY: 18 AA
AC Q75444
DE 01 NOV 1996 (TrEMBLrel. 12, last sequence update)
DE 01 NOV 1999 (TrEMBLrel. 12, last sequence update)
DE 01 NOV 1999 (TrEMBLrel. 12, last annotation update)
DE Anti Protein (Fragment).
GN AM11.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae;
OC NCBI_TaxID:9606
GN NCBI_TaxID:9606
RP SEQUENCE FROM N.A.
RX MEDLINE:96224597; PubMed:8643476
SA Levanon D., Bernstein Y., Neigam V., Omer M., Bar-Am I.,
SA Aloya K., Goldenberg D., Lotan J., Groer Y.,
SA "A large variety of alternatively spliced and differentially expressed
SA mRNAs are encoded by the human acute myeloid leukemia gene AM11."
SA ONA Cell Biol. 15:175-185(1995).
RX EMBL: X80980; CAA62467.2;
FT NON-TER 1
FT NON-TER 15
SQ SEQUENCE 15 AA: 193; MW: 226640.022; pI:4.2; CRC64:

Query Match 27.4% Score 2: DB 2: Length 15;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 0: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Q7 4 KRP 6
DB 15 KRP 6

PES-12 46
Q75444 PRELIMINARY: 18 AA
AC Q75444
DE 01 MAY 2000 (TrEMBLrel. 12, last sequence update)
DE 01 JUN 2002 (TrEMBLrel. 12, last sequence update)
DE 01 MAR 2002 (TrEMBLrel. 20, last annotation update)
DE Glycogen debranching enzyme (Fragment).
GN AG1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
OC NCBI_TaxID:9623
RP SEQUENCE FROM N.A.
RX STRAIN:2002; Landrace, and crossbred.
SA Stott J. A., Hlaskova P., Kopecky R., Matyska J., Van Packer H.,
SA Pechlan H., Fontana L., Lovell K., Sautter G., Russo G.,
SA Gellerman H.,
SA "Characterization of a SINE linked polymorphism in the porcine AM11 gene
SA and assignment of the gene to chromosome 4q32."
SA Submitted (04P-2002) to the EMBL/GenBank/DDBJ databases.
RX EMBL: AJ511347; CA054084.1;
RX EMBL: AF511348; CA054084.1;
GN Glycosidase; Hydrolase.
FT NON-TER 1
FT NON-TER 15
SQ SEQUENCE 15 AA: 1659; MW: 185961.06; pI:4.5; CRC64:

Query Match 27.4% Score 2: DB 2: Length 15;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 0: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

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```

Q7 6 TCR B
DB 9 TCR 11

PES-12 49
Q75445 PRELIMINARY: 8 AA
AC Q75445
DE 01 MAY 2000 (TrEMBLrel. 12, last sequence update)
DE 01 MAY 2000 (TrEMBLrel. 12, last sequence update)
DE 01 MAY 2000 (TrEMBLrel. 12, last annotation update)
DE Putative IS611 transposase (Fragment).
GN Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID:562
GN NCBI_TaxID:562
RP SEQUENCE FROM N.A.
RX STRAIN:A2950;
RX MEDLINE:99194747; PubMed:10094716;
SA Rahn A., Brummel-Smith J., Whitfield C.,
SA "Conserved organization in the cps gene clusters for expression of
SA Escherichia coli group 1 K antigens: relationship to the colanic acid
SA biosynthesis locus and the cps genes from Klebsiella pneumoniae."
SA J. Bacteriol. 181:2307-2313(1999).
RX EMBL: AF182531; AA050964.1;
FT NON-TER 8
FT NON-TER 8
SQ SEQUENCE 8 AA: 161; MW: 17107.149; pI:4.1406; CRC64:

Query Match 18.2% Score 2: DB 2: Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 0: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Q7 6 KRP 9
DB 2 KRP 5

PES-12 5
Q75444 PRELIMINARY: 8 AA
AC Q75444
DE 01 JUN 2002 (TrEMBLrel. 12, last sequence update)
DE 01 JUN 2002 (TrEMBLrel. 12, last sequence update)
DE 01 MAR 2002 (TrEMBLrel. 20, last annotation update)
DE Serine hydroxymethyltransferase (Fragment).
GN G1YA.
OS Archaea; Archaea; Thermococcales; Thermococcaceae;
OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
OC Micrococcales; Micrococcaceae; Actinobacter.
OC NCBI_TaxID:153021
GN NCBI_TaxID:153021
RP SEQUENCE FROM N.A.
RX STRAIN:111;
RX Keskys K., Harris K., Casalta V., Hasran J., Scrutton N.S.;
SA "Genetic organization of the genes involved in dimethylglycine and
SA sarcosine degradation in Actinobacter spp.: implications for glycine
SA betaine catabolism."
SA Submitted (DEC 2000) to the EMBL/GenBank/DDBJ databases.
RX EMBL: AF224783; AAK16496.1;
RX KWK Methylyltransferase; Transfesterase.
FT NON-TER 1
FT NON-TER 1
SQ SEQUENCE 8 AA: 698; MW: 681670.533; pI:2457; CRC64:

Query Match 18.2% Score 2: DB 2: Length 8;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 0: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

Q7 4 KRP 5
DB 4 KRP 5

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Search completed: September 30, 2003, 10:13:10
Total time: 40.5597 secs

GenePro version 1.0.6
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ORF protein protein search using s2 model

Run on: September 30, 2003, 10:23:04 Search time 6.25 seconds
(without annotations)
82,967 Matches (0.1 updates/sec)

Title: US-09-787-443-9

Perfect score: 11

Sequence: 1 AAKKTCSEPR 11

Scoring table: d1133

Gapop 60.0 % Gapext 4.0 %

Searched: 129863 seqs, 47026705 residues

Word size: 0

Total number of hits satisfying chosen parameters: 707

Maximum hit seq length: 8

Maximum hit seq length: 15

Post Processing: Listing first 500 summaries

Database: SwissProt_41.*

Note: No. is the number of residues predicted by database to have a score greater than or equal to the score of the result being viewed, and is derived by analysis of the total score distribution.

Res. ID	No.	Score	Match	Length	DB	ID	Description
1	3	27.3	6	1	PKK1_PPRAM	P82112	periplaneta
2	4	27.3	9	1	NEUT_PAVPO	P82112	periplaneta
3	4	27.3	10	1	COXK_RAT	P80431	rattus norv
4	4	27.3	10	1	XYSP_PPRAM	P80431	periplaneta
5	4	27.3	11	1	ASAP_PPRAM	P80431	periplaneta
6	4	27.3	11	1	ASAP_PPRAM	P80431	periplaneta
7	4	27.3	12	1	ASAP_PPRAM	P80431	periplaneta
8	4	27.3	12	1	ASAP_PPRAM	P80431	periplaneta
9	4	27.3	12	1	ASAP_PPRAM	P80431	periplaneta
10	4	27.3	13	1	ASAP_PPRAM	P80431	periplaneta
11	4	27.3	13	1	ASAP_PPRAM	P80431	periplaneta
12	4	27.3	13	1	ASAP_PPRAM	P80431	periplaneta
13	4	27.3	13	1	ASAP_PPRAM	P80431	periplaneta
14	4	27.3	13	1	ASAP_PPRAM	P80431	periplaneta
15	4	27.3	13	1	ASAP_PPRAM	P80431	periplaneta
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68	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
69	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
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79	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
80	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
81	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
82	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
83	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
84	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
85	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
86	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
87	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
88	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
89	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
90	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
91	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
92	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
93	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
94	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
95	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
96	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
97	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
98	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
99	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
100	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
101	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
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103	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
104	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
105	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta
106	4	27.3	15	1	ASAP_PPRAM	P80431	periplaneta

P80632 zea mays (m)
P55575 rattus norv
P30087 homo sapien
P81814 carlinus ma
P82678 chlamydomon
P38556 carlinus ma
P5487 corus stria
P16339 locusta miq
P81279 macrobachi
P4172 ascaris suu
P19346 erythrocebu
P19344 macara fusc
P19344 papio anubi
P19343 papio hanad
P19342 theropithec
P83058 bombina var
P08946 phyllomedu
P41489 locusta miq
P36884 staphylococ
P04277 homo sapien
P23879 cyprinus ca
P42998 eisenia toe
P81179 diaprepes a
P82691 periplaneta
P31929 homo sapien
P25825 azotobacter
P01022 bothrops ja
O9P21 oncorhynch
P2086 litoria cit
P56264 litoria xan
P8332 oncorhynch
P80337 ovis aries
P41468 locusta miq
P81135 mycobacteri
P11180 bos taurus
P83382 locusta miq
P4325 bacillus th
P81545 dictyosteli
Q20997 halocynthia
P19851 gallus gali
P42634 aedes aegypt
P42635 aedes aegypt
P19118 nicotiana gl
P30091 homo sapien
P32118 homo sapien
P38007 chlamydia t
P80699 bacillus su
P30423 bothrops in
P30424 bothrops in
P01021 adkistrodon
P04562 adkistrodon
P12797 megalocolla
P82087 litoria cit
P82088 litoria cit
P82089 litoria cit
P82090 litoria cit
P82091 litoria cit
P82092 litoria cit
P22790 aethina fu
P11496 periplaneta
P83321 ponacus mon
P82684 carausius m
P80464 comanonas t
P08951 rana pipien
P42341 conopholis
P82651 hoplobatrach
P88616 urolophora r
P28498 gadus morhu
P01290 equus caball
P28499 oncorhynch
P41333 scyllorhinu
P08615 physalaemus
P50983 corus imper

251	1	9,1	8	1	NPB_BSVIN	P10097 bos taurus	326	1	9,1	9	1	UN19_CLOPA	P81355 clostridium
252	1	9,1	8	1	NS1_MP1C	P81162 cyamopteri	327	1	9,1	9	1	UPA4_HUMAN	P30089 homo sapien
253	1	9,1	8	1	PL1_BRANA	P81767 brassica	328	1	9,1	9	1	UPA5_HUMAN	P40092 homo sapien
254	1	9,1	8	1	R1H_PANR	P00939 pandanus	329	1	9,1	9	1	UPA7_HUMAN	P40093 homo sapien
255	1	9,1	8	1	R1L_ERW3	P37995 erigeron	330	1	9,1	9	1	XYLA_STROG	P19149 streptomyce
256	1	9,1	8	1	R14_P6V16	P82923 bos taurus	331	1	9,1	10	1	XYLA_AGRAS	P81465 agrycybe
257	1	9,1	8	1	R16_P6V16	P36444 bos musculu	332	1	9,1	10	1	AB3_PUSE	P25261 prunus sero
258	1	9,1	8	1	UPAA_HUMAN	P30097 homo sapien	333	1	9,1	10	1	AKHX_LUCM	P81626 corusta miq
259	1	9,1	8	1	W102_HSV2P	P81742 herpes simp	334	1	9,1	10	1	AL19_CARM	P81822 carlinus ma
260	1	9,1	8	1	W11_P6V16	P81495 perkinsus o	335	1	9,1	10	1	AKPN_HPLA	P81731 helicoverpa
261	1	9,1	8	1	AL10_CARM	P82113 carlinus ma	336	1	9,1	10	1	ANG1_P6V16	P10581 bothrops ja
262	1	9,1	8	1	BS4_SERP	P81425 scyllaria po	337	1	9,1	10	1	ANG1_BOVIN	P30107 bos taurus
263	1	9,1	8	1	BK1_P6V16	P81747 clostridium	338	1	9,1	10	1	ANG1_CHICK	P81018 gallus gall
264	1	9,1	8	1	C06_P1NVE	P05486 coxus apoar	339	1	9,1	10	1	APF1_CARP1	P80474 capnocytoph
265	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	340	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
266	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	341	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
267	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	342	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
268	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	343	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
269	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	344	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
270	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	345	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
271	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	346	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
272	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	347	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
273	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	348	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
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276	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	351	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
277	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	352	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
278	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	353	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
279	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	354	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
280	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	355	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
281	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	356	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
282	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	357	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
283	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	358	1	9,1	10	1	BPP2_BOVIN	P30472 bothrops in
284	1	9,1	8	1	C06_P1NVE	P81747 coxus apoar	359						


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1  KINININ degrades aethan sulfate and to a lesser extent,
2  heparin and heparan sulfate.
3  4  ENZYME REGULATION: Inhibited by cupric ions, heparin and hepar
4  Activated by reducing agents, such as ascorbic acid, and 2
5  mercaptoethanol.
6  7  SOURCE: Monoclonal.
7  8  PIM: The N-terminus is blocked.
8  9  MISCELLANEOUS: Has an isoelectric point of 4.1. It is optically active
9  10 and optimum temperature is 41 degrees Celsius.
10 11  Lysos: heparin binding.
11 12  SUBCELLULAR LOCATION: Cytoplasm.
12 13  SUBCELLULAR LOCATION: Cytoplasm.
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200 200  SUBCELLULAR LOCATION: Cytoplasm.

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CC Amphibia: Batrachia: Anura: Neobatrachia and Southern Neobatrachia.
 CC Bufo.
 CC NCBI_TaxID: 8400;
 RN [1]
 SEQUENCE AND SYNTHESIS.
 KW MEDLINE: 9706115; PUBMED: 9706115;
 RA Walter, E.L.; Burcher, E.G.; Galloway, K.; Vassallo, M.;
 RT "Purification, characterization, and spasmolytic activity of
 peptide isolated from the toad Bufo marinus."
 RL Peptides 13:1215-1261(1996).
 CC -1- FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE. ACTIVITY OF
 APPROPRIATE BY TETRODOXIN, BUT IS SIGNIFICANTLY INHIBITED THROUGH THE
 RELEASE OF ACETYLCHOLINE.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.
 KW VASOACTIVE PYRROLIDONE CARBOXYLIC ACID.
 FT MOTIFRES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA: 1515 MW: 5606.6454 Da; CRC64:

Query Match 27.8% Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RRP 10

DB 8 RRP 10

RESULT 15

CC NEOTENSIN.
 CC NCBI_TaxID: 8400;
 RN [1]
 SEQUENCE AND SYNTHESIS.
 KW MEDLINE: 9706115; PUBMED: 9706115;
 RA Walter, E.L.; Burcher, E.G.; Galloway, K.; Vassallo, M.;
 RT "Purification, characterization, and spasmolytic activity of
 peptide isolated from the toad Bufo marinus."
 RL Peptides 13:1215-1261(1996).
 CC -1- FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE. ACTIVITY OF
 APPROPRIATE BY TETRODOXIN, BUT IS SIGNIFICANTLY INHIBITED THROUGH THE
 RELEASE OF ACETYLCHOLINE.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.
 KW VASOACTIVE PYRROLIDONE CARBOXYLIC ACID.
 FT MOTIFRES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA: 1515 MW: 5606.6454 Da; CRC64:

Query Match 27.8% Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RRP 10

DB 8 RRP 10

RESULT 16

CC NEOTENSIN.
 CC NCBI_TaxID: 8400;
 RN [1]
 SEQUENCE AND SYNTHESIS.
 KW MEDLINE: 9706115; PUBMED: 9706115;
 RA Walter, E.L.; Burcher, E.G.; Galloway, K.; Vassallo, M.;
 RT "Purification, characterization, and spasmolytic activity of
 peptide isolated from the toad Bufo marinus."
 RL Peptides 13:1215-1261(1996).
 CC -1- FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE. ACTIVITY OF
 APPROPRIATE BY TETRODOXIN, BUT IS SIGNIFICANTLY INHIBITED THROUGH THE
 RELEASE OF ACETYLCHOLINE.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.
 KW VASOACTIVE PYRROLIDONE CARBOXYLIC ACID.
 FT MOTIFRES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA: 1515 MW: 5606.6454 Da; CRC64:

Query Match 27.8% Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RRP 10

DB 8 RRP 10

RESULT 17

CC NEOTENSIN.
 CC NCBI_TaxID: 8400;
 RN [1]
 SEQUENCE AND SYNTHESIS.
 KW MEDLINE: 9706115; PUBMED: 9706115;
 RA Walter, E.L.; Burcher, E.G.; Galloway, K.; Vassallo, M.;
 RT "Purification, characterization, and spasmolytic activity of
 peptide isolated from the toad Bufo marinus."
 RL Peptides 13:1215-1261(1996).
 CC -1- FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE. ACTIVITY OF
 APPROPRIATE BY TETRODOXIN, BUT IS SIGNIFICANTLY INHIBITED THROUGH THE
 RELEASE OF ACETYLCHOLINE.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.
 KW VASOACTIVE PYRROLIDONE CARBOXYLIC ACID.
 FT MOTIFRES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA: 1515 MW: 5606.6454 Da; CRC64:

Query Match 27.8% Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RRP 10

DB 8 RRP 10

CC NEOTENSIN (NEP).
 CC Gallus gallus (chicken).
 CC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
 CC Archosauria: Aves: Neognathae: Galliformes: Phasianidae: Phasianinae:
 CC Gallus.
 CC NCBI_TaxID: 9011;
 RN [1]
 SEQUENCE.
 KW MEDLINE: 8806195; PUBMED: 882409;
 RA Iwabe, H.; Kamei, S.; Ohashi, H.; Kimura, S.;
 RT "The amino acid sequence of a smooth muscle-contracting peptide from
 chicken rectum: identity to chicken neurotensin."
 RL Jpn. J. Pharmacol. 44:455-459(1987).
 CC -1- FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.
 KW VASOACTIVE PYRROLIDONE CARBOXYLIC ACID.
 FT MOTIFRES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA: 1608 MW: 4094.9714 Da; CRC64:

Query Match 27.8% Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RRP 10

DB 8 RRP 10

RESULT 18

CC NEOTENSIN.
 CC NCBI_TaxID: 8400;
 RN [1]
 SEQUENCE AND SYNTHESIS.
 KW MEDLINE: 9706115; PUBMED: 9706115;
 RA Walter, E.L.; Burcher, E.G.; Galloway, K.; Vassallo, M.;
 RT "Purification, characterization, and spasmolytic activity of
 peptide isolated from the toad Bufo marinus."
 RL Peptides 13:1215-1261(1996).
 CC -1- FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE. ACTIVITY OF
 APPROPRIATE BY TETRODOXIN, BUT IS SIGNIFICANTLY INHIBITED THROUGH THE
 RELEASE OF ACETYLCHOLINE.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.
 KW VASOACTIVE PYRROLIDONE CARBOXYLIC ACID.
 FT MOTIFRES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA: 1515 MW: 5606.6454 Da; CRC64:

Query Match 27.8% Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RRP 10

DB 8 RRP 10

RESULT 19

CC NEOTENSIN.
 CC NCBI_TaxID: 8400;
 RN [1]
 SEQUENCE AND SYNTHESIS.
 KW MEDLINE: 9706115; PUBMED: 9706115;
 RA Walter, E.L.; Burcher, E.G.; Galloway, K.; Vassallo, M.;
 RT "Purification, characterization, and spasmolytic activity of
 peptide isolated from the toad Bufo marinus."
 RL Peptides 13:1215-1261(1996).
 CC -1- FUNCTION: SMOOTH MUSCLE-CONTRACTING PEPTIDE. ACTIVITY OF
 APPROPRIATE BY TETRODOXIN, BUT IS SIGNIFICANTLY INHIBITED THROUGH THE
 RELEASE OF ACETYLCHOLINE.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NEUROTENSIN FAMILY.
 KW VASOACTIVE PYRROLIDONE CARBOXYLIC ACID.
 FT MOTIFRES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 13 AA: 1515 MW: 5606.6454 Da; CRC64:

Query Match 27.8% Score 3; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RRP 10

DB 8 RRP 10

Query Match 16.2% Score 21 DB 1: Length 8;
 Best Local Similarity 100.0% Pred No. 1.4e-05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 BP 10
 IL 2 BP 4

RESULT 25
 ALL4 CALVO
 TD ALL4 CALVO STANDARD: PRT: B AA.
 AC F41840;
 DT 01-NOV-1995 (Rel. 42, Created)
 DT 01-NOV-1995 (Rel. 42, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Callitostatin 4 (leu-callitostatins 4)
 OS Calliphora vicina (Blue blowfly)
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 NC Neoptera; Endopterygota; Diptera; Brachycera; Oestroidea;
 OX Calliphoridae; Calliphoridae
 RN NCBI TaxID 27454;
 RP SEQUENCE
 RC TISSUE:Therapeutic database;
 RX MEDLINE:94271982; PubMed:840573;
 RA Dave H., Johnson A.H., Scott A.G., Yu G.G., Yagi K.J., Tobe S.S.,
 Thorpe A.,
 RT Callitostatins: neuropeptides from the blowfly Calliphora vicina with
 sequence homology to cockroach allatostatins.*;
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
 RN 121
 RP CHARACTERIZATION
 RX MEDLINE:94291473; PubMed:8420669;
 RA Dave H., Thorpe A.,
 RT Constitution and functional significance of leu-callitostatins in
 the blowfly Calliphora vicina.*;
 RL Cell Tissue Res. 276:467-479(1994).
 CC 1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
 A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
 INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
 BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
 EXERCISE A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
 CC 1- TISSUE SPECIFICITY: BRAIN, SUBESOPHAGEAL GANGLION, RETROCEBRAL
 COMPLEX, THORACICO-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY
 SYSTEM AND INTESTINE.
 CC 1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 DR PIR: D47393; D47393;
 KW Neuropeptide; Amidation.
 FT MOD.RES 1 1 AMINATION.
 FT UNSURE 1 1 OK N.
 SQ SEQUENCE 8 AA: 954 MW: D12879D5AH47740A CRC64;
 Query Match 16.2% Score 21 DB 1: Length 8;
 Best Local Similarity 100.0% Pred No. 1.4e-05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 BP 10
 IL 2 BP 4

RESULT 26
 ALL4 CALVO
 TD ALL4 CALVO STANDARD: PRT: B AA.
 AC F41840;
 DT 01-NOV-1995 (Rel. 42, Created)
 DT 01-NOV-1995 (Rel. 42, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Callitostatin 4 (leu-callitostatins 4)
 OS Calliphora vicina (Blue blowfly)
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 NC Neoptera; Endopterygota; Diptera; Brachycera; Oestroidea;
 OX Calliphoridae; Calliphoridae
 RN NCBI TaxID 27454;
 RP SEQUENCE
 RC TISSUE:Therapeutic database;
 RX MEDLINE:94271982; PubMed:840573;
 RA Dave H., Johnson A.H., Scott A.G., Yu G.G., Yagi K.J., Tobe S.S.,
 Thorpe A.,
 RT Callitostatins: neuropeptides from the blowfly Calliphora vicina with
 sequence homology to cockroach allatostatins.*;
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
 RN 121
 RP CHARACTERIZATION
 RX MEDLINE:94291473; PubMed:8420669;
 RA Dave H., Thorpe A.,
 RT Constitution and functional significance of leu-callitostatins in
 the blowfly Calliphora vicina.*;
 RL Cell Tissue Res. 276:467-479(1994).
 CC 1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
 A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
 INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
 BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
 EXERCISE A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
 CC 1- TISSUE SPECIFICITY: BRAIN, SUBESOPHAGEAL GANGLION, RETROCEBRAL
 COMPLEX, THORACICO-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY
 SYSTEM AND INTESTINE.
 CC 1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 DR PIR: D47393; D47393;
 KW Neuropeptide; Amidation.
 FT MOD.RES 1 1 AMINATION.
 FT UNSURE 1 1 OK N.
 SQ SEQUENCE 8 AA: 954 MW: D12879D5AH47740A CRC64;
 Query Match 16.2% Score 21 DB 1: Length 8;
 Best Local Similarity 100.0% Pred No. 1.4e-05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 BP 10
 IL 2 BP 4

Query Match 16.2% Score 21 DB 1: Length 8;
 Best Local Similarity 100.0% Pred No. 1.4e-05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 BP 10
 IL 2 BP 4

RESULT 27
 ALL4 CALVO
 TD ALL4 CALVO STANDARD: PRT: B AA.
 AC F41840;
 DT 01-NOV-1995 (Rel. 42, Created)
 DT 01-NOV-1995 (Rel. 42, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Callitostatin 4 (leu-callitostatins 4)
 OS Calliphora vicina (Blue blowfly)
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 NC Neoptera; Endopterygota; Diptera; Brachycera; Oestroidea;
 OX Calliphoridae; Calliphoridae
 RN NCBI TaxID 27454;
 RP SEQUENCE
 RC TISSUE:Therapeutic database;
 RX MEDLINE:94271982; PubMed:840573;
 RA Dave H., Johnson A.H., Scott A.G., Yu G.G., Yagi K.J., Tobe S.S.,
 Thorpe A.,
 RT Callitostatins: neuropeptides from the blowfly Calliphora vicina with
 sequence homology to cockroach allatostatins.*;
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
 RN 121
 RP CHARACTERIZATION
 RX MEDLINE:94291473; PubMed:8420669;
 RA Dave H., Thorpe A.,
 RT Constitution and functional significance of leu-callitostatins in
 the blowfly Calliphora vicina.*;
 RL Cell Tissue Res. 276:467-479(1994).
 CC 1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
 A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
 INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
 BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
 EXERCISE A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
 CC 1- TISSUE SPECIFICITY: BRAIN, SUBESOPHAGEAL GANGLION, RETROCEBRAL
 COMPLEX, THORACICO-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY
 SYSTEM AND INTESTINE.
 CC 1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 DR PIR: D47393; D47393;
 KW Neuropeptide; Amidation.
 FT MOD.RES 1 1 AMINATION.
 FT UNSURE 1 1 OK N.
 SQ SEQUENCE 8 AA: 954 MW: D12879D5AH47740A CRC64;
 Query Match 16.2% Score 21 DB 1: Length 8;
 Best Local Similarity 100.0% Pred No. 1.4e-05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 BP 10
 IL 2 BP 4

Query Match 16.2% Score 21 DB 1: Length 8;
 Best Local Similarity 100.0% Pred No. 1.4e-05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 BP 10
 IL 2 BP 4

RESULT 28
 ALL4 CALVO
 TD ALL4 CALVO STANDARD: PRT: B AA.
 AC F41840;
 DT 01-NOV-1995 (Rel. 42, Created)
 DT 01-NOV-1995 (Rel. 42, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Callitostatin 4 (leu-callitostatins 4)
 OS Calliphora vicina (Blue blowfly)
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 NC Neoptera; Endopterygota; Diptera; Brachycera; Oestroidea;
 OX Calliphoridae; Calliphoridae
 RN NCBI TaxID 27454;
 RP SEQUENCE
 RC TISSUE:Therapeutic database;
 RX MEDLINE:94271982; PubMed:840573;
 RA Dave H., Johnson A.H., Scott A.G., Yu G.G., Yagi K.J., Tobe S.S.,
 Thorpe A.,
 RT Callitostatins: neuropeptides from the blowfly Calliphora vicina with
 sequence homology to cockroach allatostatins.*;
 RL Proc. Natl. Acad. Sci. U.S.A. 90:2456-2460(1993).
 RN 121
 RP CHARACTERIZATION
 RX MEDLINE:94291473; PubMed:8420669;
 RA Dave H., Thorpe A.,
 RT Constitution and functional significance of leu-callitostatins in
 the blowfly Calliphora vicina.*;
 RL Cell Tissue Res. 276:467-479(1994).
 CC 1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR AND PLAY
 A ROLE IN THE INTEGRATION OF INFORMATION WITHIN THE BRAIN. MAY BE
 INVOLVED IN THE CONTROL OF VISCERAL MUSCLES DUE TO ITS ABILITY TO
 BEHAVE AS POTENT INHIBITORS OF PERISTALTIC MOVEMENTS. MAY ALSO
 EXERCISE A NEUROHORMONAL ROLE ON MUSCLES OF THE GUT AND HEART.
 CC 1- TISSUE SPECIFICITY: BRAIN, SUBESOPHAGEAL GANGLION, RETROCEBRAL
 COMPLEX, THORACICO-ABDOMINAL GANGLION, PERIPHERAL NEUROSECRETORY
 SYSTEM AND INTESTINE.
 CC 1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 DR PIR: D47393; D47393;
 KW Neuropeptide; Amidation.
 FT MOD.RES 1 1 AMINATION.
 FT UNSURE 1 1 OK N.
 SQ SEQUENCE 8 AA: 954 MW: D12879D5AH47740A CRC64;
 Query Match 16.2% Score 21 DB 1: Length 8;
 Best Local Similarity 100.0% Pred No. 1.4e-05;
 Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 BP 10
 IL 2 BP 4


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CX Refl TaxID 7042
CN
CP SEQUENCE
CC TISSUE S: Subesophageal ganglion; and thoracic ganglion;
CR MEDLINE 8607207; PubMed 2994100
CA FROM G.P., Miller C.A., J.J.F., Garney K.L., Girardie A.,
CT Leblond M., Schoenayda L.
CB *Identification of an atypical vasopressin-like diuretic hormone from
CF Locusta migratoria L.
CJ bloodm. biophys. Res. Commun. 149:183-186(1987).
CK
CL 1. SUBUNIT_12: 100 RESIDUES IN PROTEIN
CM 1. SUBUNIT_12 IS AN ANTIPARALLEL BETA-SHEET LINKED DIMER OF F1.
CN 1. SIMILARITY RELATES TO THE VASOPRESSIN/OXYTOCIN FAMILY.
CO
CP A29477; A29477.
CR EukEProt: 1PR000961; Neurhyp. horm.
CA EukEProt: 1PR000961; Neurhyp. horm.
CT PROSITE: P50024; NEURHYPOPHYS_HORM: 1.
CJ DISULFID 1 6 IN FL
CF DISULFID 1 1 INTERCHAIN (WITH C-6') (IN F2).
CJ DISULFID 6 6 INTERCHAIN (WITH C-1') (IN F2).
CF MOD_RES 9 9 AMIDATION.
CU SEQUENCE 9 AA: 974 MW: 5681765H45JA057 CRG64;
CV Query Match 18 Z% Score 2: DB 1: Length 9;
CW Best Local Similarity 100.0%; Pred. No. 1.3e+05;
CX Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps
CY 2 IN 4
CZ 4 IN 5
RESULT 42
FASTA_HEADERS
L1 FASTA_HEADERS STANDARD PRI 9 AA.
LP REF: 28 FEB 2003 (Ref. 41) (Created)
LT 28 FEB 2003 (Ref. 41) (Last sequence update)
LU 28 FEB 2003 (Ref. 41) (Last annotation update)
LV EMRamide-like neuropeptide F1P (DGGNPEKRF-amide).
LW Macrobrachium rosenbergii (Clariat Fresh water prawn);
LX Fakarua; Mozambique; Africa; Malacostraca;
LY Kamoharui; Hawaii; Insecta; Diptera; Phlebotomina; Caridea;
LZ Paludicola; Palaemonidae; Macrobrachium.
M1 Refl TaxID 79424
M2
M3
M4 SEQUENCE AND MASS SPEC PROPERTIES.
M5
M6 TISSUE-EYE-STALK
M7 MEDLINE 2116754; PubMed 11179612
M8 SILICOGRAPHY; P. Satoh; K. Nakai; W. Iwamoto; S.; Panchan N.;
MA SILICOGRAPHY; W. Petso; A.
MT "Three more novel EMRamide-like neuropeptide sequences from the
MU eye-stalk of the giant freshwater prawn Macrobrachium rosenbergii."
ML Peptides 22:191-197(2003).
MC 1. MASS SPEC PROPERTIES: Mw 1680.7; METHOD MALDI.
MD 1. SIMILARITY RELATES TO THE FASP (FMRFAMIDE RELATED PEPTIDE)
ME FAMILY.
MF Gq/G-proteins: G-protein coupled signaling pathway: IDA.
MG Neuropeptide: Amidation.
MH 9-29 RES 9 9 AMIDA:TON.
MI SEQUENCE 9 AA: 1041 MW: 26650729c454087B CRG64;
MQ
MR Query Match 18 Z% Score 2: DB 1: Length 9;
MS Best Local Similarity 100.0%; Pred. No. 1.3e+05;
MX Matches 2: Conservative 0; Mismatches 0; Indels 0; Gaps
MY 7 OK 4
MZ 4 OK 4

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FA59 ASO50
ID FARRASO50 STANDARD: PRD: 9 AA:
AC I43122
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE FMRFamide-like neuropeptide AFW
OS Ascaris suum (pig roundworm) (Ascaris suum roundworm)
OC Eukaryota: Metazoa: Nematoda: Chromadorea: Ascaridida: Ascarididae
OX NCBI_TaxID:6253;
RN 1;
RP SEQ_BNF:
PX MEDLINE:95465462; PubMed 7651964;
RA Gowen C., Streffer A.O.W.;
RT "Elth novel FMRFamide-like neuropeptides isolated from the nematode Ascaris suum";
RL Reprints 16:492-500(1995);
CC 1. SIMILARITY: BELONGS TO THE FARR (FMRFAMIDE RELATED PEPTIDE) FAMILY;
KW Neuropeptide; Amidation;
FT PEPTIDE 9 AA: 1012 MW: 524307374; 16.677 CR654;
SQ SEQUENCE 9 AA: 1012 MW: 524307374; 16.677 CR654;

Query Match IP:28; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CR 8
ID 11
ID 8 CR 9

RESULT: 45
ID FIBB_PALAN STANDARD: PRD: 9 AA:
AC P19344;
DT 01-NOV-1995 (Rel. 16, Created)
DT 01-NOV-1995 (Rel. 16, Last sequence update)
DE 28-FEB-2004 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB;
OS Macaca fuscata fuscata (Japanese macaque);
OC Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Cercopithecoidea: Cercopithecidae;
OX NCBI_TaxID:95543;
RN 1;
RP SEQUENCE;
PX MEDLINE:85289149; PubMed-4928610;
RA Nakamura S., Takemura O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (Erythrocebus patas): their amino acid sequences, restricted mutations, and a molecular phylogeny for macaques, quonons, and baboons";
RL J. Biochem. 97:1487-1492(1985);
CC 1. FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION;
CC 1. SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS;
CC 1. MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT;
DR EIK: 024180; 024180;
LR InterPro: IPR002181; Fibrinogen_C;
DR PROSITE: PS00514; FIBRINAG_Domain; PARTIAL;
KW Blood coagulation; Plasma;
FT PEPTIDE 1 9 FIBRINOPEPTIDE B;
FT NON_TER 9 9;
SQ SEQUENCE 9 AA: 1058 MW: 636458967; 35BB1B CR664;

Query Match IP:28; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CR 8
ID 11
ID 8 CR 9

RESULT: 46
ID FIBB_PALAN STANDARD: PRD: 9 AA:
AC P19344;
DT 01-NOV-1995 (Rel. 16, Created)
DT 01-NOV-1995 (Rel. 16, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB;
OS Papio anubis (olive baboon);
OC Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Cercopithecoidea: Cercopithecidae;
OX NCBI_TaxID:9555;
RN 1;
RP SEQUENCE 9 AA: 1020 MW: 646767673; 35BB1B CR664;

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FA59 ASO50
ID FARRASO50 STANDARD: PRD: 9 AA:
AC I43122
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE FMRFamide-like neuropeptide AFW
OS Ascaris suum (pig roundworm) (Ascaris suum roundworm)
OC Eukaryota: Metazoa: Nematoda: Chromadorea: Ascaridida: Ascarididae
OX NCBI_TaxID:6253;
RN 1;
RP SEQ_BNF:
PX MEDLINE:95465462; PubMed 7651964;
RA Gowen C., Streffer A.O.W.;
RT "Elth novel FMRFamide-like neuropeptides isolated from the nematode Ascaris suum";
RL Reprints 16:492-500(1995);
CC 1. SIMILARITY: BELONGS TO THE FARR (FMRFAMIDE RELATED PEPTIDE) FAMILY;
KW Neuropeptide; Amidation;
FT PEPTIDE 9 AA: 1012 MW: 524307374; 16.677 CR654;
SQ SEQUENCE 9 AA: 1012 MW: 524307374; 16.677 CR654;

Query Match IP:28; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CR 8
ID 11
ID 8 CR 9

RESULT: 45
ID FIBB_PALAN STANDARD: PRD: 9 AA:
AC P19344;
DT 01-NOV-1995 (Rel. 16, Created)
DT 01-NOV-1995 (Rel. 16, Last sequence update)
DE 28-FEB-2004 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB;
OS Macaca fuscata fuscata (Japanese macaque);
OC Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Cercopithecoidea: Cercopithecidae;
OX NCBI_TaxID:95543;
RN 1;
RP SEQUENCE;
PX MEDLINE:85289149; PubMed-4928610;
RA Nakamura S., Takemura O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (Erythrocebus patas): their amino acid sequences, restricted mutations, and a molecular phylogeny for macaques, quonons, and baboons";
RL J. Biochem. 97:1487-1492(1985);
CC 1. FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET AGGREGATION;
CC 1. SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS;
CC 1. MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT;
DR EIK: 024180; 024180;
LR InterPro: IPR002181; Fibrinogen_C;
DR PROSITE: PS00514; FIBRINAG_Domain; PARTIAL;
KW Blood coagulation; Plasma;
FT PEPTIDE 1 9 FIBRINOPEPTIDE B;
FT NON_TER 9 9;
SQ SEQUENCE 9 AA: 1058 MW: 636458967; 35BB1B CR664;

Query Match IP:28; Score 2; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CR 8
ID 11
ID 8 CR 9

RESULT: 46
ID FIBB_PALAN STANDARD: PRD: 9 AA:
AC P19344;
DT 01-NOV-1995 (Rel. 16, Created)
DT 01-NOV-1995 (Rel. 16, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN FGB;
OS Papio anubis (olive baboon);
OC Eukaryota: Metazoa: Chordata: Craniata; Vertebrata: Euteleostomi: Mammalia: Eutheria: Primates: Catarrhini: Cercopithecoidea: Cercopithecidae;
OX NCBI_TaxID:9555;
RN 1;
RP SEQUENCE 9 AA: 1020 MW: 646767673; 35BB1B CR664;

```


103	18.2	9	2	30.234	SRP class 1, cytosol	176	2	18.2	11	2	S71946	matrix metallopro
104	18.2	9	2	14.243	19 heavy chain CRD	177	2	18.2	11	2	P81643	19 heavy chain CRD
105	18.2	9	2	P12268	19 heavy chain CRD	178	2	18.2	11	2	C54823	olfactory receptor
106	18.2	9	2	P12268	19 heavy chain CRD	179	2	18.2	11	2	P10213	1-cell receptor al
107	18.2	9	2	A37027	transmembrane alpha	180	2	18.2	11	2	P84824	olfactory receptor
108	18.2	9	2	C66077	transmembrane alpha	181	2	18.2	11	2	S65465	cytochrome c oxid
109	18.2	9	2	S66644	transmembrane alpha	182	2	18.2	11	2	C40572	T-cell receptor be
110	18.2	9	2	144613	transmembrane alpha	183	2	18.2	11	2	P09244	T-cell receptor be
111	18.2	9	2	A28024	transmembrane alpha	184	2	18.2	11	2	P09246	T-cell receptor be
112	18.2	9	2	P37373	transmembrane alpha	185	2	18.2	11	2	P09246	T-cell receptor be
113	18.2	9	2	P10677	transmembrane alpha	186	2	18.2	11	2	P10677	T-cell receptor be
114	18.2	9	2	P10677	transmembrane alpha	187	2	18.2	11	2	P10677	T-cell receptor be
115	18.2	9	2	P37074	transmembrane alpha	188	2	18.2	11	2	P37074	T-cell receptor be
116	18.2	9	2	P37074	transmembrane alpha	189	2	18.2	11	2	P37074	T-cell receptor be
117	18.2	9	2	S76824	transmembrane alpha	190	2	18.2	11	2	P86116	nuclease Bhl (EC 3
118	18.2	9	2	S76824	transmembrane alpha	191	2	18.2	11	2	P86116	nuclease Bhl (EC 3
119	18.2	9	2	P09246	transmembrane alpha	192	2	18.2	11	2	P09246	transmembrane alpha
120	18.2	9	2	P09246	transmembrane alpha	193	2	18.2	11	2	P09246	transmembrane alpha
121	18.2	9	2	P09246	transmembrane alpha	194	2	18.2	11	2	P09246	transmembrane alpha
122	18.2	9	2	P09246	transmembrane alpha	195	2	18.2	11	2	P09246	transmembrane alpha
123	18.2	9	2	S76824	transmembrane alpha	196	2	18.2	11	2	P86116	nuclease Bhl (EC 3
124	18.2	9	2	S76824	transmembrane alpha	197	2	18.2	11	2	P86116	nuclease Bhl (EC 3
125	18.2	9	2	A44965	transmembrane alpha	198	2	18.2	11	2	P44871	transmembrane alpha
126	18.2	9	2	A44965	transmembrane alpha	199	2	18.2	11	2	P44871	transmembrane alpha
127	18.2	9	2	S13594	transmembrane alpha	200	2	18.2	11	2	P06662	transmembrane alpha
128	18.2	9	2	S13594	transmembrane alpha	201	2	18.2	11	2	P06662	transmembrane alpha
129	18.2	9	2	XAV100	transmembrane alpha	202	2	18.2	11	2	A61465	transmembrane alpha
130	18.2	9	2	P86116	transmembrane alpha	203	2	18.2	11	2	P86116	transmembrane alpha
131	18.2	9	2	P86116	transmembrane alpha	204	2	18.2	11	2	P86116	transmembrane alpha
132	18.2	9	2	A44965	transmembrane alpha	205	2	18.2	11	2	P44871	transmembrane alpha
133	18.2	9	2	A44965	transmembrane alpha	206	2	18.2	11	2	P44871	transmembrane alpha
134	18.2	9	2	JN1323	transmembrane alpha	207	2	18.2	11	2	A58592	transmembrane alpha
135	18.2	9	2	A44965	transmembrane alpha	208	2	18.2	11	2	P06662	transmembrane alpha
136	18.2	9	2	136683	transmembrane alpha	209	2	18.2	11	2	S66656	transmembrane alpha
137	18.2	9	2	S49574	transmembrane alpha	210	2	18.2	11	2	P44871	transmembrane alpha
138	18.2	9	2	P06662	transmembrane alpha	211	2	18.2	11	2	P44871	transmembrane alpha
139	18.2	9	2	P06662	transmembrane alpha	212	2	18.2	11	2	P44871	transmembrane alpha
140	18.2	9	2	P06662	transmembrane alpha	213	2	18.2	11	2	P44871	transmembrane alpha
141	18.2	9	2	P06662	transmembrane alpha	214	2	18.2	11	2	P44871	transmembrane alpha
142	18.2	9	2	P06662	transmembrane alpha	215	2	18.2	11	2	P44871	transmembrane alpha
143	18.2	9	2	P06662	transmembrane alpha	216	2	18.2	11	2	P44871	transmembrane alpha
144	18.2	9	2	P06662	transmembrane alpha	217	2	18.2	11	2	P44871	transmembrane alpha
145	18.2	9	2	P06662	transmembrane alpha	218	2	18.2	11	2	P44871	transmembrane alpha
146	18.2	9	2	A44965	transmembrane alpha	219	2	18.2	11	2	P06662	transmembrane alpha
147	18.2	9	2	P44871	transmembrane alpha	220	2	18.2	11	2	P06662	transmembrane alpha
148	18.2	9	2	S76824	transmembrane alpha	221	2	18.2	11	2	P86116	nuclease Bhl (EC 3
149	18.2	9	2	A44965	transmembrane alpha	222	2	18.2	11	2	P44871	transmembrane alpha
150	18.2	9	2	P06662	transmembrane alpha	223	2	18.2	11	2	P44871	transmembrane alpha
151	18.2	9	2	P06662	transmembrane alpha	224	2	18.2	11	2	P44871	transmembrane alpha
152	18.2	9	2	P06662	transmembrane alpha	225	2	18.2	11	2	P44871	transmembrane alpha
153	18.2	9	2	S76824	transmembrane alpha	226	2	18.2	11	2	P86116	nuclease Bhl (EC 3
154	18.2	9	2	A44965	transmembrane alpha	227	2	18.2	11	2	P44871	transmembrane alpha
155	18.2	9	2	P44871	transmembrane alpha	228	2	18.2	11	2	P44871	transmembrane alpha
156	18.2	9	2	S76824	transmembrane alpha	229	2	18.2	11	2	P86116	nuclease Bhl (EC 3
157	18.2	9	2	A44965	transmembrane alpha	230	2	18.2	11	2	P44871	transmembrane alpha
158	18.2	9	2	P06662	transmembrane alpha	231	2	18.2	11	2	P44871	transmembrane alpha
159	18.2	9	2	P06662	transmembrane alpha	232	2	18.2	11	2	P44871	transmembrane alpha
160	18.2	9	2	A44965	transmembrane alpha	233	2	18.2	11	2	P44871	transmembrane alpha
161	18.2	9	2	A44965	transmembrane alpha	234	2	18.2	11	2	P44871	transmembrane alpha
162	18.2	9	2	P44871	transmembrane alpha	235	2	18.2	11	2	P44871	transmembrane alpha
163	18.2	9	2	P44871	transmembrane alpha	236	2	18.2	11	2	P44871	transmembrane alpha
164	18.2	9	2	JN0314	transmembrane alpha	237	2	18.2	11	2	P44871	transmembrane alpha
165	18.2	9	2	S76824	transmembrane alpha	238	2	18.2	11	2	P86116	nuclease Bhl (EC 3
166	18.2	9	2	P86116	nuclease Bhl (EC 3	239	2	18.2	11	2	S65465	cytochrome c oxid
167	18.2	9	2	A27617	transmembrane alpha	240	2	18.2	11	2	P44871	transmembrane alpha
168	18.2	9	2	S76824	transmembrane alpha	241	2	18.2	11	2	P86116	nuclease Bhl (EC 3
169	18.2	9	2	P86116	nuclease Bhl (EC 3	242	2	18.2	11	2	P86116	nuclease Bhl (EC 3
170	18.2	9	2	P86116	nuclease Bhl (EC 3	243	2	18.2	11	2	P86116	nuclease Bhl (EC 3
171	18.2	9	2	S62646	transmembrane alpha	244	2	18.2	11	2	P86116	nuclease Bhl (EC 3
172	18.2	9	2	A44965	transmembrane alpha	245	2	18.2	11	2	P44871	transmembrane alpha
173	18.2	9	2	S65465	cytochrome c oxid	246	2	18.2	11	2	P44871	transmembrane alpha
174	18.2	9	2	P44871	transmembrane alpha	247	2	18.2	11	2	P44871	transmembrane alpha
175	18.2	9	2	P44871	transmembrane alpha	248	2	18.2	11	2	P44871	transmembrane alpha

449	16.2	11	2	S2349	muscle, bone, cartilage	422	2	18.2	13	1	XAV199	angiotensin convert
450	18.2	11	2	PH0929	T-cell receptor be	323	2	18.2	13	1	UNAPP	neurensin - brus
451	18.2	11	2	PH0936	T-cell receptor be	324	2	18.2	13	1	A48929	glutathione peroxi
452	18.2	11	2	PH0947	T-cell receptor be	325	2	18.2	13	2	A35245	histone H1a - mous
453	18.2	11	2	PH0957	T-cell receptor be	326	2	18.2	13	2	S78519	ribosomal protein
454	18.2	11	2	S12304	quiescent T84.1 prot	327	2	18.2	13	2	A23695	myosin heavy chain
455	18.2	11	2	A48973	transacylase A1.1E	328	2	18.2	13	2	A61361	bradykinin like pe
456	18.2	11	2	PH0773	NAB12 dehydratase	329	2	18.2	13	2	1-08543	hypothetical prote
457	18.2	11	2	S52254	cytochrome c, prote	330	2	18.2	13	2	S22945	hypothetical prote
458	18.2	11	2	S19015	cytochrome c, prote	331	2	18.2	13	2	A36042	oxix protein - Esc
459	18.2	12	1	A44975	cytochrome c, prote	332	2	18.2	13	2	S12368	arqA protein - Sal
460	18.2	12	1	A54789	cytochrome c, prote	333	2	18.2	13	2	S70723	lipamide dehydrog
461	18.2	12	2	C49215	uridine (EC 3.5.1.5	334	2	18.2	13	2	S63432	disulfidyl sulf
462	18.2	12	2	S26557	T-cell receptor be	335	2	18.2	13	2	S16658	hypothetical prote
463	18.2	12	2	S26547	T-cell receptor be	336	2	18.2	13	2	PC2371	probable endopepti
464	18.2	12	2	S65409	histone H2b - huma	337	2	18.2	13	2	A32454	phloroglucinol red
465	18.2	12	2	G49439	myo-ex polyprot	338	2	18.2	13	2	S16687	ribosomal protein
466	18.2	12	2	S36932	em protein - whea	339	2	18.2	13	2	PC4055	hypothetical 13 pr
467	18.2	12	2	S02222	translational elonga	340	2	18.2	13	2	PN0176	acidic ribosomal p
468	18.2	12	2	S65623	protophyrinogen	341	2	18.2	13	2	S09716	2S albumin large c
469	18.2	12	2	A44674	protophyrinogen	342	2	18.2	13	2	S09733	photosystem 1 prot
470	18.2	12	2	A61362	vespakinin M - hor	343	2	18.2	13	2	J02319	hypothetical 1.6K
471	18.2	12	2	A61363	vespakinin X - hor	344	2	18.2	13	2	J02319	hypothetical 1.6K
472	18.2	12	2	S24539	gene p.9 protein -	345	2	18.2	13	2	PS0250	ribulose-bisphosph
473	18.2	12	2	S64734	hypothetical prote	346	2	18.2	13	2	Q11350	hypothetical prote
474	18.2	12	2	S24774	hypothetical prote	347	2	18.2	13	2	FA0389	protein QF00053 -
475	18.2	12	2	S64123	protein-translocat	348	2	18.2	13	2	H61620	locustamytotopin 1
476	18.2	12	2	S44443	bank protein - Sta	349	2	18.2	13	2	PS0443	potassium channel
477	18.2	12	2	A60757	celastrolin C 1 -	350	2	18.2	13	2	B28955	polysialoglycoprot
478	18.2	12	2	G44426	hypothetical prote	351	2	18.2	13	2	S14273	polysialoglycoprot
479	18.2	12	2	S45547	hypothetical prote	352	2	18.2	13	2	S13273	85K glycoprotein -
480	18.2	12	2	S45547	ribosomal protein	353	2	18.2	13	2	184603	deoxyacetyllytr
481	18.2	12	2	S45547	plastocyanin 2 - A	354	2	18.2	13	2	PT5256	Ig heavy chain CRD
482	18.2	12	2	PA5547	caprin - rape fruga	355	2	18.2	13	2	PT6341	Ig heavy chain CRD
483	18.2	12	2	S45547	caprin - rape fruga	356	2	18.2	13	2	PS1316	Ig heavy chain DJ
484	18.2	12	2	S17540	aquatatin III rec	357	2	18.2	13	2	PH1369	Ig heavy chain DJ
485	18.2	12	2	PS4213	28K protein 44.2 -	358	2	18.2	13	2	G61458	Ig lambda chain V-
486	18.2	12	2	PA3698	ribosomal protein	359	2	18.2	13	2	S7C441	pancreatic elastas
487	18.2	12	2	A28955	polysialoglycoprot	360	2	18.2	13	2	S7C441	T-cell receptor V-
488	18.2	12	2	A39000	lydin 1 - Africa	361	2	18.2	13	2	S7C441	T-cell antigen rec
489	18.2	12	2	S13626	lipovitelin - Afr	362	2	18.2	13	2	S47357	T-cell antigen rec
490	18.2	12	2	A43261	calculation factor	363	2	18.2	13	2	S47376	T-cell antigen rec
491	18.2	12	2	S24655	3-hydroxyanthranilic	364	2	18.2	13	2	PH1148	T-cell receptor be
492	18.2	12	2	PH1255	Ig heavy chain CRD	365	2	18.2	13	2	G56046	mannose-1-phosphat
493	18.2	12	2	PH1255	Ig heavy chain CRD	366	2	18.2	13	2	B47435	sperm motility inh
494	18.2	12	2	S45547	8-hydroxyanthranilic	367	2	18.2	13	2	S66235	diethyl-ly-peptida
495	18.2	12	2	PH1255	T-cell antigen rec	368	2	18.2	13	2	B56864	6-phosphofructokin
496	18.2	12	2	PH1255	T-cell receptor di	369	2	18.2	13	2	S33879	Ig kappa-1 chain,
497	18.2	12	2	PH1255	T-cell receptor di	370	2	18.2	13	2	S25446	Ig H chain V-D-J r
498	18.2	12	2	A49044	T-cell receptor de	371	2	18.2	13	2	PH1636	Ig H chain V-D-J r
499	18.2	12	2	S74396	5-hydroxy-tryptoph	372	2	18.2	13	2	PH1620	Ig H chain V-D-J r
500	18.2	12	2	146942	basic beta protola	373	2	18.2	13	2	PH1593	Ig H chain V-D-J r
501	18.2	12	2	S68454	NAB11-elycoprote	374	2	18.2	13	2	PH1596	Ig H chain V-D-J r
502	18.2	12	2	PH1255	Ig gamma 2b chain,	375	2	18.2	13	2	G37266	Ig heavy chain C r
503	18.2	12	2	PH1255	Ig H chain V-D-J r	376	2	18.2	13	2	D37267	Ig heavy chain C r
504	18.2	12	2	PH1255	T-cell receptor al	377	2	18.2	13	2	PH0795	T-cell receptor al
505	18.2	12	2	PH1255	T-cell receptor al	378	2	18.2	13	2	PH0795	T-cell receptor al
506	18.2	12	2	PH1255	T-cell receptor be	379	2	18.2	13	2	PH0795	T-cell receptor al
507	18.2	12	2	PH1255	T-cell receptor be	380	2	18.2	13	2	PH0786	T-cell receptor al
508	18.2	12	2	B32621	hexokinase (EC 2.7	381	2	18.2	13	2	S66558	serine proteinase
509	18.2	12	2	B32621	hexokinase (EC 2.7	382	2	18.2	13	2	A86126	hypothetical prote
510	18.2	12	2	PH0795	T-cell receptor be	383	2	18.2	13	2	S33063	Ig lambda chain J
511	18.2	12	2	PH0795	T-cell receptor be	384	2	18.2	13	2	S24344	glyceroldehyde-3-p
512	18.2	12	2	PC4377	telomeric and tetra	385	2	18.2	13	2	1-08543	mastoparan - yello
513	18.2	12	2	S24136	2 protein - guinea	386	2	18.2	14	1	QMVAVV	mastoparan M - hor
514	18.2	12	2	S24136	protein 1 isozyme	387	2	18.2	14	1	QMVHXX	mastoparan X - hor
515	18.2	12	2	S24136	protein 1 isozyme	388	2	18.2	14	1	QMVHXX	mastoparan C - Eur
516	18.2	12	2	A54252	protein matrix alter	389	2	18.2	14	1	QMVHXX	polistes mastopara
517	18.2	12	2	A61342	Na+/K+ exchanger	390	2	18.2	14	1	NTKX1M	alpha-conotoxin M1
518	18.2	12	2	S21133	NAB A5P ribosylate	391	2	18.2	14	1	LEF8WC	tip operon leader
519	18.2	12	2	PS0286	NAB12 dehydratase	392	2	18.2	14	1	LEF8WC	tip operon leader
520	18.2	12	2	PS0286	NAB12 dehydratase	393	2	18.2	14	1	PS0286	somatostatin - S11
521	18.2	12	2	A54524	20 protein, cytochr	394	2	18.2	14	2	PS0286	somatostatin - C

Annotation: Bovine probosin tetradecapeptide contains amino acid sequence from secretory
 A:Reference number: JH0328; M010:91113172; PMID:167411

A:Accession: JH0328
 A:Molecule type: protein
 A:Residues: 1-14 <ARG>
 C:Comment: Infant probosin has the biological activity of both secretory and protein
 C:Superfamily: mammalian animal peptides
 C:Keywords: amidated carboxyl end; hormone
 P:1-8/produced in fetus status predicted only
 P:14/produced in fetus status predicted only
 P:11/Modified sites amidated carboxyl end (1-14) (amide chain mature form from following cly

Query Match 27.4% Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 GRR 9
 II
 LB 12 GRR 14

RESULT 19

PH1621
 In H chain V D region (clone B less 47) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02 Jun 1994 #sequence_revision 02 Jun 1994 #text_change 08 Oct 1994

A:Accession: PH1621
 A:Molecule type: protein

A:Residues: 1-14 <ARG>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 27.4% Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 9 GRR 9
 II
 LB 9 GRR 11

RESULT 20

PH1622
 In H chain V D region (clone B less 47) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02 Jun 1994 #sequence_revision 02 Jun 1994 #text_change 08 Oct 1994

A:Accession: PH1622
 A:Molecule type: protein

A:Residues: 1-14 <ARG>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 27.4% Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 9 GRR 9
 II
 LB 9 GRR 11

RESULT 21

PH1623
 In H chain V D region (clone B less 47) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02 Jun 1994 #sequence_revision 02 Jun 1994 #text_change 08 Oct 1994

A:Accession: PH1623
 A:Molecule type: protein

A:Residues: 1-14 <ARG>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 27.4% Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 9 GRR 9
 II
 LB 9 GRR 11

RESULT 22

PH1624
 In H chain V D region (clone B less 47) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02 Jun 1994 #sequence_revision 02 Jun 1994 #text_change 17 Mar 1999

A:Accession: PH1624
 A:Molecule type: protein

A:Residues: 1-14 <ARG>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 27.4% Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 9 GRR 9
 II
 LB 9 GRR 11

Annotation: Bovine probosin tetradecapeptide contains amino acid sequence from secretory
 A:Reference number: JH0328; M010:91113172; PMID:167411

A:Accession: JH0328
 A:Molecule type: protein
 A:Residues: 1-14 <ARG>
 C:Comment: Infant probosin has the biological activity of both secretory and protein
 C:Superfamily: mammalian animal peptides
 C:Keywords: amidated carboxyl end; hormone
 P:1-8/produced in fetus status predicted only
 P:14/produced in fetus status predicted only
 P:11/Modified sites amidated carboxyl end (1-14) (amide chain mature form from following cly

Query Match 27.4% Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 7 GRR 9
 II
 LB 4 GRR 5

RESULT 23

PH1625
 In H chain V D region (clone B less 47) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02 Jun 1994 #sequence_revision 02 Jun 1994 #text_change 17 Mar 1999

A:Accession: PH1625
 A:Molecule type: protein

A:Residues: 1-14 <ARG>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 27.4% Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 9 GRR 9
 II
 LB 5 GRR 5

RESULT 24

PH1626
 In H chain V D region (clone B less 47) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02 Jun 1994 #sequence_revision 02 Jun 1994 #text_change 17 Mar 1999

A:Accession: PH1626
 A:Molecule type: protein

A:Residues: 1-14 <ARG>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 27.4% Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 9 GRR 9
 II
 LB 5 GRR 5

RESULT 25

PH1627
 In H chain V D region (clone B less 47) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 18 Aug 2000 #sequence_revision 18 Aug 2000 #text_change 18 Aug 2000

A:Accession: PH1627
 A:Molecule type: protein

A:Residues: 1-14 <ARG>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 27.4% Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 9 GRR 9
 II
 LB 5 GRR 5

RESULT 26

PH1628
 In H chain V D region (clone B less 47) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 18 Aug 2000 #sequence_revision 18 Aug 2000 #text_change 18 Aug 2000

A:Accession: PH1628
 A:Molecule type: protein

A:Residues: 1-14 <ARG>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 27.4% Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 9 GRR 9
 II
 LB 5 GRR 5

RESULT 27

PH1629
 In H chain V D region (clone B less 47) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 18 Aug 2000 #sequence_revision 18 Aug 2000 #text_change 18 Aug 2000

A:Accession: PH1629
 A:Molecule type: protein

A:Residues: 1-14 <ARG>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 27.4% Score 4; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 9 GRR 9
 II
 LB 5 GRR 5

Query Match 27.0% Score 31.06 21 Length 15
 Best Local Similarity 100.0% Ident. No. 4 20+0%
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 1 AIN 4

IN 1 AIN 4

RESULT 41
 PA0099
 Cytochrome P-450 1A2 (human) (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 20 Feb 1999 #sequence_revision 20 Feb 1999 #text_change 20 Feb 1999
 C:Accession: PA0099
 K:Gotoh, T., Kikuchi, N., Sakurai, Y., Ito, Y., Ito, K., Ito, A.
 Submitted to JPIB, October 1994
 A:Title: Two dimensional polyacrylamide gel electrophoresis of P-450 1A2
 A:Reference number: PA0051
 A:Accession: PA0099
 A:Molecule type: protein
 A:Residues: 1-15 SK08

QY 5 KID 7

IN 2 KID 4

RESULT 41
 PA0066
 Protein 429-662 - fungus (Fusarium sporotrichoides) (fragment)
 C:Species: Fusarium sporotrichoides
 C:Date: 20 Feb 1995 #sequence_revision 20 Feb 1995 #text_change 20 Mar 1995
 C:Accession: PA0066
 K:Gotoh, T., Kikuchi, N., Sakurai, Y., Ito, Y., Ito, K., Ito, A.
 Submitted to JPIB, October 1994
 A:Title: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichoides
 A:Reference number: PA0051
 A:Accession: PA0066
 A:Molecule type: protein
 A:Residues: 1-15 SK08

Query Match 27.0% Score 31.06 21 Length 15
 Best Local Similarity 100.0% Ident. No. 4 20+0%
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 1 AIN 4

IN 1 AIN 4

RESULT 42
 A42971
 Hepatocellular carcinoma - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 12 Oct 1989 #sequence_revision 12 Oct 1989 #text_change 12 Oct 1989
 C:Accession: A42971
 K:Gotoh, T., Kikuchi, N., Sakurai, Y., Ito, Y., Ito, K., Ito, A.
 Submitted to JPIB, October 1994
 A:Title: Hepatocellular carcinoma - human (fragment)
 A:Reference number: A42971
 A:Accession: A42971
 A:Molecule type: protein
 A:Residues: 1-15 SK08
 A:Keywords: hepatocellular carcinoma

Query Match 27.0% Score 31.06 21 Length 15
 Best Local Similarity 100.0% Ident. No. 4 20+0%
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 9 RER 11

IN 11 RER 14

RESULT 43
 B42800
 Cytochrome P-450 1A2 (human) (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 22 Nov 1999 #sequence_revision 22 Nov 1999 #text_change 30 Sep 1999
 C:Accession: B42800
 K:Gotoh, T., Kikuchi, N., Sakurai, Y., Ito, Y., Ito, K., Ito, A.
 Submitted to JPIB, October 1994
 A:Title: Primary structure of a human mitochondrial protein homologous to the bacte
 A:Reference number: A42800
 A:Accession: B42800
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-15 c11N
 A:Cross references: GENE2292

Query Match 27.0% Score 31.06 21 Length 15
 Best Local Similarity 100.0% Ident. No. 4 20+0%
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 8 RSP 13

IN 11 RSP 14

RESULT 44
 PH1443
 T-cell receptor alpha chain (mouse A4/H2K) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 10 Mar 1994 #sequence_revision 10 Mar 1994 #text_change 11 Apr 1995
 C:Accession: PH1443
 K:Gotoh, T., Kikuchi, N., Sakurai, Y., Ito, Y., Ito, K., Ito, A.
 Submitted to JPIB, October 1994
 A:Title: T-cell receptor alpha chain (mouse A4/H2K) - mouse (fragment)
 A:Reference number: PH1443
 A:Accession: PH1443
 A:Molecule type: mRNA
 A:Residues: 1-15 c11N
 A:Keywords: T-cell receptor

Query Match 27.0% Score 31.06 21 Length 15
 Best Local Similarity 100.0% Ident. No. 4 20+0%
 Matches 4: Conservative 0: Mismatches 0: Gaps 0:

QY 9 RER 11

IN 11 RER 14

RESULT 45
 PH0760
 T-cell receptor beta chain (Hz) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 17 Jul 1992 #sequence_revision 17 Jul 1992 #text_change 05 Nov 1999
 C:Accession: PH0760
 K:Gotoh, T., Kikuchi, N., Sakurai, Y., Ito, Y., Ito, K., Ito, A.
 Submitted to JPIB, October 1994
 A:Title: T-cell receptor beta chain (Hz) - mouse (fragment)
 A:Reference number: PH0760
 A:Accession: PH0760
 A:Molecule type: mRNA
 A:Residues: 1-15 c11N
 A:Cross references: EMBL3445, F000000000, F000000000, F000000000
 A:Keywords: T-cell receptor

Cysteine protease 1 (pro.) receptor

Query Match 27.28% Score 21.14 E-2 Length 8,
 Best Local Similarity 100.0%, Pred. No. 2.8e+05;
 Matches 21: Conservative 0; Mismatches 0; Gaps 0;

QY 6 13R 9
 LB 6 13R 9

RESULT 0
 A28004
 A.Hypoxanthine kinase G, two spectrophotometric

Citation: J Biol Chem 271:10411-10414 (1996)
 C.Dates: 16-Jun-1999 #sequence_revision 24 20-Apr-2000 #text_change 24 20-Apr-2000

C.Accession: A28004
 C.Keywords: A28004

A.Molecule type: protein
 A.Residues: 138 6A22

A.Note: the amino-terminal residue (Met138) is a phosphorylation site. The residue is a phosphorylation site. The residue is a phosphorylation site.

A.Status: preliminary
 A.Molecule type: RNA
 A.Residues: 138 6A22

A.Note: this GFF is not annotated in GenBank entry PSENRIC, release 113.0

Query Match 18.28% Score 21.14 E-2 Length 8,
 Best Local Similarity 100.0%, Pred. No. 2.8e+05;
 Matches 21: Conservative 0; Mismatches 0; Gaps 0;

QY 6 13R 9
 LB 6 13R 9

RESULT 0
 A28004
 A.Hypoxanthine kinase G, two spectrophotometric

Citation: J Biol Chem 271:10411-10414 (1996)
 C.Dates: 16-Jun-1999 #sequence_revision 24 20-Apr-2000 #text_change 24 20-Apr-2000

C.Accession: A28004
 C.Keywords: A28004

A.Molecule type: protein
 A.Residues: 138 6A22

A.Note: this GFF is not annotated in GenBank entry PSENRIC, release 113.0

Query Match 18.28% Score 21.14 E-2 Length 8,
 Best Local Similarity 100.0%, Pred. No. 2.8e+05;
 Matches 21: Conservative 0; Mismatches 0; Gaps 0;

QY 6 13R 9
 LB 6 13R 9

RESULT 0
 A28004
 A.Hypoxanthine kinase G, two spectrophotometric

Citation: J Biol Chem 271:10411-10414 (1996)
 C.Dates: 16-Jun-1999 #sequence_revision 24 20-Apr-2000 #text_change 24 20-Apr-2000

A.Reference number: 716441; PMID:9425427; PMID:8021188

A.Accession: 716441
 A.Status: preliminary
 A.Molecule type: RNA
 A.Residues: 138 6A22

A.Cross-references: EMBL:426373; NID:4561911; PION:AAB46955.1; PIR:Q561999
 A.Experiment: submitted to GenBank

A.Note: this GFF is not annotated in GenBank entry PSENRIC, release 113.0

Query Match 18.28% Score 21.14 E-2 Length 8,
 Best Local Similarity 100.0%, Pred. No. 2.8e+05;
 Matches 21: Conservative 0; Mismatches 0; Gaps 0;

QY 6 13R 9
 LB 6 13R 9

RESULT 0
 A28004
 A.Hypoxanthine kinase G, two spectrophotometric

Citation: J Biol Chem 271:10411-10414 (1996)
 C.Dates: 16-Jun-1999 #sequence_revision 24 20-Apr-2000 #text_change 24 20-Apr-2000

C.Accession: A28004
 C.Keywords: A28004

A.Molecule type: protein
 A.Residues: 138 6A22

A.Note: this GFF is not annotated in GenBank entry PSENRIC, release 113.0

Query Match 18.28% Score 21.14 E-2 Length 8,
 Best Local Similarity 100.0%, Pred. No. 2.8e+05;
 Matches 21: Conservative 0; Mismatches 0; Gaps 0;

QY 6 13R 9
 LB 6 13R 9

RESULT 0
 A28004
 A.Hypoxanthine kinase G, two spectrophotometric

Citation: J Biol Chem 271:10411-10414 (1996)
 C.Dates: 16-Jun-1999 #sequence_revision 24 20-Apr-2000 #text_change 24 20-Apr-2000

C.Accession: A28004
 C.Keywords: A28004

A.Molecule type: protein
 A.Residues: 138 6A22

A.Note: this GFF is not annotated in GenBank entry PSENRIC, release 113.0

Query Match 18.28% Score 21.14 E-2 Length 8,
 Best Local Similarity 100.0%, Pred. No. 2.8e+05;
 Matches 21: Conservative 0; Mismatches 0; Gaps 0;

QY 6 13R 9
 LB 6 13R 9

RESULT 0
 A28004
 A.Hypoxanthine kinase G, two spectrophotometric

Citation: J Biol Chem 271:10411-10414 (1996)
 C.Dates: 16-Jun-1999 #sequence_revision 24 20-Apr-2000 #text_change 24 20-Apr-2000

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RR 9
 11
 DB 3 RR 4

RESULT 47
 PI0279
 L4 heavy chain CDR3 region (clone 4 91A) - Korman (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 02-Jul-1996 #text_change 16-Aug-1996
 C:Accession: PI0279
 R:Yamada, M.; Wasserman, R.; Reichardt, P.A.; Shane, S.; Gatten, A.; Korman, J.
 J. Exp. Med. 173, 345-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PI0222; M01D:910637; PMID:169162
 A:Accession: PI0279
 A:Molecule type: DNA
 A:Residues: 1-8 AYAR
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RR 9
 11
 DB 3 RR 4

RESULT 48
 PI0279
 L4 heavy chain CDR3 region (clone 12 10b) - Korman (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 02-Jul-1996 #text_change 16-Aug-1996
 C:Accession: PI0279
 R:Yamada, M.; Wasserman, R.; Reichardt, P.A.; Shane, S.; Gatten, A.; Korman, J.
 J. Exp. Med. 173, 345-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PI0222; M01D:910637; PMID:169162
 A:Accession: PI0279
 A:Molecule type: DNA
 A:Residues: 1-8 AYAR
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RR 9
 11
 DB 3 RR 4

RESULT 49
 PI0279
 L4 heavy chain CDR3 region (clone 12 10b) - Korman (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 02-Jul-1996 #text_change 16-Aug-1996
 C:Accession: PI0279
 R:Yamada, M.; Wasserman, R.; Reichardt, P.A.; Shane, S.; Gatten, A.; Korman, J.
 J. Exp. Med. 173, 345-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A:Reference number: PI0222; M01D:910637; PMID:169162
 A:Accession: PI0279
 A:Molecule type: DNA
 A:Residues: 1-8 AYAR
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RR 9
 11
 DB 3 RR 4

RESULT 50
 PI0279
 L4 heavy chain CDR3 region (clone 12 10b) - Korman (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: PI0279
 R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau
 Mamm. Genome 5, 349-355, 1994
 A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
 A:Reference number: PI0222; M01D:9439082; PMID:8043949
 A:Accession: PI0279
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-8 <RES>
 A:Cross-references: EMBL:U05691; NID:9497010; PIRN:AAB60462.1; PIR:q642826

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RR 9
 11
 DB 3 RR 4

RESULT 51
 PI0279
 L4 heavy chain CDR3 region (clone 12 10b) - Korman (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: PI0279
 R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau
 Mamm. Genome 5, 349-355, 1994
 A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
 A:Reference number: PI0222; M01D:9439082; PMID:8043949
 A:Accession: PI0279
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-8 <RES>
 A:Cross-references: EMBL:U05691; NID:9497010; PIRN:AAB60462.1; PIR:q642826

Query Match: 18.2%; Score 2; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RR 9
 11
 DB 3 RR 4

RESULT 52
 PI0279
 L4 heavy chain CDR3 region (clone 12 10b) - Korman (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
 C:Accession: PI0279
 R:Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau
 Mamm. Genome 5, 349-355, 1994
 A:Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
 A:Reference number: PI0222; M01D:9439082; PMID:8043949
 A:Accession: PI0279
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-8 <RES>
 A:Cross-references: EMBL:U05691; NID:9497010; PIRN:AAB60462.1; PIR:q642826

Search completed: September 30, 2003, 10:09:46
 Job time: 13.4367 secs

GeneCore version 5.1.2
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us-09-787-443-12

Search: 263308 seqs, 9616862 residues
Word size: 8
Total number of hits satisfying chosen parameters: 2064
Maximum db seq length: 9
Maximum db seq length: 15
Last processing: Lasting first 500 sequences
Database: 1: pir1; 2: pir2; 3: pir3; 4: pir4; 5: pir5; 6: pir6; 7: pir7; 8: pir8; 9: pir9; 10: pir10; 11: pir11; 12: pir12; 13: pir13; 14: pir14; 15: pir15; 16: pir16; 17: pir17; 18: pir18; 19: pir19; 20: pir20; 21: pir21; 22: pir22; 23: pir23; 24: pir24; 25: pir25; 26: pir26; 27: pir27; 28: pir28; 29: pir29; 30: pir30; 31: pir31; 32: pir32; 33: pir33; 34: pir34; 35: pir35; 36: pir36; 37: pir37; 38: pir38; 39: pir39; 40: pir40; 41: pir41; 42: pir42; 43: pir43; 44: pir44; 45: pir45; 46: pir46; 47: pir47; 48: pir48; 49: pir49; 50: pir50; 51: pir51; 52: pir52; 53: pir53; 54: pir54; 55: pir55; 56: pir56; 57: pir57; 58: pir58; 59: pir59; 60: pir60; 61: pir61; 62: pir62; 63: pir63; 64: pir64; 65: pir65; 66: pir66; 67: pir67; 68: pir68; 69: pir69; 70: pir70; 71: pir71; 72: pir72; 73: pir73; 74: pir74; 75: pir75; 76: pir76; 77: pir77; 78: pir78; 79: pir79; 80: pir80; 81: pir81; 82: pir82; 83: pir83; 84: pir84; 85: pir85; 86: pir86; 87: pir87; 88: pir88; 89: pir89; 90: pir90; 91: pir91; 92: pir92; 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107	2	18.2	2	176	2	18.2	11	4	154081	retinoic acid rece
108	2	18.2	2	177	2	18.2	12	1	A43975	locustamytroptin -
109	2	18.2	2	178	2	18.2	12	1	A43975	alpha-conotoxin Ia
110	2	18.2	2	179	2	18.2	12	2	SL1286	exo-alpha-stiloidas
111	2	18.2	2	180	2	18.2	12	2	A49215	urease (EC 3.5.1.5
112	2	18.2	2	181	2	18.2	12	2	A61309	glycoprotein hormo
113	2	18.2	2	182	2	18.2	12	2	S26056	24 heavy chain m
114	2	18.2	2	183	2	18.2	12	2	S36742	Em protein - wheat
115	2	18.2	2	184	2	18.2	12	2	S01222	translation elonga
116	2	18.2	2	185	2	18.2	12	2	S45191	probable minor cap
117	2	18.2	2	186	2	18.2	12	2	A44874	proboscipedia fr
118	2	18.2	2	187	2	18.2	12	2	S13579	tachykinin - Afri
119	2	18.2	2	188	2	18.2	12	2	A61459	vespakinin X - hor
120	2	18.2	2	189	2	18.2	12	2	S26859	gene p10 protein -
121	2	18.2	2	190	2	18.2	12	2	S49215	urease (EC 3.5.1.5
122	2	18.2	2	191	2	18.2	12	2	S24479	hypothetical prote
123	2	18.2	2	192	2	18.2	12	2	S4447	blink protein - Sta
124	2	18.2	2	193	2	18.2	12	2	A60757	enterotoxin C 1 -
125	2	18.2	2	194	2	18.2	12	2	A49763	sucrose-6-phosphat
126	2	18.2	2	195	2	18.2	12	2	S45663	bma protein - clos
127	2	18.2	2	196	2	18.2	12	2	S49547	hypothetical prote
128	2	18.2	2	197	2	18.2	12	2	A43919	acidic ribosomal p
129	2	18.2	2	198	2	18.2	12	2	PT0083	protein QA600022 -
130	2	18.2	2	199	2	18.2	12	2	PA0098	ribosomal protein
131	2	18.2	2	200	2	18.2	12	2	SL6204	6-phosphotriutokin
132	2	18.2	2	201	2	18.2	12	2	S65740	hemoglobin, extrac
133	2	18.2	2	202	2	18.2	12	2	C51306	hemocyanin chain 6
134	2	18.2	2	203	2	18.2	12	2	A39000	hydriin 1 - African
135	2	18.2	2	204	2	18.2	12	2	SL6266	lipovitellin - Afr
136	2	18.2	2	205	2	18.2	12	2	A41503	sterol carrier pro
137	2	18.2	2	206	2	18.2	12	2	PT0255	1q heavy chain CRD
138	2	18.2	2	207	2	18.2	12	2	S41170	kinesin light chd1
139	2	18.2	2	208	2	18.2	12	2	S47363	1 cell antigen rec
140	2	18.2	2	209	2	18.2	12	2	S41196	3-hydroxy-3-methyl
141	2	18.2	2	210	2	18.2	12	2	Q26937	1q kappa 1 chain: J
142	2	18.2	2	211	2	18.2	12	2	PT0093	1q gamma-2b chain
143	2	18.2	2	212	2	18.2	12	2	PH1695	1q H chain V-D-J r
144	2	18.2	2	213	2	18.2	12	2	PH1696	1q H chain V-D-J r
145	2	18.2	2	214	2	18.2	12	2	PH1551	1q H chain V-D-J r
146	2	18.2	2	215	2	18.2	12	2	S25343	1q heavy chain V r
147	2	18.2	2	216	2	18.2	12	2	S39693	neura; cell adhesi
148	2	18.2	2	217	2	18.2	12	2	S23468	2 protein; galinea
149	2	18.2	2	218	2	18.2	12	2	Q07756	1obelin 1 isotorm
150	2	18.2	2	219	2	18.2	12	2	S49073	NADH2 dehydrogenas
151	2	18.2	2	220	2	18.2	12	2	XAV135	frame shifted cya
152	2	18.2	2	221	2	18.2	13	1	U61181	angiostatin concer
153	2	18.2	2	222	2	18.2	13	1	U61181	neurotensin - brus
154	2	18.2	2	223	2	18.2	13	1	U61181	melanotropin alpha
155	2	18.2	2	224	2	18.2	13	1	M1HWA3	melanotropin alpha
156	2	18.2	2	225	2	18.2	13	1	A38929	glutathione peroxi
157	2	18.2	2	226	2	18.2	13	1	A53628	neurotensin - quin
158	2	18.2	2	227	2	18.2	13	1	A28335	neurotensin [valid
159	2	18.2	2	228	2	18.2	13	1	A61057	neurotensin - comm
160	2	18.2	2	229	2	18.2	13	1	A23697	myosin heavy chain
161	2	18.2	2	230	2	18.2	13	1	E39778	lactose phosphotri
162	2	18.2	2	231	2	18.2	13	1	PH1122	oil protein - vacu
163	2	18.2	2	232	2	18.2	13	1	S21152	tryptophyllin reia
164	2	18.2	2	233	2	18.2	13	1	A05114	tryptophyllin-13 -
165	2	18.2	2	234	2	18.2	13	1	PH0460	corticostatic pept
166	2	18.2	2	235	2	18.2	13	1	A04558	protocatheuatin 3,
167	2	18.2	2	236	2	18.2	13	1	PH1533	hypothetical prote
168	2	18.2	2	237	2	18.2	13	1	S44004	acq-46.5 protein -
169	2	18.2	2	238	2	18.2	13	1	S22095	hypothetical prote
170	2	18.2	2	239	2	18.2	13	1	A39342	oxix protein - Esc
171	2	18.2	2	240	2	18.2	13	1	S70723	lipamide dehydroq
172	2	18.2	2	241	2	18.2	13	1	A64124	hyperhelical prote
173	2	18.2	2	242	2	18.2	13	1	S63472	dissimilatory sulf
174	2	18.2	2	243	2	18.2	13	1	PH1231	probable endopepti
175	2	18.2	2	244	2	18.2	13	1	S66647	ribosomal protein
176	2	18.2	2	245	2	18.2	13	1	S20179	ribosomal protein
177	2	18.2	2	246	2	18.2	13	1	S09214	photosystem 2 prot
178	2	18.2	2	247	2	18.2	13	1	S60376	early madalin 4b -
179	2	18.2	2	248	2	18.2	13	1	PH1231	hypothetical 1.6k

252	18.2	13	2	184757	protein, b2 - human	322	18.2	14	2	PR0147	omega-gliadin, b1 a
250	18.2	13	2	1502419	hypophthalmal, b6K	323	18.2	14	2	PR0151	omega-gliadin, b2'
251	18.2	13	2	1011450	hypophthalmal, p350	324	18.2	14	2	S33834	chaperone, trp1 re
252	18.2	13	2	PR0168	phosphorylase, b1	325	18.2	14	2	PA0104	protein QF20070 -
253	18.2	13	2	PA0189	protein, b20.55.1	326	18.2	14	2	S45625	cathepsin, b1 (EC 3)
254	18.2	13	2	163396	protein, b20.55.1	327	18.2	14	2	S43376	collagen alpha cha
255	18.2	13	2	PR0120	protein, b20.55.1	328	18.2	14	2	PA0152	metal-binding prot
256	18.2	13	2	PR0143	protein, b20.55.1	329	18.2	14	2	G61308	hemocyanin chain, 3
257	18.2	13	2	184553	protein, b20.55.1	330	18.2	14	2	S48307	DEB-A protein - fr
258	18.2	13	2	S52356	protein, b20.55.1	331	18.2	14	2	S12904	protein kinase (EC
259	18.2	13	2	PR0105	protein, b20.55.1	332	18.2	14	2	184283	CI-inhibitor, hum
260	18.2	13	2	PR0106	protein, b20.55.1	333	18.2	14	2	PR0223	Ig heavy chain CDR
261	18.2	13	2	PR0109	protein, b20.55.1	334	18.2	14	2	PR0254	Ig heavy chain CDR
262	18.2	13	2	S47356	protein, b20.55.1	335	18.2	14	2	PR0294	Ig heavy chain CDR
263	18.2	13	2	S47357	protein, b20.55.1	336	18.2	14	2	PR0347	Ig heavy chain DJ
264	18.2	13	2	S47359	protein, b20.55.1	337	18.2	14	2	PR0327	Ig heavy chain DJ
265	18.2	13	2	S47365	protein, b20.55.1	338	18.2	14	2	PR0356	Ig heavy chain DJ
266	18.2	13	2	S47371	protein, b20.55.1	339	18.2	14	2	PR0342	Ig heavy chain DJ
267	18.2	13	2	S47372	protein, b20.55.1	340	18.2	14	2	PR0321	Ig heavy chain DJ
268	18.2	13	2	S47373	protein, b20.55.1	341	18.2	14	2	PR0321	Ig heavy chain DJ
269	18.2	13	2	S47376	protein, b20.55.1	342	18.2	14	2	PR0305	Ig heavy chain DJ
270	18.2	13	2	S47377	protein, b20.55.1	343	18.2	14	2	PR0306	Ig heavy chain DJ
271	18.2	13	2	S47380	protein, b20.55.1	344	18.2	14	2	S57574	T-cell receptor V-
272	18.2	13	2	S47381	protein, b20.55.1	345	18.2	14	2	PR0135	T-cell receptor be
273	18.2	13	2	S47382	protein, b20.55.1	346	18.2	14	2	PR0040	glycogen phosphory
274	18.2	13	2	S47384	protein, b20.55.1	347	18.2	14	2	A43847	Ig mu chain V regi
275	18.2	13	2	S47385	protein, b20.55.1	348	18.2	14	2	JS0272	hypothetical, b1.5K
276	18.2	13	2	S47386	protein, b20.55.1	349	18.2	14	2	PR0625	Ig H chain V-D-J r
277	18.2	13	2	S47387	protein, b20.55.1	350	18.2	14	2	PR0627	Ig H chain V-D-J r
278	18.2	13	2	S47388	protein, b20.55.1	351	18.2	14	2	PR0627	Ig H chain V-D-J r
279	18.2	13	2	S47389	protein, b20.55.1	352	18.2	14	2	PR0628	Ig H chain V-D-J r
280	18.2	13	2	S62328	protein, b20.55.1	353	18.2	14	2	PR0617	Ig H chain V-D-J r
281	18.2	13	2	A58366	protein, b20.55.1	354	18.2	14	2	PR0624	Ig H chain V-D-J r
282	18.2	13	2	A58366	protein, b20.55.1	355	18.2	14	2	PR0586	Ig H chain V-D-J r
283	18.2	13	2	S53275	protein, b20.55.1	356	18.2	14	2	PR0594	Ig H chain V-D-J r
284	18.2	13	2	PR0120	protein, b20.55.1	357	18.2	14	2	PR0597	Ig H chain V-D-J r
285	18.2	13	2	PR0153	protein, b20.55.1	358	18.2	14	2	PR0608	Ig H chain V-D-J r
286	18.2	13	2	PR0156	protein, b20.55.1	359	18.2	14	2	PR0213	Ig H chain V-D-J r
287	18.2	13	2	PR0156	protein, b20.55.1	360	18.2	14	2	PR0765	T-cell receptor al
288	18.2	13	2	PR0156	protein, b20.55.1	361	18.2	14	2	PR0762	T-cell receptor be
289	18.2	13	2	S52356	protein, b20.55.1	362	18.2	14	2	S65392	cytochrome-c oxida
290	18.2	13	2	S52357	protein, b20.55.1	363	18.2	14	2	PR0945	T-cell receptor be
291	18.2	13	2	PR0290	protein, b20.55.1	364	18.2	14	2	PR0945	T-cell receptor be
292	18.2	13	2	PR0805	protein, b20.55.1	365	18.2	14	2	S83754	hypothetical prote
293	18.2	13	2	PR0805	protein, b20.55.1	366	18.2	14	2	PR0778	hypothetical prote
294	18.2	13	2	PR0805	protein, b20.55.1	367	18.2	14	2	PR0836	trp operon leader
295	18.2	13	2	PR0805	protein, b20.55.1	368	18.2	14	2	PR0761	nucleoside-diphosp
296	18.2	13	2	PR0805	protein, b20.55.1	369	18.2	14	2	PR0761	alpha-glucosidase
297	18.2	13	2	PR0805	protein, b20.55.1	370	18.2	14	2	PR0761	glucan 1,4-alpha-g
298	18.2	13	2	PR0805	protein, b20.55.1	371	18.2	14	2	S22237	leukocyte elastase
299	18.2	13	2	PR0805	protein, b20.55.1	372	18.2	14	2	S22237	basic proteinase 1
300	18.2	13	2	PR0805	protein, b20.55.1	373	18.2	14	2	PR0805	ubiquitin-carrier
301	18.2	13	2	PR0805	protein, b20.55.1	374	18.2	14	2	PR0805	hemoglobin alpha c
302	18.2	13	2	PR0805	protein, b20.55.1	375	18.2	14	2	PR0805	heterogeneous ribo
303	18.2	13	2	PR0805	protein, b20.55.1	376	18.2	14	2	PR0805	ribosomal protein
304	18.2	13	2	PR0805	protein, b20.55.1	377	18.2	14	2	PR0805	Dp116 - human
305	18.2	13	2	PR0805	protein, b20.55.1	378	18.2	14	2	PR0805	trypsin - rabbit
306	18.2	13	2	PR0805	protein, b20.55.1	379	18.2	14	2	PR0805	placental calcium-
307	18.2	13	2	PR0805	protein, b20.55.1	380	18.2	14	2	PR0805	fibrinogen alpha c
308	18.2	13	2	PR0805	protein, b20.55.1	381	18.2	14	2	PR0805	ubiquitin thioest
309	18.2	13	2	PR0805	protein, b20.55.1	382	18.2	14	2	PR0805	hypothetical leade
310	18.2	13	2	PR0805	protein, b20.55.1	383	18.2	14	2	PR0805	hypothetical prote
311	18.2	13	2	PR0805	protein, b20.55.1	384	18.2	14	2	PR0805	capsid protein VP1
312	18.2	13	2	PR0805	protein, b20.55.1	385	18.2	14	2	PR0805	
313	18.2	13	2	PR0805	protein, b20.55.1	386	18.2	14	2	PR0805	
314	18.2	13	2	PR0805	protein, b20.55.1	387	18.2	14	2	PR0805	
315	18.2	13	2	PR0805	protein, b20.55.1	388	18.2	14	2	PR0805	
316	18.2	13	2	PR0805	protein, b20.55.1	389	18.2	14	2	PR0805	
317	18.2	13	2	PR0805	protein, b20.55.1	390	18.2	14	2	PR0805	
318	18.2	13	2	PR0805	protein, b20.55.1	391	18.2	14	2	PR0805	
319	18.2	13	2	PR0805	protein, b20.55.1	392	18.2	14	2	PR0805	
320	18.2	13	2	PR0805	protein, b20.55.1	393	18.2	14	2	PR0805	
321	18.2	13	2	PR0805	protein, b20.55.1	394	18.2	14	2	PR0805	

glycine reductase (EC 1.4.99.-) salt hydrolyl protein of alpha chain. Clostridium sticklandii
 C:Species: Clostridium sticklandii
 C:Date: 19-Jun-1997 #sequence_revision 19-Jun-1997 #text_change 15-Aug-1997
 C:Accession: S43308
 R:Stadman, E.C.; Davis, J.N.
 A:Biochem. 266, 22147-22153, 1991
 A:Title: Glycine reductase protein: C1. Properties and characterization of this form B: The
 A:Accession: S43308
 A:Status: Preliminary
 A:Molecule type: Protein
 A:Residues: 1-6 358A
 C:Function:
 A:Description: Glycine reductase complex catalyzes the reductive decarboxylation of glycine
 C:Keywords: Alpha oxidoreductase

Query Match: 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity: 100.0%; Prod. No. 2e-03;
 Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPR 9
 II
 LB 1 KPR 4

RESULT 5
 S43306
 Substance P: Atlantic cod
 C:Species: Gadus morhua (Atlantic cod)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
 C:Accession: S23306
 R:Jensen, J.; Conlon, J.M.
 A:Biochem. 266, 659-664, 1992
 A:Title: Substance-P-related and neurokinin-A-related peptides from the brain of the
 A:Reference number: S23306; MUID:9229992; PMID:1376687
 A:Accession: S23306
 A:Molecule type: Protein
 A:Residues: 1-11 358A
 A:Experimental source: brain
 C:Function:
 A:Description: may play a physiological role in the regulation of cardiovascular and
 A:Note: substance P is derived by post-translational processing of preprotachykinin
 C:Superfamily: unassigned animal peptides
 C:Keywords: neuropeptide; amidated carboxyl end; tachykinin
 F:1/Modified site: amidated carboxyl end (Met) #status predicted

Query Match: 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity: 100.0%; Prod. No. 2e-03;
 Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPR 9
 II
 LB 1 KPR 4

RESULT 6
 S65606
 quinoline 2-oxidoreductase alpha chain Comamonas testosteroni (fragment)
 C:Species: Comamonas testosteroni
 C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C:Accession: S65606
 R:Schach, S.; Tshisaka, B.; Feizer, S.; Lingens, F.
 A:Biochem. 252, 536-544, 1995
 A:Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase 1
 A:Reference number: S65606; MUID:9259889; PMID:7556204
 A:Accession: S65606
 A:Molecule type: Protein
 A:Residues: 1-11 358B
 A:Experimental source: strain 63

Query Match: 27.4%; Score 3; DB 2; Length 11;
 Best Local Similarity: 100.0%; Prod. No. 2e-03;
 Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPR 9
 III
 LB 9 KPR 11

RESULT 7
 S43300
 Probable substance P - smaller spotted catshark
 C:Species: Scyliorhinus reticulatus (smaller spotted catshark, smaller spotted dogfish)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Mar-1999
 C:Accession: S43300
 R:Wang, D.; Wang, Y.; Hazer, N.; Baiment, R.J.; Conlon, J.M.
 A:Biochem. 214, 469-474, 1993
 A:Title: Primary structures and biological activities of substance-P-related peptide
 A:Reference number: S43300; MUID:93292509; PMID:7685693

glycine reductase (EC 1.4.99.-) salt hydrolyl protein of alpha chain. Clostridium sticklandii
 C:Species: Clostridium sticklandii
 C:Date: 19-Jun-1997 #sequence_revision 19-Jun-1997 #text_change 15-Aug-1997
 C:Accession: S43308
 R:Stadman, E.C.; Davis, J.N.
 A:Biochem. 266, 22147-22153, 1991
 A:Title: Glycine reductase protein: C1. Properties and characterization of this form B: The
 A:Accession: S43308
 A:Status: Preliminary
 A:Molecule type: Protein
 A:Residues: 1-6 358A
 C:Function:
 A:Description: Glycine reductase complex catalyzes the reductive decarboxylation of glycine
 C:Keywords: Alpha oxidoreductase

Query Match: 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity: 100.0%; Prod. No. 2e-03;
 Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPR 9
 II
 LB 1 KPR 4

RESULT 4
 S71948
 Matrix metalloproteinase 3 precursor - bovine (transmembrane)
 N:Alternate names: MMP-3 protein; Stromelysin precursor; MMP-4
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1999 #text_change 07-May-1999
 C:Accession: S71948
 R:Arar, E.C.; Fratta, M.A.; Freidmark, B.; Lischke, M.; Trassack, J.E.; Matzuda, K.; W
 A:Biochem. J. 338, 417-424, 1996
 A:Title: Isothiazolones interfere with normal matrix metalloproteinase activation and in
 A:Reference number: S71948; MUID:9454867; PMID:8469928
 A:Accession: S71948
 A:Molecule type: Protein
 A:Residues: 1-5,6-10 358A
 C:Function:
 A:Description: degrades a wide range of extracellular matrix components, including carti
 A:Note: may be involved in arthritis formation

Query Match: 27.3%; Score 3; DB 2; Length 11;
 Best Local Similarity: 100.0%; Prod. No. 2e-03;
 Matches: 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 KPR 9
 II
 LB 4 KPR 6

RESULT 4
 S23306
 Substance P: rainbow trout
 C:Species: Oncorhynchus mykiss (rainbow trout)
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 18-Aug-2000
 C:Accession: S23306
 R:Jensen, J.; Conlon, J.M.
 A:Biochem. 266, 659-664, 1992
 A:Title: Substance-P-related and neurokinin-A-related peptides from the brain of the cod
 A:Reference number: S23306; MUID:9229992; PMID:1376687
 A:Accession: S23306
 A:Molecule type: Protein
 A:Residues: 1-11 358A
 A:Experimental source: brain
 C:Function:
 A:Description: may play a physiological role in the regulation of cardiovascular and gas
 A:Note: substance P is derived by post-translational processing of preprotachykinin A
 C:Superfamily: unassigned animal peptides
 C:Keywords: neuropeptide; amidated carboxyl end; tachykinin
 F:1/Modified site: amidated carboxyl end (Met) #status predicted

QY 2 KR 10
DL 6 KR 2

RESULT 30
339745
endolysosomal acid hydrolase (EC 3.2.1.224) 1 - Rhodococcus sp. (fragment)
Citation: 30-Sep-1991 #sequence, revision 30-Sep-1991 #text_change 1 Dec-1993
C:Accession: A39745
R:Title: M. J. Ikegami, Y. Yamagata, I. J. Biol. Chem. 265, 7919-7926, 1991
A:Title: Activator proteins for glycosylated lipid hydrolysis by endolysosomal enzymes. EL
Life science base activator proteins.
A:Reference number: A39745; M01059120421; M01059120427
A:Accession: A39745
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8-170
C:Keywords: glycosidase; hydrolase

Query Match 18.2% Score 2: DB 2: Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 4 KR 4
DL 6 KR 2

RESULT 31
134936
hypothalamic protein - parsley
Citation: 20-Sep-1999 #sequence, revision 20-Sep-1999 #text_change 2 Sep-1999
C:Accession: T14936
R:Fieldbridge, M.; Spranger, M.; Eickholt, M.; Vazani, K.; Harten, K.; Weissmann, R. Plant Cell 6, 1677-1721, 1994
A:Title: Functional analysis of a highly conserved plant MAP kinase transcript and localization.
A:Reference number: 21825; M01059128722; M01059128714
A:Accession: T14936
A:Status: preliminary; translated from GenBank/1496
A:Molecule type: RNA
A:Residues: 1-8-SEEL
A:Cross-references: EMBL:575495; NID:5913263; GH:591417

Query Match 18.2% Score 2: DB 2: Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 6 KR 7
DL 1 KR 4

RESULT 32
P00162
paramyosin, mollusk quaker (fragment)
Citation: 31-Dec-1990 #sequence, revision 31-Dec-1990 #text_change 1 May-2000
C:Accession: P00162
R:Watabe, S.; Tsuchiya, T.; Hartshorne, D. J. Comp. Biochem. Physiol. B 94, 813-821, 1991
A:Title: Phosphorylation of paramyosin.
A:Reference number: P00162; M010590157485; M01059015741
A:Accession: P00162
A:Molecule type: protein
A:Residues: 1-8-SWAT
A:Experimental source: white adductor muscle
A:Note: The sequence is the phosphorylated tryptic peptide.
Comment: This protein is thought to exist as a dimer of two subunits formed after part on the carboxyl-terminal end of the molecule. Only alpha-paramyosin is phosphorylated by

C:Keywords: muscle; phosphoprotein
P:5/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 18.2% Score 2: DB 2: Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 10 KR 11
DL 2 KR 3

RESULT 33
A23967
leucopyrokinin - Madeira cockroach
Citation: 31-Mar-1988 #sequence, revision 26-May-1994 #text_change 11-Jul-1997
C:Accession: A23967
R:Nachman, R.J.; Holman, G.M.; Cook, B.J. Biochem. Biophys. Res. Commun. 137, 936-942, 1986
A:Title: Active fragments and analogs of the insect neuropeptide leucopyrokinin: st:
A:Reference number: A23967; M010586264541; M010586264540
A:Accession: A23967
A:Molecule type: protein
A:Residues: 1-8-NAGS
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
P:2/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
P:8/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 18.2% Score 2: DB 2: Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 8 KR 9
DL 6 KR 7

RESULT 34
S66646
cardioacceleratory protein 2b - tobacco hornworm
Citation: 15-Feb-1997 #sequence, revision 15-Mar-1997 #text_change 17-Mar-1999
C:Accession: S66646
R:Büschmann, G.R.; Cheung, G.C.; Lee, P.K.; Lee, T.D.; Swiderok, K.M.; Tublitz, N.J. FEBS Lett. 371, 311-314, 1995
A:Title: Amino acid sequence of CAP(2b), an insect cardioacceleratory peptide from t
A:Reference number: S66646; M010596014159; M010596014158
A:Accession: S66646
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-8-SHEE

Query Match 18.2% Score 2: DB 2: Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2: Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 8 KR 9
DL 6 KR 7

RESULT 35
A39892
P element, P cytotype-determining - fruit fly (Drosophila melanogaster) (fragment)
Citation: 24-Jan-1992 #sequence, revision 24-Jan-1992 #text_change 16-Feb-1997
C:Accession: A39892
R:Nittasaka, F.; Mukai, T.; Yamazaki, T. PROC. Natl. Acad. Sci. U.S.A. 84, 7605-7608, 1987
A:Title: Repressor of P elements in Drosophila melanogaster: cytotypic determination
A:Reference number: A39892
A:Accession: A39892

A:Status: Preliminary
A:Residue type: DNA
A:Residues: 1-8 <LEV>
C:GeneID:108
A:Gene: Flybase: P element
A:Cross-references: Flybase: FB0000055

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 11

DB 7 RS 4

RESULT 36

PT0423

C:Species: Mus musculus (man)
C:Title: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 10-Aug-1994

C:Accession: PT0423

R:Kamada, M.; Wasserman, R.; Reichardt, S.A.; Shaner, S.; Cohen, A.; Kovetz, G.
J. Exp. Med. 173, 355-407, 1991

A:Title: Preferential utilization of specific amino-acids in heavy chain diversity and
A:Reference number: PT0222; MOID:910637; PMID:159936

A:Accession: PT0423

A:Molecule type: DNA

A:Residues: 1-8 <YAW>

A:Experimental source: B lymphocyte
A:Keywords: heterotrimer; immunoglobulin

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RR 10

DB 6 RR 7

RESULT 37

PT0600

C:Species: Mus musculus (man)

C:Title: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 10-Aug-1994

C:Accession: PT0600

R:Cartagena, R.E.; Roach, D.E.; Barber, W. E. J. Exp. Med.
J. Immunol. 143, 1680-1684, 1989

A:Title: Structures of histamine releasing peptides formed by the action of acid protease
A:Reference number: A45800; MOID:894146; PMID:273496

A:Accession: PT0600

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <CAR>

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2

DB 2 AR 3

RESULT 38

PT0618

C:Species: Mus musculus (house mouse)
C:Title: 02-Jan-1994 #sequence_revision 02-Jan-1994 #text_change 17-Mar-1999

C:Accession: PT0618

R:Kawashima, S.A.; Campos-Torres, S.; Leder, P.

J. Exp. Med. 178, 417-429, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less
A:Reference number: PT0580; MOID:9301609; PMID:8315387

A:Accession: PT0618

A:Molecule type: DNA

A:Residues: 1-8 <LEV>

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2

DB 2 AR 3

RESULT 39

PT0623

C:Species: Mus musculus (house mouse)

C:Title: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999

C:Accession: A54823

R:Cross, A.; Simon, L.; Cedar, H.; Axel, R.

Cell 78, 823-834, 1994

A:Title: Allelic inactivation regulates olfactory receptor gene expression.
A:Reference number: A54823; MOID:94373818; PMID:8087849

A:Accession: A54823

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-8 <CHE>

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 RR 10

DB 4 RR 4

RESULT 40

PT0639

C:Species: Mus musculus (house mouse)

C:Title: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0639

R:Feeney, A.

J. Exp. Med. 174, 115-124, 1991

A:Title: Junctional sequences of fetal T cell receptor beta chains have low N region
A:Reference number: PT0509; MOID:9127601; PMID:1711558

A:Accession: PT0639

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-8 <FEF>

A:Experimental source: newborn thymus, strain BALB/c

C:Keywords: T cell receptor

Query Match 18.2% Score 2; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AR 2

DB 7 AR 8

RESULT 41

PT0691

C:Species: Mus musculus (house mouse)

C:Title: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C:Accession: PT0691

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AM protein: Protein search, using SW model

Run on: September 30, 2003, 10:07:04 : Search time 6.25 seconds
(with gap additions)
82,757 Million characters/sec

Title: US-09-787-443-12

Perfect score: 11

Sequence: 1 AK0TKMPRS 11

Scoring table: all33

Gap: 60.0 : Gapext: 60.0

Searches: 127863 seqs, 47026705 residues

Word size: 3

Total number of hits satisfying chosen parameters: 707

Minimum hit seq length: 8

Maximum hit seq length: 15

Post processing: listing first 500 summaries

Database: SwissProt_41.*

Prod. No. is the number of results produced by choice to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	EB	ID	Description
1	3	27.3	11	1	32	1	Q2-A1-ORCE	P01474 oryctolagus
2	3	27.3	11	1	32	1	Q2-A1-ORCE	P25438 rat
3	3	27.3	11	1	32	1	Q2-A1-ORCE	P25439 rat
4	3	27.3	11	1	32	1	Q2-A1-ORCE	P25440 rat
5	3	27.3	11	1	32	1	Q2-A1-ORCE	P25441 rat
6	3	27.3	15	1	32	1	Q2-A1-ORCE	P25442 rat
7	3	27.3	15	1	32	1	Q2-A1-ORCE	P25443 rat
8	3	27.3	15	1	32	1	Q2-A1-ORCE	P25444 rat
9	3	27.3	15	1	32	1	Q2-A1-ORCE	P25445 rat
10	3	27.3	15	1	32	1	Q2-A1-ORCE	P25446 rat
11	3	27.3	15	1	32	1	Q2-A1-ORCE	P25447 rat
12	3	27.3	15	1	32	1	Q2-A1-ORCE	P25448 rat
13	3	27.3	15	1	32	1	Q2-A1-ORCE	P25449 rat
14	3	27.3	15	1	32	1	Q2-A1-ORCE	P25450 rat
15	3	27.3	15	1	32	1	Q2-A1-ORCE	P25451 rat
16	3	27.3	15	1	32	1	Q2-A1-ORCE	P25452 rat
17	3	27.3	15	1	32	1	Q2-A1-ORCE	P25453 rat
18	3	27.3	15	1	32	1	Q2-A1-ORCE	P25454 rat
19	3	27.3	15	1	32	1	Q2-A1-ORCE	P25455 rat
20	3	27.3	15	1	32	1	Q2-A1-ORCE	P25456 rat
21	3	27.3	15	1	32	1	Q2-A1-ORCE	P25457 rat
22	3	27.3	15	1	32	1	Q2-A1-ORCE	P25458 rat
23	3	27.3	15	1	32	1	Q2-A1-ORCE	P25459 rat
24	3	27.3	15	1	32	1	Q2-A1-ORCE	P25460 rat
25	3	27.3	15	1	32	1	Q2-A1-ORCE	P25461 rat
26	3	27.3	15	1	32	1	Q2-A1-ORCE	P25462 rat
27	3	27.3	15	1	32	1	Q2-A1-ORCE	P25463 rat
28	3	27.3	15	1	32	1	Q2-A1-ORCE	P25464 rat
29	3	27.3	15	1	32	1	Q2-A1-ORCE	P25465 rat
30	3	27.3	15	1	32	1	Q2-A1-ORCE	P25466 rat
31	3	27.3	15	1	32	1	Q2-A1-ORCE	P25467 rat
32	3	27.3	15	1	32	1	Q2-A1-ORCE	P25468 rat
33	3	27.3	15	1	32	1	Q2-A1-ORCE	P25469 rat

34	2	18.2	10	1	BPP2_BOTJA	P01022 bothrops ja
35	2	18.2	10	1	CATR_SHEEP	P83205 ovis aries
36	2	18.2	10	1	COXK_ONCMY	P80332 oncorhynchu
37	2	18.2	10	1	COXM_RAT	P80431 rattus norv
38	2	18.2	10	1	COXQ_RABIT	P80336 eryctolagus
39	2	18.2	10	1	COXQ_SHEEP	P80337 ovis aries
40	2	18.2	10	1	FIBB_CERS1	P14537 coratotheri
41	2	18.2	10	1	GON1_CHEPR	P80677 cheiYosoma
42	2	18.2	10	1	GON1_PETMA	P04378 petromyzon
43	2	18.2	10	1	GON3_PETMA	P10948 petromyzon
44	2	18.2	10	1	MP2_LCCM1	P41488 locusta miq
45	2	18.2	10	1	MP2_MQCC	P81533 micropplitis
46	2	18.2	10	1	PVK_LCCM1	P83382 locusta miq
47	2	18.2	10	1	QZOB_COMTE	P80465 comamonas t
48	2	18.2	10	1	SLAP_BACTG	P49325 bacillus th
49	2	18.2	10	1	TKNB_CHICK	P19851 gallus gall
50	2	18.2	10	1	TKU1_UREUN	P40751 urechis uni
51	2	18.2	10	1	TKU2_UREUN	P40752 urechis uni
52	2	18.2	10	1	UPA9_HUMAN	P30095 homo sapien
53	2	18.2	10	1	XYNB_D1CH4	P80717 dictyoclomu
54	2	18.2	11	1	BPP3_BOTIN	P30423 bothrops in
55	2	18.2	11	1	BPP4_BOTIN	P30424 bothrops in
56	2	18.2	11	1	BPPB_AGRHA	P01021 eukistirodon
57	2	18.2	11	1	CS15_BACSU	P81095 bacillus su
58	2	18.2	11	1	ESL1_RAT	P56571 rattus norv
59	2	18.2	11	1	MHE1_KLEIN	P80580 kiebsella
60	2	18.2	11	1	PKC1_CARMO	P82684 carausius m
61	2	18.2	11	1	RR2_CONAM	P42341 conopholis
62	2	18.2	11	1	RS30_ONCMY	P83328 oncorhynch
63	2	18.2	11	1	TIN1_HOPTI	P82651 hoplobatr
64	2	18.2	11	1	TKN2_UREPU	P88616 uperoleia r
65	2	18.2	11	1	TKNA_CHICK	P19850 gallus gall
66	2	18.2	11	1	TKNA_HORSE	P01290 equus cabal
67	2	18.2	11	1	TKNA_RANCA	P22688 rana catesb
68	2	18.2	11	1	TKNA_RANCI	P29207 rana ridibu
69	2	18.2	11	1	TKND_RANCA	P22691 rana catesb
70	2	18.2	11	1	UXS2_YEAST	P99013 saccharomyc
71	2	18.2	12	1	UXS2_YEAST	P50983 conus imper
72	2	18.2	12	1	FA77_PENMO	P83322 penaeus mon
73	2	18.2	12	1	GVAB_RANBU	P40754 rana rugosa
74	2	18.2	12	1	LMT1_LCCM1	P22395 locusta miq
75	2	18.2	12	1	N040_LOTJA	O22426 lotus japon
76	2	18.2	12	1	N040_SFESRO	O24369 sesbania ro
77	2	18.2	12	1	PK4_PERAM	P82619 periplaneta
78	2	18.2	12	1	PK4_PERFE	P82690 periplaneta
79	2	18.2	12	1	PK2_PERAM	P81555 periplaneta
80	2	18.2	12	1	RS19_CLEYP	O46490 clover yell
81	2	18.2	12	1	RS19_TORHP	O56251 tomato big
82	2	18.2	12	1	TKN1_KASMA	P88613 kassina mac
83	2	18.2	12	1	V14K_WSSV	P82006 white spot
84	2	18.2	12	1	A3FB_TENMO	P83109 tenebrio mo
85	2	18.2	12	1	AH4_PUSE	P29262 prunus sero
86	2	18.2	12	1	BP37_LEUMA	P81754 leucophaea
87	2	18.2	13	1	HPP1_BOTJA	P01020 bothrops ja
88	2	18.2	13	1	CH6C_CANFA	P49818 canis fami
89	2	18.2	13	1	F1BB_HYLLA	P14472 hylobates l
90	2	18.2	13	1	F1BB_RABIT	P14478 oryctolagus
91	2	18.2	13	1	LMA1_LOCM1	P38496 locusta miq
92	2	18.2	13	1	LMT4_LOCM1	P41490 locusta miq
93	2	18.2	13	1	MLA_ANCRA	P41589 anolis caro
94	2	18.2	13	1	MLA_CAMDR	P01198 camelus dro
95	2	18.2	13	1	NEU7_BUPFA	P81796 bufo marinu
96	2	18.2	13	1	NEUT_CAVPO	P12560 cavia porce
97	2	18.2	13	1	NEUT_CHICK	P13724 gallus gall
98	2	18.2	13	1	NEUT_RANVE	P41536 rana tempor
99	2	18.2	13	1	NEUT_TRIVU	P31745 trichosurus
100	2	18.2	13	1	N040_PEA	P55959 pisum sativ
101	2	18.2	13	1	N040_VICSA	P55961 vicia sativ
102	2	18.2	13	1	PKC_ORCLI	P37086 orconectes
103	2	18.2	13	1	PSAJ_PEA	P17229 pisum sativ
104	2	18.2	13	1	SAZA_ONCMY	P82238 oncorhynch
105	2	18.2	13	1	SAZB_ONCMY	P82239 oncorhynch
106	2	18.2	13	1	TV11_PHYRO	P04096 phyllomedus

107	2	18.2	14	1	CAT2_FASHE	18.2	180	1	9.1	8	1	FAR4_MACRS	P81275	macrobrachi
108	2	18.2	14	1	EPIU_PANEA	181	181	1	9.1	8	1	FAR4_HCRAM	P41486	homarus ame
109	2	18.2	14	1	HV14_PIG	182	182	1	9.1	8	1	FAR4_HCRAM	P41487	homarus ame
110	2	18.2	14	1	JAVI_KANIA	183	183	1	9.1	8	1	FAR4_MACRS	P83277	macrobriachi
111	2	18.2	14	1	LPW_CITFR	184	184	1	9.1	8	1	FAR4_CALVO	P41863	calliphora
112	2	18.2	14	1	LPW_POCIL	185	185	1	9.1	8	1	FUSS_FUSSO	P81010	fusarium so
113	2	18.2	14	1	LPW_RHIME	186	186	1	9.1	8	1	GLUR_HUMAN	P02729	homo sapien
114	2	18.2	14	1	MAH_AALSP	187	187	1	9.1	8	1	HTE1_PERAM	P04548	periplaneta
115	2	18.2	14	1	PKK1_FERAM	188	188	1	9.1	8	1	HTE2_PERAM	P04549	periplaneta
116	2	18.2	14	1	RSD1_GLOPO	189	189	1	9.1	8	1	HTE2_PENMO	P25419	tenebrio mo
117	2	18.2	14	1	RSD1_GLOMB	190	190	1	9.1	8	1	LOK1_LEUMA	P21140	leucophaea
118	2	18.2	14	1	RSD1_FKZAP	191	191	1	9.1	8	1	LOK1_LEUMA	P21141	leucophaea
119	2	18.2	14	1	SMS1_PYCSO	192	192	1	9.1	8	1	LOK4_LEUMA	P21142	leucophaea
120	2	18.2	14	1	SMS1_PYCSO	193	193	1	9.1	8	1	LOK5_LEUMA	P21143	leucophaea
121	2	18.2	14	1	TA3_HVIM2	194	194	1	9.1	8	1	LOK5_LEUMA	P19987	leucophaea
122	2	18.2	14	1	TA3_HVIM2	195	195	1	9.1	8	1	LOK6_LEUMA	P19988	leucophaea
123	2	18.2	14	1	ACT1_FNPIS	196	196	1	9.1	8	1	LOK7_LEUMA	P19989	leucophaea
124	2	18.2	14	1	AFIL1_MALVA	197	197	1	9.1	8	1	LOK8_LEUMA	P19990	leucophaea
125	2	18.2	14	1	AFIL1_MALVA	198	198	1	9.1	8	1	LPMS_STAEP	P23211	staphylococ
126	2	18.2	14	1	AB21_PUSE	199	199	1	9.1	8	1	NPB_HOVIN	P15507	bos taurus
127	2	18.2	14	1	ALL5_MANSE	200	200	1	9.1	8	1	NS3_MYCTU	P81152	mycobacteri
128	2	18.2	14	1	CARL1_FKZAI	201	201	1	9.1	8	1	ORMY_ORCLI	P82455	orconectes
129	2	18.2	14	1	CARL1_FKZAI	202	202	1	9.1	8	1	RECH_PANBO	P08939	pandalus bo
130	2	18.2	14	1	CARL1_FKZAI	203	203	1	9.1	8	1	RS1_ERWCH	P37985	erwinia chr
131	2	18.2	14	1	CARL1_FKZAI	204	204	1	9.1	8	1	RT34_HOVIN	P82929	bos taurus
132	2	18.2	14	1	CFR1_FKZAI	205	205	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
133	2	18.2	14	1	CFR1_FKZAI	206	206	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
134	2	18.2	14	1	CFR1_FKZAI	207	207	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
135	2	18.2	14	1	CFR1_FKZAI	208	208	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
136	2	18.2	14	1	CFR1_FKZAI	209	209	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
137	2	18.2	14	1	CFR1_FKZAI	210	210	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
138	2	18.2	14	1	CFR1_FKZAI	211	211	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
139	2	18.2	14	1	CFR1_FKZAI	212	212	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
140	2	18.2	14	1	CFR1_FKZAI	213	213	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
141	2	18.2	14	1	CFR1_FKZAI	214	214	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
142	2	18.2	14	1	CFR1_FKZAI	215	215	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
143	2	18.2	14	1	CFR1_FKZAI	216	216	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
144	2	18.2	14	1	CFR1_FKZAI	217	217	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
145	2	18.2	14	1	CFR1_FKZAI	218	218	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
146	2	18.2	14	1	CFR1_FKZAI	219	219	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
147	2	18.2	14	1	CFR1_FKZAI	220	220	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
148	2	18.2	14	1	CFR1_FKZAI	221	221	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
149	2	18.2	14	1	CFR1_FKZAI	222	222	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
150	2	18.2	14	1	CFR1_FKZAI	223	223	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
151	2	18.2	14	1	CFR1_FKZAI	224	224	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
152	2	18.2	14	1	CFR1_FKZAI	225	225	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
153	2	18.2	14	1	CFR1_FKZAI	226	226	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
154	2	18.2	14	1	CFR1_FKZAI	227	227	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
155	2	18.2	14	1	CFR1_FKZAI	228	228	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
156	2	18.2	14	1	CFR1_FKZAI	229	229	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
157	2	18.2	14	1	CFR1_FKZAI	230	230	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
158	2	18.2	14	1	CFR1_FKZAI	231	231	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
159	2	18.2	14	1	CFR1_FKZAI	232	232	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
160	2	18.2	14	1	CFR1_FKZAI	233	233	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
161	2	18.2	14	1	CFR1_FKZAI	234	234	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
162	2	18.2	14	1	CFR1_FKZAI	235	235	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
163	2	18.2	14	1	CFR1_FKZAI	236	236	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
164	2	18.2	14	1	CFR1_FKZAI	237	237	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
165	2	18.2	14	1	CFR1_FKZAI	238	238	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
166	2	18.2	14	1	CFR1_FKZAI	239	239	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
167	2	18.2	14	1	CFR1_FKZAI	240	240	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
168	2	18.2	14	1	CFR1_FKZAI	241	241	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
169	2	18.2	14	1	CFR1_FKZAI	242	242	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
170	2	18.2	14	1	CFR1_FKZAI	243	243	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
171	2	18.2	14	1	CFR1_FKZAI	244	244	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
172	2	18.2	14	1	CFR1_FKZAI	245	245	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
173	2	18.2	14	1	CFR1_FKZAI	246	246	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
174	2	18.2	14	1	CFR1_FKZAI	247	247	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
175	2	18.2	14	1	CFR1_FKZAI	248	248	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
176	2	18.2	14	1	CFR1_FKZAI	249	249	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
177	2	18.2	14	1	CFR1_FKZAI	250	250	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
178	2	18.2	14	1	CFR1_FKZAI	251	251	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu
179	2	18.2	14	1	CFR1_FKZAI	252	252	1	9.1	8	1	UF06_MOUSE	P38644	mus musculu

[illegible]

DE 1
1 AR 2

RESULT 9

P44K P-493

ID P44K P-493 STANDARD PRT 8 AA

AC P44K P-493

DE 01-MAY-2000 (Rel. 19, Created)

DI 01-MAY-2000 (Rel. 19, Last sequence update)

DI 01-MAY-2000 (Rel. 19, Last annotation update)

DE 44 kDa immunogenic protein (Fragment)

OS Porphyromonas gingivalis (Bacteroides fragilis)

CC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales

CC Porphyromonadaceae; Porphyromonas

CX NCBI TaxID 557

RN 11

RP SEQUENCE

RC STRAIN VIB 3492

RX MEDLINE 20195497; PubMed 10731013

RA Norris J.M., Love D.N.

RT "Serum antibody responses of rats to soluble whole cell antigens of

RT feline porphyromonas gingivalis"

RL Vols. Microbiol. 73:37-49(200)

CC 1- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A

KW Antigen

FT NCBI TaxID 557

SQ SEQUENCE 8 AA: 989 MW: 95545.32054761 CS 9

Query Match

Best Local Similarity 100.0%; Score 23; DB 1; Length 8;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PK 4

QZ 4 PK 5

RESULT 10

FAR7 AS-50

ID FAR7 AS-50 STANDARD PRT 8 AA

AC P44371

DE 01-MAY-1995 (Rel. 32, Created)

DI 01-MAY-1995 (Rel. 32, Last sequence update)

DI 01-FEB-1996 (Rel. 33, Last annotation update)

DE FMRFamide-like neuropeptide AF7

OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides)

CC Eukaryota; Metazoa; Nematoda; Chordata; Ascarididae; Ascarididae

CC Ascarididae; Ascaris

CX NCBI TaxID 6251

RN 11

RP SEQUENCE

RX MEDLINE 95140362; PubMed 7651954

RA Cowan C., Strickland A.O.W.

RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode

RT Ascaris suum"

RL Peptides 10:491-500(1995)

CC 1- SIMILARITY: BELONGS TO THE FAR7 (PREFAMINE RELATED PEPTIDE)

CC FAMILY

KW Neuropeptide; Amidation

FT NCBI TaxID 6251

SQ SEQUENCE 8 AA: 963 MW: 96340.594176823 CS 9

Query Match

Best Local Similarity 100.0%; Score 23; DB 1; Length 8;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 9

QZ 5 PK 4

RESULT 11

LMT2_LUCM:

ID LMT2_LUCM STANDARD PRT 8 AA

AC P22396

DI 01-AUG-1991 (Rel. 19, Created)

DI 01-AUG-1991 (Rel. 19, Last sequence update)

DI 01-AUG-1991 (Rel. 19, Last annotation update)

DE Locust myotropin 2 (LMM-MP-2)

OS Locusta migratoria (Military locust)

CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

CC Neoptera; Orthoptera; Orthoptera; Caelifera; Acridomorpha;

CC Acrididae; Acrididae; Caelifera; Locusta

CX NCBI TaxID 7004

RN 11

RP SEQUENCE

RC TISSUE Corpora cardiaca

RA Schoofs L., Holman G.M., Hayes J.K., Nachman R.J., de Loof A.

RT "Isolation, identification and synthesis of locust myotropin II, an

RT additional neuropeptide of Locusta migratoria. Member of the

RT cephalomyotropic peptide family"

RL Insect Biochem. 20:479-484(1996)

CC 1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTIONS ACTIVITY

CC (MYOTROPIC ACTIVITY)

CC 1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY

CC InterPro: IPR001484; PYROKININ

CC PROSITE: PS00539; PYROKININ_1

CC KW Neuropeptide; Amidation; Pyrokinin

CC FT NCBI TaxID 6988

CC SQ SEQUENCE 8 AA: 934 MW: 26417719CAA87B CRC64;

Query Match

Best Local Similarity 100.0%; Score 23; DB 1; Length 8;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PK 9

QZ 5 PK 7

RESULT 12

LPM_LEUMA

ID LPM_LEUMA STANDARD PRT 8 AA

AC P13049

DI 01-JAN-1990 (Rel. 13, Created)

DI 01-FEB-1994 (Rel. 28, Last sequence update)

DI 28-FEB-2003 (Rel. 41, Last annotation update)

DE Leukopyrokinin (LPM)

OS Leucophaea maderae (Madeira cockroach)

CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

CC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;

CC Blaberidae; Leucophaea

CX NCBI TaxID 6988

RN 11

RP SEQUENCE

RX MEDLINE 86269041; PubMed 3015140

RA Nachman R.J., Holman G.M., Cook B.J.

RT "Active fragments and analogs of the insect neuropeptide

RT leucopyrokinin: structure-function studies"

RL Biochem. Biophys. Res. Commun. 137:936-942(1986)

CC 1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTIONS ACTIVITY

CC (MYOTROPIC ACTIVITY)

CC 1- MISCELLANEOUS: AN ANALOG WITHOUT THE N-TERMINAL PCA RESIDUE WAS

CC SYNTHESIZED AND FOUND TO EXHIBIT GREATER ACTIVITY (144%) THAN THE

CC PARENT NEUROPEPTIDE. THE PORTION OF THE SEQUENCE OF LPM MOST

CC CRITICAL FOR THE MYOTROPIC PROPERTIES IS LIMITED TO THE

CC PENTAPEPTIDE FRAGMENT PTPRL

